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(54) Title: THREE–DIMENSIONAL MODEL OF A FC EPSILON RECEPTOR ALPHA CHAIN AND USES THEREOF

(57) Abstract

The present invention includes three–dimensional models of antibody receptor proteins, such as FcεRIα proteins, and methods to produce such models. The present invention also includes muteins having increased stability and/or antibody binding activity, as well as methods to produce such muteins, preferably using information derived from three–dimensional models of the present invention. Also included are nucleic acid sequences encoding muteins of the present invention and use of those sequences to produce such muteins. Also included is the use of the model to identify compounds that inhibit the binding of an antibody receptor protein to an antibody. The present invention also includes uses of such muteins and inhibitory compounds, for example, in methods to diagnose and protect animals from allergy and other abnormal immune responses.

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THREE-DIMENSIONAL MODEL OF A Fc EPSILON RECEPTOR ALPHA CHAIN AND USES THEREOF

-FIELD OF THE INVENTION

The present invention relates to a crystal and a three-dimensional (3-D) model of a Fc epsilon receptor alpha chain as well as to the use of that model to produce muteins and inhibitors useful in the diagnosis and treatment of allergy and the regulation of other

10 immune responses in an animal.

BACKGROUND OF THE INVENTION

Antibody Fc-receptors (FcRs) play an important role in the immune response by coupling the specificity of secreted antibodies to a variety of cells of the immune system. A number of cell types, including macrophages, mast cells, eosinophils, and basophils,

15 express membrane-bound FcRs at their surfaces. The binding of antibodies to FcRs provides antigen-specificity to these cells, which upon activation release further cell-specific mediators of the immune response, such as interleukins, initiators of inflammation, leukotrienes, prostaglandins, histamines, or cytotoxic proteins. The adoptive specificity of the FcRs allows a combinatorial approach to pathogen

20 elimination, by coupling the diversity of antibody antigen-recognition sites to the variety of cell-types expressing these receptors.

FcR-initiated mechanisms are important in normal immunity to infectious disease as well as in allergies, antibody-mediated tumor recognition, autoimmune diseases, and other diseases in which immune responses are abnormal (i.e., not

25 regulated). Recent experiments with transgenic mice have demonstrated that the FcRs control key steps in the immune response, including antibody-directed cellular cytotoxicity and inflammatory cascades associated with the formation of immune complexes; see, for example, Ravetch et al., 1998, *Annu Rev Immunolo 16*, 421-432. Receptors that bind IgG (FcgRI, FcgRII, and FcgRIII, known collectively as FcgRs)

30 mediate a variety of inflammatory reactions, regulate B-cell activation, and also trigger hypersensitivity reactions. The high affinity Fc epsilon receptor (also known as the IgE

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receptor or FceRI) is associated with the activation of mast cells and the triggering of allergic reactions and anaphylactic shock. Knockout mice for the FceRI alpha chain (FcεRIα) are unable to mount IgE-mediated anaphylaxis (see for example, Dombrowicz et al., 1993, *Cell 75*, 969-976), although FcgRs are still able to activate mast cells (see,

5   for example, Dombrowicz et al., 1997, *J. Clin. Invest. 99*, 915-925; Oettgen et al., 1994, *Nature 370*, 367-370). FceRI has also been shown to trigger anti-parasitic reactions from platelets and eosinophils as well as deliver antigen into the MHC class II presentation pathway for the activation of T cells; see, for example, Gounni et al., 1994, *Nature 367*, 183-186; Joseph et al., 1997, *Eur. J. Immunol. 27*, 2212-2218; Maurer et al., 1998, *J.*

10   *Immunol. 161*, 2731-2739. The b-subunit of FceRI has been associated with asthma in genetic studies; see, for example, Hill et al., 1996, *Hum. Mol. Genet. 5*, 959-962; Hill et al., 1995, *Bmj 311*, 776-779; Kim et al., 1998, *Curr. Opin. Pulm. Med. 4*, 46-48; Mao et al., 1998, *Clin. Genet. 53*, 54-56; Shirakawa et al., 1994, *Nat. Genet. 7*, 125-129. A significant fraction of the population (~20%) may be affected by allergies, and this

15   century has seen a substantial increase in asthma. Since IgE binding to FceRI is a requisite event in the reaction to different allergens, therapeutic strategies aimed at inhibiting FceRI could provide a useful treatment for these diseases. For example, monoclonal antibodies that target IgE and block receptor binding have shown therapeutic potential; see, for example, Heusser et al., 1997, *Curr. Opin. Immunol. 9*,

20   805-813.

FceRI is found as a tetrameric (abg$_2$) or trimeric (ag$_2$) membrane bound receptor on the surface of mast cells, basophils, eosinophils, langerhans cells and platelets. The alpha chain, also referred to as FcεRIα, of FceRI binds IgE molecules with high affinity (K_D of about 10^{-9} to 10^{-10} moles/liter (M)), and can be secreted as a 172-amino acid

25   soluble, IgE-binding fragment by the introduction of a stop codon before the single C-terminal transmembrane anchor; see, for example, Blank et al.,1991, *E. J. Biol. Chem. 266*, 2639-2646, which describes the secretion of a soluble IgE-binding fragment of 172 amino acids. The extracellular domains of the human FcεRIα protein belong to the immunoglobulin (Ig) superfamily and contain seven N-linked glycosylation sites.

30   Glycosylation of FcεRIα affects the secretion and stability of the receptor, but is not required for IgE-binding; see, for example, LaCroix et al., 1993, *Mol. Immunol. 30*,

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321-330; Letourneur et al.,1995, *J. Biol. Chem. 270*, 8249-8256; Robertson, 1993, *J. Biol. Chem. 268*, 12736-12743; Scarselli et al., 1993, *FEBS Lett 329*, 223-226. The beta and gamma chains of FceRI are signal transduction modules.

 Prior investigators have disclosed the nucleic acid sequence for human FcεRIα;

5 see, for example, U.S. Patent No. 4,962,035, by Leder, issued October 9, 1990; U.S. Patent No. 5,639,660, by Kinet et al., issued June 17, 1997; Kochan et al., 1988, *Nucleic Acids Res. 16*, 3584; Shimizu et al., 1988, *Proc. Natl. Acad. Sci. USA 85*, 1907-1911; and Pang et al., 1993, *J. Immunol. 151*, 6166-6174. Nucleic acid sequences have also been reported for the human FcεRI beta and gamma chains; see, respectively, Kuster et

10 al., 1992, *J. Biol. Chem. 267*, 12782-12787; Kuster et al., 1990, *J. Biol. Chem. 265*, 6448-6452. Nucleic acid sequences have also been reported for nucleic acid molecules encoding canine FcεRIα, murine FcεRIα, rat FcεRIα, feline FcεRIα and equine FcεRIα proteins; see, respectively, GenBank™ accession number D16413; Swiss-Prot accession number P20489 (represents encoded protein sequence); GenBank accession number

15 J03606; PCT Publication No. WO 98/27208, by Frank et al., published June 25, 1998, referred to herein as WO 98/27208; and PCT Publication No. WO 99/38974, by Weber et al., published August 5, 1999, referred to herein as WO 99/38974. In addition, methods to detect IgE antibodies using a FcεRIα protein have been reported in PCT Publication No. WO 98/23964, by Frank et al., published June 4, 1998, referred to

20 herein as WO 98/23964; WO 98/27208, *ibid.*; PCT Publication No. WO 98/45707, by Frank et al., published October 15, 1998, referred to herein as WO 98/45707; and WO 99/38974, *ibid.*. WO 98/23964, WO 98/27208, WO 98/45707 and WO 99/38974.

 There have been several reports of the use of mutagenesis and swapping techniques to attempt to identify amino acids of either FcεRIα or IgE involved in the

25 binding of (i.e., interaction between) those respective proteins, reports attempting to model FcεRIα proteins based on homology to other Ig-superfamily members, and reports that identify compounds that apparently inhibit such binding; see, for example, Cook et al., 1997, *Biochemistry 36*, 15579-15588; Hulett et al., 1994, *J. Biol. Chem. 269*, 15287-15293; Hulett et al., 1995, *J. Biol. Chem 270*, 21188-21194; Mallamaci et

30 al., 1993, *J. Biol. Chem. 268*, 22076-22083; Robertson, 1993, *ibid.*; Scarselli et al., 1993, *ibid.* McDonnell et al., 1997, *Biochem. Soc. Trans. 25*, 387-392; McDonnell et al.,

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1996, *Nat. Struc. Biol.* 3, 419-426; PCT Publication No. WO 97/40033, by Cheng et al.,

published October 30, 1997; U.S. Patent No. 5,180,805, by Gould et al, issued

January 19, 1993; U.S. Patent No. 5,693,758, by Gould et al., issued December 2, 1997;

PCT Publication No. WO 96/01643, by Gould et al., published January 25, 1996; PCT

5   Publication No. WO 95/14779, by Gould et al., published June 1, 1995. None of these

references, however, describe isolated crystals of FcεRIα proteins or 3-D models derived

from crystals.

        Despite what is known about FcRs and their interaction with antibodies, there

remains a need for FcRs with improved characteristics, such as enhanced affinity for

10   antibodies, altered substrate specificity, increased stability, and increased solubility for

use in diagnosis, treatment and prevention of allergy and other abnormal immune

responses. Also needed for safe and efficacious compounds to prevent or treat allergy

and to regulate other immune responses in an animal.

                        SUMMARY OF THE INVENTION

15   The present invention includes isolated crystals of the extracellular domains of

antibody receptor proteins (FcRs), three-dimensional (3-D) models of such crystals and

modifications of such models. The present invention also includes compounds that

inhibit the ability of FcRs to bind to antibodies as well as FcR muteins and other

modified FcRs. Also included in the present invention are methods to produce and use

20   such crystals, models, inhibitory compounds, muteins, and other modified proteins. As

such, the present invention includes FcRs with improved functions such as increased

stability, increased affinity for an Fc domain of an antibody, altered substrate specificity,

and increased solubility, including but not limited to reduced aggregation. Such

proteins, also referred to as muteins, are useful to detect allergy and other immune

25   response abnormalities as well as to protect an animal from such abnormalities. The

present invention also provides safe and efficacious inhibitory compounds to protect

(e.g., prevent, treat, reduce the consequences of) an animal from allergy and to regulate

other immune responses in an animal.

        The present invention includes a 3-D model of an extracellular domain of a

30   human high affinity Fc epsilon receptor alpha chain (FcεRIα) protein, wherein the model

substantially represents the atomic coordinates specified in Table 1, Table 5, Table 6,

Table 7 or Table 8. The present invention also includes a 3-D model comprising a modification of a model substantially representing the atomic coordinates specified in Table 1, Table 5, Table 6, Table 7 or Table 8. Also included in the present invention are methods to produce such models.

5   The present invention also includes an isolated crystal of an extracellular domain of a FcεRIα protein and methods to produce such a crystal.

The present invention also includes an isolated FcεRIα protein consisting of SEQ ID NO:2 or of SEQ ID NO:4 except that the isoleucine at position 170 is replaced by a cysteine, as well as a protein that is structurally homologous to either such protein. Also

10 included are nucleic acid molecules encoding such proteins, recombinant molecules and recombinant cells including such proteins, and methods to produce such proteins.

The present invention includes a method to identify a compound that inhibits the binding between an IgE antibody and a FcεRIα protein. The method includes the step of using a 3-D model of an extracellular domain of a human FcεRIα protein to identify the

15 compound. Such a model substantially represents the atomic coordinates specified in Table 1, Table 5, Table 6, Table 7 or Table 8. Also included in the present invention are inhibitory compounds identified using such a method. Also included are therapeutic compositions that include such inhibitory compounds and methods to use such therapeutic compositions to protect an animal from allergy or to regulate other immune

20 responses (e.g., protect an animal from other abnormal immune responses).

The present invention also includes a mutein that binds to a Fc domain of an antibody. Such a mutein has an improved function compared to a protein that includes SEQ ID NO:2 or SEQ ID NO:4. Examples of such an improved function include increased stability, increased affinity for an Fc domain of an antibody, altered substrate

25 specificity, decreased aggregation, and increased solubility. Such a mutein is produced by a method that includes the following steps: (a) analyzing a 3-D model substantially representing the atomic coordinates specified in Table 1, Table 5, Table 6, Table 7 or Table 8 to identify at least one amino acid of the protein represented by the model which if replaced by a specified amino acid would effect an improved function of the protein;

30 and (b) replacing the identified amino acid(s) to produce the mutein having such an improved function. The present invention also includes a mutein having an improved

function compared to an unmodified FcεRIα protein, wherein the amino acid sequence of the mutein differs in at least one position from the amino acid sequence of the unmodified protein. Such a position(s) is in at least one of the following regions: a crystal contact cluster, a tryptophan-containing hydrophobic ridge, a FG loop in D2, a

5 D1D2 interface, a cleft between D1 and D2, a domain 1, a domain 2, a hydrophobic core, a A'B loop of D1, a EF loop of D1, a BC loop of D2, a C strand of D2, a CC' loop of D2, C'E loop of D2, a strand of D2, the amino terminal five residues of the protein, the carboxyl terminal five residues of the protein, and N-linked glycosylation sites.

Also included are muteins that are chemically modified FcεRIα proteins. Also

10 included are nucleic acid molecules that encode muteins of the present invention, recombinant molecules and recombinant cells including such nucleic acid molecules and methods to produce such muteins. Also included are diagnostic reagents and diagnostic kits including such muteins, therapeutic compositions including such muteins, and methods to detect or protect an animal from allergy or other abnormal immune

15 responses.

The present invention also includes a method to improve a function of a FcεRIα protein which includes the steps of: (a) analyzing a 3-D model of an extracellular domain of a human high affinity FcεRIα protein substantially representing the atomic coordinates specified in Table 1, Table 5, Table 6, Table 7 or Table 8, to identify at least

20 one amino acid of the protein which if replaced by a specified amino acid improves at least one of the functions of the protein; and (b) replacing the identified amino acid(s) to produce a mutein having at least one of the improved functions.

BRIEF DESCRIPTION OF THE FIGURES

Fig. 1 depicts electron density maps and overall structure of a human FcεRIα

25 model. (A) The 3.0 angstrom experimental electron density map, calculated using the MIRAS phases followed by density modification with the program DM is shown along with a refined model for human FcεRIα. The density is contoured at 1.4σ for residues 147-153. (B) Electron density for carbohydrate moieties linked to N42. The |2Fo-Fc| electron density map, contoured at 1σ, was calculated to 2.4 angstroms using combined

30 MIRAS and model phases (prior to inclusion of carbohydrate in the model). Two N-acetylglucosamines and a mannose moiety were built into the density as shown.

Fig. 2 depicts a ribbon diagram of a human FcεRIα model showing the positions of the disulfides and the FG loop in domain 2 (D2) that is implicated in receptor specificity. Domain 1 (D1) is shown to the right and D2 is shown to the left.

Fig. 3 depicts a topology diagram of the two domains of a human FcεRIα model showing the hydrogen-bonding patterns of the beta sheet structure. The short stretch of parallel beta-sheet in D1 and D2 caused by the cross-over of the A strand is highlighted. Note that the FG strands of D2 are longer than those of D1, contributing to the prominence of the D2-FG loop.

Fig. 4 demonstrates that a human FcεRIα model has a novel tertiary arrangement of tandem Ig domains.

Fig. 5 depicts sequence alignments of human FcRs. The secondary structure of the two domains is indicated with labeled bars above those residues which form beta-sheet in FcεRI. Below the sequences, carbohydrate attachment sites found in seventeen different FcR sequences are indicated with a (+). This analysis is based on the seven human receptors shown and the non-human receptors listed in Table 4.

Fig. 6 depicts the four surface-exposed tryptophans at the top of the D2 domain of a human FcεRIα model that are implicated in IgE binding.

Fig. 7 depicts residues in the D2 FG loop and D1 E strand of a human FcεRIα model that are highly variable in human FcR sequences. The residues in the D2-FG loop have been directly implicated in IgE binding. The residues in the D1 E strand and the D1 A'B loop are located near the top of the D2 domain and could form part of an extended IgE-binding surface between the two domains.

Fig. 8 depicts a juxtaposition of a human FcεRIα model with a model for the intact IgE antibody structure. The insertion of the Cε2 domains in the IgE molecule are indicated by dotted lines. The FcεRIα protein is shown relative to the mast cell membrane near the top of the Cε3 domains that bind to the receptor.

DETAILED DESCRIPTION OF THE INVENTION

The present invention includes isolated crystals of the extracellular domains of FcRs, 3-D models of such crystals and modifications of such models. The present invention also includes compounds that inhibit the ability of FcRs to bind to antibodies as well as muteins and other modified FcRs. Also included in the present invention are

methods to produce and use such crystals, models, inhibitory compounds, muteins, and other modified proteins.

The present invention includes an isolated crystal of an extracellular domain of a high affinity Fc epsilon receptor alpha chain (FcεRIα), a 3-D model of such a crystal and
5   a modification of such a model. As used herein, the term "a" entity or "an" entity refers to one or more of that entity; for example, a crystal or a model refers to one or more crystals or models, respectively. As such, the terms "a" (or "an"), "one or more" and "at least one" can be used interchangeably herein. It is also to be noted that the terms "comprising", "including", and "having" can be used interchangeably. Furthermore, a
10   compound "selected from the group consisting of" refers to one or more of the compounds in the list that follows, including mixtures, or combinations, of two or more of the compounds.

As used herein, an extracellular domain of a FcεRIα protein is the portion of the FceRI alpha chain that is exposed to the environment outside the cell and that binds to
15   the Fc domain of an IgE antibody. Such an extracellular domain can be (a) a complete extracellular domain which is a domain that extends from the first amino acid of a mature FceRI alpha chain through the last amino acid prior to the start of the transmembrane region or a domain that is functionally equivalent, in that such a domain includes a D1 and D2 domain, displays a similar affinity for the IgE antibody to which
20   such an FcεRIα protein naturally binds, and produces crystals having sufficient quality to enable structure determination, or (b) a fragment of any of the extracellular domains of (a), wherein the fragment retains its ability to bind to the Fc domain of an antibody. As used herein, the terms binding to an antibody and binding to the Fc domain (i.e., constant region) of an antibody can be used interchangeably since it is recognized that a
25   FcR binds to the Fc domain of an antibody. A FcR (i.e., a protein that can bind to an antibody), such as a FcεRIα protein, can be a full-length FcR (e.g., a full-length FceRI alpha chain), or any fragment thereof, wherein the fragment binds to an antibody. Similarly an antibody, or an Fc domain thereof, can be a full-length antibody, or full-length Fc domain thereof, or any fragment thereof that binds to a FcR. Preferably a FcR
30   binds to an antibody with an affinity (K_A) of at least about 10^8 liters/mole (M^{-1}), more preferably of at least about $10^9 M^{-1}$, and even more preferably of at least about $10^{10} M^{-1}$.

The present invention is surprising in several aspects. For example, this is the first report of an isolated crystal of an extracellular domain of a FcεRIα protein, and in particular of an isolated crystal of sufficient quality that a crystal structure, i.e., a 3-D model, could be derived therefrom. The inventors believe that this protein also

5   represents the most highly glycosylated protein for which a crystal and a 3-D model have been reported to date. Not only does glycosylation interfere with protein crystal formation but it also is difficult to consistently produce recombinant proteins having a uniform glycosylation pattern. Generation of such a crystal was very difficult and non-obvious and has been attempted by others without success. The inventors tried many

10   approaches before discovering that a preferred FcεRIα protein from which to make a useful crystal is a FcεRIα protein that consists of amino acids 1 through 176 of the mature human FcεRIα protein. This protein is denoted herein as PhFcεRIα$_{1-176}$, or the hFcεRIα$_{1-176}$ protein, and has an amino acid sequence denoted herein as SEQ ID NO:2. An example of a nucleotide acid molecule encoding PhFcεRIα$_{1-176}$ is referred to herein

15   as nhFcεRIα$_{1-528}$, the nucleic acid sequence of which is denoted herein as SEQ ID NO:1. It was also discovered that better crystals are generated when PhFcεRIα$_{1-176}$ is produced in insect cells, using a method such as that described in the Examples. Determination of the crystal structure of PhFcεRIα$_{1-176}$ produced in *Trichoplusia ni* (Hi-5) cells resulted in a 3-D model that substantially represents the atomic coordinates specified in Table 1,

20   referred to herein as form M1. Amino acids are represented herein by their standard three or one letter codes; see, for example, Sambrook et al., *Molecular Cloning: A Laboratory Manual*, Cold Spring Harbor Labs Press, 1989. Prior to obtaining a crystal of sufficient quality to solve its crystal structure using insect-cell produced PhFcεRIα$_{1-176}$, a number of other proteins were tried, including a FcεRIα protein spanning from

25   amino acid 1 through 171 of SEQ ID NO:2 produced in *Pichia pastoris*, and FcεRIα proteins spanning from amino acid 1 through 172 of SEQ ID NO:2 produced in Chinese hamster ovary cells, *Trichoplusia ni* cells, and *Spodoptera frugiperda* cells without success. Without being bound by theory, it is believed that PhFcεRIα$_{1-176}$ was a better candidate because it apparently represents a complete extracellular domain. Based on

30   the 3-D model of PhFcεRIα$_{1-176}$, the inventors believe, without being bound by theory, that the amino acid at position 172 is important in the structure determination and that,

in order to form a crystal of sufficient quality to determine the first 3-D model of a FcεRIα protein, at least one additional amino acid was required carboxyl-terminal to that at position 172; the inventors further believe that an optimal protein would span from the amino acid at position 3 through the amino acid at position 174 of SEQ ID NO:2. It

5 should be noted, however, that having solved the crystal structure of a first FcεRIα protein enables the solving of crystal structures of additional FcεRIα proteins as well as of additional FcRs in general. For example, the crystal structures of two additional crystals cited in the Examples can be solved using a combination of X-ray diffraction data of the crystals per se and information derived from the 3-D model of $PhFcεRIα_{1-176}$.

10 The examples also describe the solution of an additional four crystal structures using such information, namely the examples present 3-D models of: (a) a human FcεRIα protein spanning amino acids 1-172 of SEQ ID NO:2 (i.e., $PhFcεRIα_{1-172}$, the amino acid sequence of which is represented herein as SEQ ID NO:4) expressed in lec1 Chinese hamster ovary (CHO) cells, the structural form being referred to herein as Form T1; (b) a

15 second structural form of $PhFcεRIα_{1-172}$ produced in lec1 CHO cells, referred to herein as Form T2; (c) a second structural form of a $PhFcεRIα_{1-176}$ protein expressed in *T. ni* (Hi5) cells, referred to herein as Form M2; and (d) a $PhFcεRIα_{1-172}$ protein in which the isoleucine at position 170 of SED ID NO:4 is replaced with a cysteine, expressed in Sf9 insect cells, a structural form referred to herein as H1. The atomic coordinates of the

20 crystal structural forms T1, T2, M2 and H1 are presented, respectively, in Tables 5, 6, 7, and 8.

The 3-D model of the $hFcεRIα_{1-176}$ protein form M1 is also very surprising in view of the knowledge of the structure of proteins containing immunoglobulin domains, herein also referred to as Ig domains. The most striking differences, which are described

25 in greater detail below, include, but are not limited to: domain 1 (D1) and domain 2 (D2) of the model of $PhFcεRIα_{1-176}$ are much smaller than known Ig domains; the packing and orientation of D1 and D2 of the $hFcεRIα_{1-176}$ protein are significantly different from known Ig domain-containing proteins in that, for example, the bend angle between D1 and D2 of the $PhFcεRIα_{1-176}$ structure is much more acute than for other proteins, the

30 relative rotational orientation of the two domains is much different, D1 and D2 of $PhFcεRIα_{1-176}$ form an unusual interface and cleft, D1 and D2 of $PhFcεRIα_{1-176}$ are

antiparallel, the presence of a hydrophobic surface on the two faces of the model of PhFcεRIα$_{1-176}$ which appear to be nearby or directly involved in binding to IgE antibodies; the FG loop of D2 of PhFcεRIα$_{1-176}$, also apparently involved in binding to IgE antibodies, projects much more significantly above the D2 domain than is seen for
5   known D2-containing proteins; and the interruption in structure between strands A and A' in D1 which apparently leads to interaction between the two domains. It is to be noted that although most known Ig domain pairs which are parallel, some Ig domains are antiparallel (e.g., hemolin) but the domain:domain orientation and specifics of packing of those domains are very different from the orientation and packing of PhFcεRIα$_{1-176}$. It
10   is also surprising that the model of the hFcεRIα$_{1-176}$ protein predicts that an IgE antibody interacts with D1 as well as D2 in view of the mutagenesis analysis studies conducted to date all of which have only identified mutations in D2 that lead to decreased, or increased, binding between a FcεRIα protein and an IgE antibody. As such, a model of the present invention is necessary for proper interpretation and refinement of
15   mutagenesis and region swapping studies that have been reported. Such a model for the first time permits the differentiation between amino acids directly or indirectly influencing binding of IgE to FcεRIα and demonstrates where amino acids and amino acid segments identified in mutagenesis and swapping studies are positioned on the protein. It is to be noted that the 3-D models of FcεRIα crystal structure forms T1, T2,
20   M2 and H1 are quite similar to that of form M1, with the following differences. The principal differences in the structures from the various crystal forms occur in the BC loop in domain 1 (the "30 loop"), the C' strand in domain 2 (the "130 region") and the carbohydrate sites. There are also smaller differences in the termini of the structures and the FG loop in domain 1 (the "72 loop"). These differences are described in more detail
25   in the Examples.

One embodiment of the present invention is an isolated crystal of an extracellular domain of a FcεRIα protein. As used herein, an isolated crystal is a crystal of a protein that has been produced in a laboratory; that is, an isolated crystal is produced by an individual and is not an object found *in situ* in nature. It is appreciated by those skilled
30   in the art that there are a variety of techniques to produce crystals including, but not limited to, vapor diffusion using a hanging or sitting drop methodology, vapor diffusion

under oil, and batch methods; see, for example, Ducruix et al., eds., 1991, *Crystallization of nucleic acids and proteins; A practical approach*, Oxford University Press, and Wyckoff et al., eds., 1985, *Methods in Enzymology 11*, 49-185. It is also to be appreciated that crystallization conditions can be adjusted depending on a protein's

5   inherent characteristics as well as on a protein's concentration in a solution and that a variety of precipitants can be added to a protein solution in order to effect crystallization; such precipitants are known to those skilled in the art. In a preferred embodiment, a crystal of a FcεRIα protein is produced in a solution by adding a precipitant such as polyethylene glycol (PEG) or PEG monomethylether. In a particularly preferred

10   embodiment, the precipitant PEG is added to .. solution to achieve a final concentration of from about 10 percent (%) to about 40%, preferably from about 12% to about 32% PEG per volume solution. It is also to be noted that a FcεRIα protein used to produce a crystal can be produced by a variety of methods, including purification of a native protein, chemical synthesis of a protein, or recombinant production of a protein.

15   Although a number of cell types can be used to recombinantly produce such a protein, insect cells, such as, but not limited to *Trichoplusia ni* and *Spodoptera frugiperda*, are preferred, with *Trichoplusia ni* cells being more preferred. Also preferred are Chinese hamster ovary cells. Additional methods to produce proteins are disclosed below.

Isolated crystals of the present invention can include heavy atom derivatives,

20   such as, but not limited to, gold, platinum, mercury, selenium, and lead. Such heavy atoms can be introduced randomly or introduced in a manner based on knowledge of 3-D models of the present invention. Additional crystals of the present invention are not derivatized. In one embodiment, an isolated crystal of the present invention is a co-crystal of a FcεRIα protein bound to a Fc domain of an IgE antibody. In another

25   embodiment, an isolated crystal of the present invention is a co-crystal of a FcεRIα protein and a compound that inhibits the binding of a FcεRIα protein to a Fc domain of an IgE antibody. Additional crystals of the present invention include crystals produced from proteins that are muteins of the present invention or other proteins that are represented by a 3-D model of the present invention.

30   An isolated crystal of the present invention can be the crystal of any suitable extracellular domain of a FcεRIα protein. Suitable FcεRIα proteins include mammalian

FcεRIα proteins, with human, canine, feline, equine, rat and murine FcεRIα proteins being preferred, and human FcεRIα proteins being even more preferred. A preferred crystal of the present invention diffracts X-rays to a resolution of about 4.0 angstroms or higher (i.e., lower number meaning higher resolution), with resolutions of about

5   3.5 angstroms or higher, about 3 angstroms or higher, about 2.5 angstroms or higher, about 2 angstroms or higher, about 1.5 angstroms or higher, and about 1 angstrom or higher being increasingly more preferred. It is appreciated, however, that additional crystals of lower resolutions can have utility in discerning overall topology of the structures, e.g., location of a binding site or where a molecule binds to a receptor. A

10   particularly preferred isolated crystal of the present invention has the amino acid sequence SEQ ID NO:2, amino acid sequence SEQ ID NO:4, or a sequence essentially equivalent that represents an extracellular domain of another mammalian FcεRIα protein. SEQ ID NO:4 is the amino acid sequence of a protein consisting of the first 172 residues of a mature human FcεRIα protein denoted herein as $PhFcεRIα_{1-172}$; i.e., SEQ

15   ID NO:4 spans from amino acid residue 1 through amino acid residue 172 of SEQ ID NO:2. An example of a nucleotide acid molecule encoding $PhFcεRIα_{1-172}$ is referred to herein as $nhFcεRIα_{1-516}$, the nucleic acid sequence of which is denoted herein as SEQ ID NO:3. Preferred are crystals that belong to monoclinic space group C2 or monoclinic space group P6122. Particularly preferred crystals include: a crystal of $PhFcεRIα_{1-176}$

20   that belongs to monoclinic space group C2, has cell dimensions of 88.6 angstroms x 69.6 angstroms x 49.3 angstroms, alpha=gamma=90.0 degrees, beta=116.69 degrees, and diffracts X-rays to a resolution of about 2.4 angstroms (form M1); a crystal of $PhFcεRIα_{1-176}$ that belongs to monoclinic space group C2, has cell dimensions of 136.02 angstroms x 75.01 angstroms x 79.28 angstroms, alpha=gamma=90 degrees, beta=117.8

25   degrees, and diffracts X-rays to a resolution of about 3.0 angstroms; and a crystal of $PhFcεRIα_{1-172}$ that belongs to monoclinic space group P6122, has cell dimensions of 58 angstroms x 58 angstroms x 226 angstroms, alpha=beta=90 degrees, gamma=120 degrees, and diffracts X-rays to a resolution of about 3.2 angstroms. Also preferred crystals include: a crystal of $PhFcεRIα_{1-172}$ that belongs to tetragonal space group $P4_3$,

30   has cell dimensions of 145.08 angstroms x 145.08 angstroms x 62.74 angstroms, alpha=beta=gamma=90.0 degrees, and diffracts X-rays to a resolution of about 3.1

angstroms (form T1); a crystal of PhFcεRIα$_{1-172}$ that belongs to tetragonal space group P4$_3$, has cell dimensions of 150.50 angstroms x 150.50 angstroms x 74.18 angstroms, alpha=beta=gamma=90.0 degrees, and diffracts X-rays to a resolution of about 3.8 angstroms (form T2); a crystal of PhFcεRIα$_{1-176}$ that belongs to monoclinic space group

5   C2, has cell dimensions of 136.90 angstroms x 73.79 angstroms x 79.40 angstroms, alpha=gamma=90.0 degrees, beta=117.74 degrees, and diffracts X-rays to a resolution of about 3.2 angstroms (form M2); and a crystal of PhFcεRIα$_{1-172}$ that belongs to hexagonal space group P6$_1$22, has cell dimensions of 58.62 angstroms x 58.62 angstroms x 229.19 angstroms, alpha=gamma=90.0 degrees, beta=120 degrees, and diffracts X-rays to a

10   resolution of about 3.2 angstroms (form H1)

        The present invention includes a 3-D model of an extracellular domain of a FcεRIα protein that substantially represents the atomic coordinates specified in Table 1, Table 5, Table 6, Table 7 or Table 8. The present invention also includes 3-D models that comprise modifications of the model substantially represented by the atomic

15   coordinates specified in Table 1, Table 5, Table 6, Table 7 or Table 8. Each such modification represents a protein that binds to a Fc domain of an antibody. A 3-D model of an extracellular domain of a FcεRIα protein is a representation, or image, that predicts the actual structure of the corresponding protein. As such, a 3-D model is a tool that can be used to probe the relationship between the protein's structure and function at the

20   atomic level and to design muteins (i.e., genetically and/or chemically altered FcRs) having an improved function, such as, but not limited to: increased (i.e., enhanced) stability; increased antibody binding activity, for example, by, increasing the affinity for an antibody by, for example, increasing the association rate and/or decreasing the dissociation rate between a FcR and an antibody or by altering substrate specificity (e.g.,

25   enhancing the ability of a FcR of a certain species and class to bind to antibody from another species and/or another antibody class); and/or increased solubility (e.g., reduced aggregation). It is well known to those skilled in the art, however, that a 3-D model of a protein derived by analysis of protein crystals is not identical to the inherent structure of the protein. See, for example, Branden et al., *Introduction to Protein Structure*, Garland

30   Publishing Inc., New York and London, 1991, especially on page 277, which states "not surprisingly the model never corresponds precisely to the actual crystal." Furthermore,

the model can be subjected to further refinements to more closely correspond to the actual structure of a FcR. Such a refined model, which is an example of a modification of the present invention, is a better predictor of the actual structure and mechanism of action of the protein that the model represents. A refinement of a 3-D model of the

5 present invention refers to an improved model of a FcεRIα protein that can be obtained in a variety of ways known to those skilled in the art. Refinements can include models determined to more preferred degrees of resolution, preferably to about 3.5 angstroms, more preferably to about 3 angstroms, more preferably to about 2.5 angstroms, more preferably to about 2 angstroms, more preferably to about 1.5 angstroms, and even more

10 preferably to about 1 angstrom. Preferred refinements are obtained using the 3-D model as a basis for such improvements.

One embodiment of the present invention is a 3-D model of an extracellular domain of a FcεRIα protein that substantially represents the atomic coordinates specified (i.e., listed) in Table 1.

Table 1. Atomic coordinates of PhFcεRIα$_{1-176}$, Form M1

ATOM NUMBER	ATOM TYPE	RESIDUE	#	X	Y	Z	OCC	B
1	CB	LYS	4	23.345	19.877	27.253	1.00	114.16
2	CG	LYS	4	23.455	20.034	25.744	1.00	114.16
3	CD	LYS	4	23.900	21.444	25.387	1.00	114.16
4	CE	LYS	4	24.017	21.633	23.885	1.00	114.16
5	NZ	LYS	4	24.406	23.028	23.539	1.00	114.16
6	C	LYS	4	23.899	17.439	27.171	1.00	98.73
7	O	LYS	4	24.999	17.777	26.726	1.00	98.73
8	N	LYS	4	22.817	18.457	29.211	1.00	98.73
9	CA	LYS	4	22.920	18.482	27.721	1.00	98.73
10	N	PRO	5	23.522	16.148	27.224	1.00	89.31
11	CD	PRO	5	22.385	15.565	27.963	1.00	81.52
12	CA	PRO	5	24.397	15.093	26.708	1.00	89.31
13	CB	PRO	5	23.912	13.858	27.454	1.00	81.52
14	CG	PRO	5	22.445	14.102	27.562	1.00	81.52
15	C	PRO	5	24.212	14.980	25.190	1.00	89.31
16	O	PRO	5	23.503	15.784	24.581	1.00	89.31
17	N	LYS	6	24.844	13.992	24.575	1.00	79.33
18	CA	LYS	6	24.719	13.835	23.137	1.00	79.33
19	CB	LYS	6	25.816	14.639	22.433	1.00	122.37
20	CG	LYS	6	25.411	15.180	21.073	1.00	122.37
21	CD	LYS	6	26.324	16.320	20.643	1.00	122.37
22	CE	LYS	6	25.774	17.040	19.421	1.00	122.37
23	NZ	LYS	6	26.602	18.225	19.060	1.00	122.37
24	C	LYS	6	24.794	12.368	22.740	1.00	79.33
25	O	LYS	6	25.644	11.622	23.231	1.00	79.33
26	N	VAL	7	23.884	11.948	21.866	1.00	65.03
27	CA	VAL	7	23.879	10.567	21.409	1.00	65.03
28	CB	VAL	7	22.479	10.128	20.951	1.00	74.25
29	CG1	VAL	7	22.530	8.711	20.408	1.00	74.25
30	CG2	VAL	7	21.515	10.205	22.113	1.00	74.25
31	C	VAL	7	24.846	10.463	20.244	1.00	65.03
32	O	VAL	7	24.829	11.290	19.328	1.00	65.03
33	N	SER	8	25.713	9.462	20.299	1.00	46.54
34	CA	SER	8	26.686	9.255	19.238	1.00	46.54
35	CB	SER	8	28.123	9.513	19.749	1.00	64.02
36	OG	SER	8	28.482	8.670	20.836	1.00	64.02
37	C	SER	8	26.517	7.815	18.780	1.00	46.54
38	O	SER	8	26.109	6.955	19.567	1.00	46.54
39	N	LEU	9	26.840	7.556	17.515	1.00	55.36
40	CA	LEU	9	26.674	6.227	16.945	1.00	55.36
41	CB	LEU	9	25.796	6.283	15.679	1.00	45.99
42	CG	LEU	9	24.626	7.256	15.529	1.00	45.99
43	CD1	LEU	9	23.773	6.849	14.338	1.00	45.99
44	CD2	LEU	9	23.784	7.246	16.761	1.00	45.99
45	C	LEU	9	27.983	5.585	16.555	1.00	55.36
46	O	LEU	9	28.894	6.250	16.091	1.00	55.36
47	N	ASN	10	28.060	4.274	16.713	1.00	52.82
48	CA	ASN	10	29.244	3.556	16.318	1.00	52.82
49	CB	ASN	10	30.174	3.353	17.510	1.00	77.87
50	CG	ASN	10	31.366	2.495	17.166	1.00	77.87
51	OD1	ASN	10	32.032	2.717	16.155	1.00	77.87
52	ND2	ASN	10	31.645	1.504	18.004	1.00	77.87
53	C	ASN	10	28.816	2.215	15.753	1.00	52.82
54	O	ASN	10	28.320	1.361	16.492	1.00	52.82
55	N	PRO	11	28.966	2.024	14.432	1.00	54.26
56	CD	PRO	11	28.755	0.707	13.793	1.00	46.78
57	CA	PRO	11	29.503	2.975	13.454	1.00	54.26
58	CB	PRO	11	29.512	2.179	12.155	1.00	46.78

59	CG	PRO	11	29.707	0.774	12.631	1.00	46.78
60	C	PRO	11	28.692	4.268	13.348	1.00	54.26
61	O	PRO	11	27.541	4.332	13.775	1.00	54.26
62	N	PRO	12	29.286	5.303	12.742	1.00	56.88
63	CD	PRO	12	30.615	5.189	12.120	1.00	56.23
64	CA	PRO	12	28.751	6.646	12.514	1.00	56.88
65	CB	PRO	12	29.888	7.348	11.788	1.00	56.23
66	CG	PRO	12	31.093	6.592	12.191	1.00	56.23
67	C	PRO	12	27.458	6.798	11.736	1.00	56.88
68	O	PRO	12	26.680	7.710	12.003	1.00	56.88
69	N	TRP	13	27.255	5.930	10.751	1.00	54.29
70	CA	TRP	13	26.079	5.991	9.881	1.00	54.29
71	CB	TRP	13	26.203	4.929	8.794	1.00	47.07
72	CG	TRP	13	27.629	4.697	8.423	1.00	47.07
73	CD2	TRP	13	28.502	5.622	7.767	1.00	47.07
74	CE2	TRP	13	29.762	4.998	7.659	1.00	47.07
75	CE3	TRP	13	28.341	6.919	7.266	1.00	47.07
76	CD1	TRP	13	28.372	3.584	8.676	1.00	47.07
77	NE1	TRP	13	29.655	3.756	8.218	1.00	47.07
78	CZ2	TRP	13	30.853	5.6⁚⁚	7.064	1.00	47.07
79	CZ3	TRP	13	29.419	7.536	6.679	1.00	47.07
80	CH2	TRP	13	30.664	6.890	6.582	1.00	47.07
81	C	TRP	13	24.753	5.836	10.602	1.00	54.29
82	O	TRP	13	24.571	4.?12	11.389	1.00	54.29
83	N	ASN	14	23.838	6.759	10.323	1.00	44.90
84	CA	ASN	14	22.513	6.758	10.925	1.00	44.90
85	CB	ASN	14	22.099	8.179	11.291	1.00	62.66
86	CG	ASN	14	21.713	8.992	10.083	1.00	62.66
87	OD1	ASN	14	22.501	9.154	9.152	1.00	62.66
88	ND2	ASN	14	20.489	9.505	10.085	1.00	62.66
89	C	ASN	14	21.504	6.158	9.935	1.00	44.90
90	O	ASN	14	20.302	6.059	10.229	1.00	44.90
91	N	ARG	15	22.006	5.777	8.759	1.00	43.26
92	CA	ARG	15	21.189	5.130	7.735	1.00	43.26
93	CB	ARG	15	21.196	5.926	6.426	1.00	51.24
94	CG	ARG	15	21.031	7.419	6.623	1.00	51.24
95	CD	ARG	15	21.112	8.161	5.311	1.00	51.24
96	NE	ARG	15	19.813	8.119	4.637	1.00	51.24
97	CZ	ARG	15	19.648	7.770	3.375	1.00	51.24
98	NH1	ARG	15	20.693	7.441	2.652	1.00	51.24
99	NH2	ARG	15	18.442	7.743	2.849	1.00	51.24
100	C	ARG	15	21.902	3.799	7.545	1.00	43.26
101	O	ARG	15	23.017	3.759	7.031	1.00	43.26
102	N	ILE	16	21.258	2.719	7.981	1.00	47.47
103	CA	ILE	16	21.845	1.386	7.893	1.00	47.47
104	CB	ILE	16	22.222	0.864	9.308	1.00	38.74
105	CG2	ILE	16	23.163	1.866	10.026	1.00	38.74
106	CG1	iLE	16	20.944	0.673	10.139	1.00	38.74
107	CD1	iLE	16	21.166	0.154	11.568	1.00	38.74
108	C	ILE	16	20.912	0.357	7.257	1.00	47.47
109	O	ILE	16	19.711	0.579	7.111	1.00	47.47
110	N	PHE	17	21.480	-0.785	6.900	1.00	45.27
111	CA	PHE	17	20.721	-1.874	6.309	1.00	45.27
112	CB	PHE	17	21.636	-2.758	5.473	1.00	33.04
113	CG	PHE	17	21.911	-2.218	4.113	1.00	33.04
114	CD1	PHE	17	23.185	-2.237	3.598	1.00	33.04
115	CD2	PHE	17	20.864	-1.725	3.322	1.00	33.04
116	CE1	PHE	17	23.432	-1.782	2.307	1.00	33.04
117	CE2	PHE	17	21.106	-1.272	2.036	1.00	33.04
118	CZ	PHE	17	22.387	-1.299	1.523	1.00	33.04
119	C	PHE	17	20.026	-2.748	7.334	1.00	45.27
120	O	PHE	17	20.540	-2.971	8.433	1.00	45.27
121	N	LYS	18	18.847	-3.240	6.959	1.00	48.86
122	CA	LYS	18	18.074	-4.137	7.806	1.00	48.86

	123	CB	LYS	18	16.848	-4.630	7.035	1.00	55.91
	124	CG	LYS	18	16.039	-5.694	7.731	1.00	55.91
	125	CD	LYS	18	14.629	-5.696	7.175	1.00	55.91
	126	CE	LYS	18	13.744	-6.718	7.865	1.00	55.91
5	127	NZ	LYS	18	13.936	-8.075	7.298	1.00	55.91
	128	C	LYS	18	19.003	-5.299	8.149	1.00	48.86
	129	O	LYS	18	19.635	-5.875	7.267	1.00	48.86
	130	N	GLY	19	19.106	-5.627	9.429	1.00	53.46
	131	CA	GLY	19	19.993	-6.705	9.832	1.00	53.46
10	132	C	GLY	19	21.381	-6.284	10.311	1.00	53.46
	133	O	GLY	19	22.111	-7.117	10.837	1.00	53.46
	134	N	GLU	20	21.758	-5.016	10.134	1.00	46.04
	135	CA	GLU	20	23.073	-4.533	10.576	1.00	46.04
	136	CB	GLU	20	23.553	-3.372	9.700	1.00	45.53
15	137	CG	GLU	20	23.544	-3.671	8.197	1.00	45.53
	138	CD	GLU	20	24.253	-2.611	7.347	1.00	45.53
	139	OE1	GLU	20	24.049	-1.393	7.587	1.00	45.53
	140	OE2	GLU	20	25.008	-3.004	6.423	1.00	45.53
	141	C	GLU	20	23.046	-4.083	12.039	1.00	46.04
20	142	O	GLU	20	21.980	-3.958	12.654	1.00	46.04
	143	N	ASN	21	24.223	-3.845	12.607	1.00	50.99
	144	CA	ASN	21	24.297	-3.422	13.994	1.00	50.99
	145	CB	ASN	21	25.255	-4.321	14.790	1.00	67.08
	146	CG	ASN	21	24.817	-5.776	14.825	1.00	67.08
25	147	OD1	ASN	21	23.634	-6.077	15.049	1.00	67.08
	148	ND2	ASN	21	25.782	-6.675	14.619	1.00	67.08
	149	C	ASN	21	24.765	-1.985	14.118	1.00	50.99
	150	O	ASN	21	25.533	-1.493	13.290	1.00	50.99
	151	N	VAL	22	24.291	-1.317	15.164	1.00	48.02
30	152	CA	VAL	22	24.674	0.058	15.453	1.00	48.02
	153	CB	VAL	22	23.752	1.086	14.742	1.00	39.09
	154	CG1	VAL	22	22.313	0.924	15.215	1.00	39.09
	155	CG2	VAL	22	24.243	2.499	15.023	1.00	39.09
	156	C	VAL	22	24.552	0.241	16.964	1.00	48.02
35	157	O	VAL	22	23.568	-0.203	17.577	1.00	48.02
	158	N	THR	23	25.558	0.870	17.570	1.00	52.73
	159	CA	THR	23	25.530	1.102	19.013	1.00	52.73
	160	CB	THR	23	26.848	0.666	19.686	1.00	65.60
	161	OG1	THR	23	26.999	-0.754	19.570	1.00	65.60
40	162	CG2	THR	23	26.849	1.059	21.162	1.00	65.60
	163	C	THR	23	25.313	2.577	19.294	1.00	52.73
	164	O	THR	23	25.946	3.422	18.673	1.00	52.73
	165	N	LEU	24	24.407	2.883	20.214	1.00	47.77
	166	CA	LEU	24	24.136	4.267	20.576	1.00	47.77
45	167	CB	LEU	24	22.632	4.561	20.543	1.00	58.94
	168	CG	LEU	24	21.813	4.200	19.303	1.00	58.94
	169	CD1	LEU	24	20.429	4.824	19.406	1.00	58.94
	170	CD2	LEU	24	22.509	4.704	18.068	1.00	58.94
	171	C	LEU	24	24.673	4.528	21.980	1.00	47.77
50	172	O	LEU	24	24.287	3.858	22.950	1.00	47.77
	173	N	THR	25	25.563	5.510	22.085	1.00	57.92
	174	CA	THR	25	26.155	5.867	23.371	1.00	57.92
	175	CB	THR	25	27.700	5.784	23.316	1.00	61.52
	176	OG1	THR	25	28.091	4.446	22.995	1.00	61.52
55	177	CG2	THR	25	28.292	6.164	24.669	1.00	61.52
	178	C	THR	25	25.738	7.275	23.818	1.00	57.92
	179	O	THR	25	25.732	8.211	23.018	1.00	57.92
	180	N	CYS	26	25.397	7.394	25.101	1.00	87.83
	181	CA	CYS	26	24.998	8.662	25.685	1.00	87.83
60	182	C	CYS	26	26.319	9.363	26.031	1.00	87.83
	183	O	CYS	26	27.330	8.698	26.256	1.00	87.83
	184	CB	CYS	26	24.149	8.404	26.926	1.00	68.33
	185	SG	CYS	26	23.114	9.775	27.559	1.00	68.33
	186	N	ASN	27	26.315	10.692	26.067	1.00	98.51

187	CA	ASN	27	27.538	11.474	26.307	1.00	98.51
188	CB	ASN	27	27.183	12.865	26.803	1.00	123.41
189	CG	ASN	27	27.922	13.945	26.038	1.00	123.41
190	OD1	ASN	27	29.067	13.760	25.618	1.00	123.41
191	ND2	ASN	27	27.268	15.085	25.851	1.00	98.51
192	C	ASN	27	28.671	10.911	27.174	1.00	98.51
193	O	ASN	27	28.481	9.968	27.937	1.00	98.51
194	N	GLY	28	29.849	11.531	27.053	1.00	112.08
195	CA	GLY	28	31.050	11.111	27.774	1.00	112.08
196	C	GLY	28	31.283	11.487	29.235	1.00	112.08
197	O	GLY	28	32.175	10.929	29.874	1.00	112.08
198	N	ASN	29	30.513	12.430	29.772	1.00	117.67
199	CA	ASN	29	30.674	12.818	31.175	1.00	117.67
200	CB	ASN	29	30.018	14.176	31.464	1.00	132.23
201	CG	ASN	29	30.579	15.301	30.619	1.00	132.23
202	OD1	ASN	29	31.792	15.505	30.559	1.00	132.23
203	ND2	ASN	29	29.693	16.049	29.971	1.00	132.23
204	C	ASN	29	30.009	11.779	32.077	1.00	117.67
205	O	ASN	29	30.259	11.737	33.277	1.00	117.67
206	N	ASN	30	29.158	10.943	31.489	1.00	110.72
207	CA	ASN	30	28.423	9.921	32.235	1.00	110.72
208	CB	ASN	30	27.236	9.430	31.395	1.00	135.09
209	CG	ASN	30	26.331	8.468	32.153	1.00	135.09
210	OD1	ASN	30	26.684	7.989	33.231	1.00	135.09
211	ND2	ASN	30	25.163	8.183	31.590	1.00	135.09
212	C	ASN	30	29.267	8.721	32.680	1.00	110.72
213	O	ASN	30	29.834	8.000	31.853	1.00	110.72
214	N	PHE	31	29.338	8.509	33.995	1.00	129.04
215	CA	PHE	31	30.095	7.397	34.559	1.00	129.04
216	CB	PHE	31	31.178	7.900	35.519	1.00	95.73
217	CG	PHE	31	32.321	8.589	34.837	1.00	95.73
218	CD1	PHE	31	32.106	9.716	34.059	1.00	95.73
219	CD2	PHE	31	33.619	8.127	34.993	1.00	95.73
220	CE1	PHE	31	33.166	10.380	33.440	1.00	95.73
221	CE2	PHE	31	34.687	8.784	34.378	1.00	95.73
222	CZ	PHE	31	34.458	9.915	33.603	1.00	95.73
223	C	PHE	31	29.181	6.440	35.308	1.00	129.04
224	O	PHE	31	28.188	6.850	35.908	1.00	129.04
225	N	PHE	32	29.531	5.160	35.260	1.00	141.76
226	CA	PHE	32	28.775	4.109	35.937	1.00	141.76
227	CB	PHE	32	29.529	2.765	35.876	1.00	141.76
228	CG	PHE	32	30.787	2.788	35.031	1.00	141.76
229	CD1	PHE	32	31.814	3.706	35.280	1.00	141.76
230	CD2	PHE	32	30.953	1.870	33.993	1.00	141.76
231	CE1	PHE	32	32.985	3.712	34.501	1.00	141.76
232	CE2	PHE	32	32.118	1.867	33.209	1.00	141.76
233	CZ	PHE	32	33.134	2.787	33.464	1.00	141.76
234	C	PHE	32	28.562	4.481	37.408	1.00	141.76
235	O	PHE	32	29.410	5.140	38.017	1.00	141.76
236	N	GLU	33	27.433	4.055	37.969	1.00	141.76
237	CA	GLU	33	27.103	4.330	39.369	1.00	141.76
238	CB	GLU	33	28.229	3.831	40.292	1.00	141.76
239	CG	GLU	33	28.491	2.332	40.223	1.00	141.76
240	CD	GLU	33	27.251	1.496	40.515	1.00	141.76
241	OE1	GLU	33	26.216	2.073	40.920	1.00	141.76
242	OE2	GLU	33	27.313	0.256	40.344	1.00	141.76
243	C	GLU	33	26.784	5.802	39.682	1.00	141.76
244	O	GLU	33	26.382	6.125	40.803	1.00	141.76
245	N	VAL	34	26.967	6.689	38.705	1.00	137.33
246	CA	VAL	34	26.663	8.105	38.896	1.00	137.33
247	CB	VAL	34	27.428	8.997	37.878	1.00	109.45
248	CG1	VAL	34	26.940	10.441	37.974	1.00	109.45
249	CG2	VAL	34	28.929	8.922	38.140	1.00	109.45
250	C	VAL	34	25.167	8.237	38.637	1.00	137.33

	251	O	VAL	34	24.368	8.503	39.545	1.00	137.33
	252	N	SER	35	24.807	8.021	37.375	1.00	141.76
	253	CA	SER	35	23.432	8.110	36.909	1.00	141.76
	254	CB	SER	35	23.189	9.522	36.351	1.00	133.69
5	255	OG	SER	35	21.955	9.652	35.667	1.00	133.69
	256	C	SER	35	23.164	7.055	35.828	1.00	141.76
	257	O	SER	35	23.825	7.036	34.785	1.00	141.76
	258	N	SER	36	22.226	6.148	36.087	1.00	88.62
	259	CA	SER	36	21.891	5.151	35.080	1.00	88.62
10	260	CB	SER	36	20.818	4.198	35.591	1.00	92.65
	261	OG	SER	36	19.623	4.905	35.850	1.00	92.65
	262	C	SER	36	21.335	6.012	33.959	1.00	88.62
	263	O	SER	36	20.928	7.150	34.193	1.00	88.62
	264	N	THR	37	21.332	5.495	32.741	1.00	66.50
15	265	CA	THR	37	20.833	6.279	31.625	1.00	66.50
	266	CB	THR	37	21.718	6.049	30.395	1.00	64.10
	267	OG1	THR	37	23.085	6.313	30.748	1.00	64.10
	268	CG2	THR	37	21.299	6.969	29.254	1.00	64.10
	269	C	THR	37	19.369	6.003	31.268	1.00	66.50
20	270	O	THR	37	18.855	4.912	31.478	1.00	66.50
	271	N	LYS	38	18.693	7.025	30.764	1.00	59.63
	272	CA	LYS	38	17.304	6.899	30.331	1.00	59.63
	273	CB	LYS	38	16.430	7.945	31.017	1.00	48.08
	274	CG	LYS	38	15.696	7.418	32.220	1.00	48.08
25	275	CD	LYS	38	15.075	8.535	33.017	1.00	48.08
	276	CE	LYS	38	14.471	7.971	34.289	1.00	48.08
	277	NZ	LYS	38	13.893	9.058	35.108	1.00	48.08
	278	C	LYS	38	17.274	7.120	28.820	1.00	59.63
	279	O	LYS	38	17.770	8.140	28.343	1.00	59.63
30	280	N	TRP	39	16.719	6.166	28.068	1.00	49.53
	281	CA	TRP	39	16.634	6.286	26.599	1.00	49.53
	282	CB	TRP	39	17.250	5.060	25.919	1.00	52.24
	283	CG	TRP	39	18.742	4.956	26.016	1.00	52.24
	284	CD2	TRP	39	19.701	5.542	25.124	1.00	52.24
35	285	CE2	TRP	39	20.985	5.189	25.598	1.00	52.24
	286	CE3	TRP	39	19.601	6.338	23.972	1.00	52.24
	287	CD1	TRP	39	19.461	4.288	26.966	1.00	52.24
	288	NE1	TRP	39	20.809	4.422	26.720	1.00	52.24
	289	CZ2	TRP	39	22.158	5.601	24.961	1.00	52.24
40	290	CZ3	TRP	39	20.772	6.750	23.339	1.00	52.24
	291	CH2	TRP	39	22.032	6.380	23.837	1.00	52.24
	292	C	TRP	39	15.194	6.450	26.090	1.00	49.53
	293	O	TRP	39	14.270	5.831	26.608	1.00	49.53
	294	N	PHE	40	15.000	7.283	25.079	1.00	52.82
45	295	CA	PHE	40	13.662	7.470	24.529	1.00	52.82
	296	CB	PHE	40	13.159	8.894	24.792	1.00	55.71
	297	CG	PHE	40	13.062	9.229	26.255	1.00	55.71
	298	CD1	PHE	40	14.209	9.497	27.000	1.00	55.71
	299	CD2	PHE	40	11.833	9.208	26.909	1.00	55.71
50	300	CE1	PHE	40	14.140	9.719	28.368	1.00	55.71
	301	CE2	PHE	40	11.755	9.437	28.287	1.00	55.71
	302	CZ	PHE	40	12.916	9.691	29.012	1.00	55.71
	303	C	PHE	40	13.637	7.159	23.029	1.00	52.82
	304	O	PHE	40	14.294	7.823	22.228	1.00	52.82
55	305	N	HIS	41	12.896	6.117	22.665	1.00	42.70
	306	CA	HIS	41	12.766	5.703	21.269	1.00	42.70
	307	CB	HIS	41	12.801	4.176	21.186	1.00	48.50
	308	CG	HIS	41	12.708	3.643	19.795	1.00	48.50
	309	CD2	HIS	41	12.249	2.462	19.318	1.00	48.50
60	310	ND1	HIS	41	13.128	4.360	18.698	1.00	48.50
	311	CE1	HIS	41	12.931	3.647	17.604	1.00	48.50
	312	NE2	HIS	41	12.397	2.490	17.954	1.00	48.50
	313	C	HIS	41	11.408	6.261	20.842	1.00	42.70
	314	O	HIS	41	10.387	5.917	21.434	1.00	42.70

	315	N	ASN	42	11.419	7.145	19.845	1.00	49.72
	316	CA	ASN	42	10.184	7.785	19.375	1.00	49.72
	317	CB	ASN	42	9.253	6.782	18.668	1.00	43.66
	318	CG	ASN	42	9.743	6.393	17.280	1.00	43.66
5	319	OD1	ASN	42	10.632	7.053	16.729	1.00	43.66
	320	ND2	ASN	42	9.156	5.340	16.708	1.00	43.66
	321	C	ASN	42	9.447	8.391	20.562	1.00	49.72
	322	O	ASN	42	8.220	8.372	20.609	1.00	49.72
	323	N	GLY	43	10.202	8.901	21.533	1.00	60.04
10	324	CA	GLY	43	9.588	9.505	22.706	1.00	60.04
	325	C	GLY	43	9.100	8.539	23.778	1.00	60.04
	326	O	GLY	43	8.465	8.961	24.748	1.00	60.04
	327	N	SER	44	9.377	7.247	23.615	1.00	55.75
	328	CA	SER	44	8.948	6.249	24.592	1.00	55.75
15	329	CB	SER	44	8.280	5.058	23.908	1.00	71.51
	330	OG	SER	44	6.988	5.397	23.456	1.00	71.51
	331	C	SER	44	10.118	5.744	25.405	1.00	55.75
	332	O	SER	44	11.122	5.289	24.855	1.00	55.75
	333	N	LEU	45	9.981	5.821	26.723	1.00	58.69
20	334	CA	LEU	45	11.040	5.380	27.609	1.00	58.69
	335	CB	LEU	45	10.639	5.585	29.068	1.00	58.46
	336	CG	LEU	45	11.647	5.140	30.129	1.00	58.46
	337	CD1	LEU	45	12.963	5.906	30.005	1.00	58.46
	338	CD2	LEU	45	11.017	5.358	31.491	1.00	58.46
25	339	C	LEU	45	11.375	3.925	27.366	1.00	58.69
	340	O	LEU	45	10.508	3.054	27.398	1.00	58.69
	341	N	SER	46	12.650	3.677	27.116	1.00	59.18
	342	CA	SER	46	13.138	2.336	26.864	1.00	59.18
	343	CB	SER	46	14.437	2.402	26.077	1.00	54.40
30	344	OG	SER	46	15.025	1.120	26.000	1.00	54.40
	345	C	SER	46	13.388	1.591	28.165	1.00	59.18
	346	O	SER	46	13.461	2.192	29.236	1.00	59.18
	347	N	GLU	47	13.507	0.274	28.073	1.00	69.21
	348	CA	GLU	47	13.785	-0.524	29.252	1.00	69.21
35	349	CB	GLU	47	13.256	-1.944	29.080	1.00	88.33
	350	CG	GLU	47	11.752	-2.050	29.190	1.00	88.33
	351	CD	GLU	47	11.284	-3.483	29.278	1.00	88.33
	352	OE1	GLU	47	11.349	-4.198	28.256	1.00	88.33
	353	OE2	GLU	47	10.860	-3.898	30.377	1.00	88.33
40	354	C	GLU	47	15.297	-0.541	29.433	1.00	69.21
	355	O	GLU	47	15.807	-0.973	30.462	1.00	69.21
	356	N	GLU	48	16.003	-0.057	28.415	1.00	63.82
	357	CA	GLU	48	17.456	0.011	28.433	1.00	63.82
	358	CB	GLU	48	17.980	0.306	27.025	1.00	75.50
45	359	CG	GLU	48	19.483	0.478	26.950	1.00	75.50
	360	CD	GLU	48	20.223	-0.738	27.466	1.00	75.50
	361	OE1	GLU	48	20.152	-1.802	26.810	1.00	75.50
	362	OE2	GLU	48	20.863	-0.628	28.534	1.00	75.50
	363	C	GLU	48	17.902	1.113	29.394	1.00	63.82
50	364	O	GLU	48	17.454	2.255	29.284	1.00	63.82
	365	N	THR	49	18.792	0.772	30.322	1.00	72.39
	366	CA	THR	49	19.275	1.737	31.303	1.00	72.39
	367	CB	THR	49	18.867	1.316	32.727	1.00	60.69
	368	OG1	THR	49	19.140	-0.079	32.907	1.00	60.69
55	369	CG2	THR	49	17.381	1.573	32.953	1.00	60.69
	370	C	THR	49	20.780	2.007	31.294	1.00	72.39
	371	O	THR	49	21.247	2.896	31.998	1.00	72.39
	372	N	ASN	50	21.543	1.251	30.509	1.00	68.99
	373	CA	ASN	50	22.991	1.473	30.445	1.00	68.99
60	374	CB	ASN	50	23.710	0.247	29.879	1.00	96.77
	375	CG	ASN	50	23.508	-0.989	30.733	1.00	96.77
	376	OD1	ASN	50	23.625	-0.933	31.956	1.00	96.77
	377	ND2	ASN	50	23.209	-2.114	30.092	1.00	96.77
	378	C	ASN	50	23.294	2.693	29.579	1.00	68.99

379	O	ASN	50	22.424	3.178	28.856	1.00	68.99
380	N	SER	51	24.527	3.186	29.655	1.00	51.99
381	CA	SER	51	24.927	4.369	28.892	1.00	51.99
382	CB	SER	51	26.304	4.843	29.349	1.00	64.53
383	OG	SER	51	27.281	3.878	28.998	1.00	64.53
384	C	SER	51	24.978	4.074	27.391	1.00	51.99
385	O	SER	51	25.024	4.987	26.569	1.00	51.99
386	N	SER	52	24.998	2.793	27.045	1.00	68.17
387	CA	SER	52	25.xxx	2.395	25.650	1.00	68.17
388	CB	SER	52	26.351	1.690	25.346	1.00	64.58
389	OG	SER	52	27.361	2.655	25.123	1.00	64.58
390	C	SER	52	23.866	1.502	25.248	1.00	68.17
391	O	SER	52	23.621	0.468	25.864	1.00	68.17
392	N	LEU	53	23.136	1.927	24.221	1.00	42.59
393	CA	LEU	53	22.001	1.160	23.704	1.00	42.59
394	CB	LEU	53	20.856	2.108	23.328	1.00	56.84
395	CG	LEU	53	19.581	1.569	22.678	1.00	56.84
396	CD1	LEU	53	19.134	0.285	23.349	1.00	56.84
397	CD2	LEU	53	18.501	2.627	22.801	1.00	56.84
398	C	LEU	53	22.xx4	0.407	22.473	1.00	42.59
399	O	LEU	53	23.049	1.009	21.545	1.00	42.59
400	N	ASN	54	22.330	-0.911	22.479	1.00	55.75
401	CA	ASN	54	22.762	-1.722	21.349	1.00	55.75
402	CB	ASN	54	23.53?	-2.950	21.820	1.00	73.05
403	CG	ASN	54	24.921	-2.613	22.300	1.00	73.05
404	OD1	ASN	54	25.717	-2.024	21.565	1.00	73.05
405	ND2	ASN	54	25.225	-2.984	23.539	1.00	73.05
406	C	ASN	54	21.592	-2.177	20.493	1.00	55.75
407	O	ASN	54	20.643	-2.806	20.979	1.00	55.75
408	N	ILE	55	21.660	-1.835	19.212	1.00	67.23
409	CA	ILE	55	20.623	-2.237	18.281	1.00	67.23
410	CB	ILE	55	20.258	-1.098	17.338	1.00	49.71
411	CG2	ILE	55	19.390	-1.625	16.199	1.00	49.71
412	CG1	ILE	55	19.512	-0.026	18.124	1.00	49.71
413	CD1	ILE	55	19.172	1.189	17.333	1.00	49.71
414	C	ILE	55	21.209	-3.398	17.498	1.00	67.23
415	O	ILE	55	22.197	-3.231	16.776	1.00	67.23
416	N	VAL	56	20.618	-4.576	17.674	1.00	59.54
417	CA	VAL	56	21.101	-5.774	16.993	1.00	59.54
418	CB	VAL	56	21.340	-6.907	18.013	1.00	69.51
419	CG1	VAL	56	21.949	-8.114	17.311	1.00	69.51
420	CG2	VAL	56	22.262	-6.419	19.125	1.00	69.51
421	C	VAL	56	20.152	-6.270	15.898	1.00	59.54
422	O	VAL	56	18.932	-6.289	16.086	1.00	59.54
423	N	ASN	57	20.716	-6.684	14.763	1.00	58.29
424	CA	ASN	57	19.932	-7.171	13.618	1.00	58.29
425	CB	ASN	57	19.399	-8.588	13.869	1.00	80.36
426	CG	ASN	57	20.503	-9.631	13.901	1.00	80.36
427	OD1	ASN	57	21.319	-9.723	12.977	1.00	80.36
428	ND2	ASN	57	20.534	-10.428	14.966	1.00	80.36
429	C	ASN	57	18.788	-6.195	13.433	1.00	58.29
430	O	ASN	57	17.619	-6.517	13.660	1.00	58.29
431	N	ALA	58	19.166	-4.991	13.027	1.00	46.57
432	CA	ALA	58	18.252	-3.885	12.847	1.00	46.57
433	CB	ALA	58	18.982	-2.774	12.075	1.00	27.34
434	C	ALA	58	16.915	-4.227	12.170	1.00	46.57
435	O	ALA	58	16.880	-4.920	11.141	1.00	46.57
436	N	LYS	59	15.823	-3.732	12.737	1.00	53.79
437	CA	LYS	59	14.520	-3.949	12.146	1.00	53.79
438	CB	LYS	59	13.543	-4.514	13.169	1.00	70.29
439	CG	LYS	59	14.035	-5.733	13.911	1.00	70.29
440	CD	LYS	59	13.157	-5.989	15.115	1.00	70.29
441	CE	LYS	59	13.770	-7.023	16.036	1.00	70.29
442	NZ	LYS	59	12.856	-7.266	17.181	1.00	70.29

	443	C	LYS	59	14.033	-2.579	11.682	1.00	53.79
	444	O	LYS	59	14.593	-1.549	12.062	1.00	53.79
	445	N	PHE	60	13.011	-2.563	10.839	1.00	57.14
	446	CA	PHE	60	12.473	-1.301	10.359	1.00	57.14
5	447	CB	PHE	60	11.350	-1.549	9.355	1.00	75.29
	448	CG	PHE	60	11.823	-2.022	8.019	1.00	75.29
	449	CD1	PHE	60	11.028	-2.876	7.259	1.00	75.29
	450	CD2	PHE	60	13.043	-1.596	7.499	1.00	75.29
	451	CE1	PHE	60	11.437	-3.304	5.999	1.00	75.29
10	452	CE2	PHE	60	13.465	-2.016	6.237	1.00	75.29
	453	CZ	PHE	60	12.657	-2.873	5.485	1.00	75.29
	454	C	PHE	60	11.922	-0.568	11.567	1.00	57.14
	455	O	PHE	60	11.895	0.659	11.609	1.00	57.14
	456	N	GLU	61	11.484	-1.345	12.550	1.00	62.19
15	457	CA	GLU	61	10.921	-0.803	13.778	1.00	93.34
	458	CB	GLU	61	10.401	-1.937	14.671	1.00	93.34
	459	CG	GLU	61	9.199	-2.699	14.121	1.00	93.34
	460	CD	GLU	61	9.496	-3.449	12.827	1.00	93.34
	461	OE1	GLU	61	10.425	-4.285	12.815	1.00	93.34
20	462	OE2	GLU	61	8.792	-3.203	11.823	1.00	93.34
	463	C	GLU	61	11.960	0.013	14.552	1.00	62.19
	464	O	GLU	61	11.609	0.932	15.285	1.00	62.19
	465	N	ASP	62	13.235	-0.315	14.384	1.00	48.05
	466	CA	ASP	62	14.272	0.406	15.107	1.00	48.05
25	467	CB	ASP	62	15.573	-0.389	15.119	1.00	36.56
	468	CG	ASP	62	15.420	-1.725	15.809	1.00	36.56
	469	OD1	ASP	62	14.696	-1.799	16.822	1.00	36.56
	470	OD2	ASP	62	16.025	-2.703	15.355	1.00	36.56
	471	C	ASP	62	14.516	1.790	14.535	1.00	48.05
30	472	O	ASP	62	15.250	2.587	15.110	1.00	48.05
	473	N	SER	63	13.896	2.076	13.399	1.00	39.66
	474	CA	SER	63	14.076	3.386	12.809	1.00	39.66
	475	CB	SER	63	13.420	3.454	11.428	1.00	51.20
	476	OG	SER	63	14.091	2.604	10.524	1.00	51.20
35	477	C	SER	63	13.419	4.361	13.759	1.00	39.66
	478	O	SER	63	12.647	3.966	14.630	1.00	39.66
	479	N	GLY	64	13.722	5.637	13.613	1.00	35.00
	480	CA	GLY	64	13.108	6.589	14.521	1.00	35.00
	481	C	GLY	64	14.014	7.568	15.260	1.00	35.00
40	482	O	GLY	64	15.207	7.696	14.975	1.00	35.00
	483	N	GLU	65	13.406	8.261	16.214	1.00	46.87
	484	CA	GLU	65	14.075	9.259	17.020	1.00	46.87
	485	CB	GLU	65	13.101	10.390	17.340	1.00	64.86
	486	CG	GLU	65	13.685	11.460	18.222	1.00	64.86
45	487	CD	GLU	65	12.647	12.430	18.727	1.00	64.86
	488	OE1	GLU	65	11.819	12.030	19.574	1.00	64.86
	489	OE2	GLU	65	12.658	13.596	18.274	1.00	64.86
	490	C	GLU	65	14.594	8.683	18.327	1.00	46.87
	491	O	GLU	65	13.873	7.988	19.046	1.00	46.87
50	492	N	TYR	66	15.845	8.985	18.632	1.00	50.39
	493	CA	TYR	66	16.453	8.533	19.882	1.00	50.39
	494	CB	TYR	66	17.565	7.535	19.607	1.00	40.76
	495	CG	TYR	66	17.085	6.188	19.143	1.00	40.76
	496	CD1	TYR	66	17.117	5.843	17.800	1.00	40.76
55	497	CE1	TYR	66	16.746	4.585	17.382	1.00	40.76
	498	CD2	TYR	66	16.652	5.236	20.056	1.00	40.76
	499	CE2	TYR	66	16.273	3.973	19.646	1.00	40.76
	500	CZ	TYR	66	16.330	3.653	18.311	1.00	40.76
	501	OH	TYR	66	16.024	2.378	17.910	1.00	40.76
60	502	C	TYR	66	17.032	9.711	20.658	1.00	50.39
	503	O	TYR	66	17.732	10.535	20.075	1.00	50.39
	504	N	LYS	67	16.719	9.785	21.955	1.00	55.49
	505	CA	LYS	67	17.221	10.837	22.854	1.00	55.49
	506	CB	LYS	67	16.106	11.762	23.379	1.00	68.70

	507	CG	LYS	67	15.118	12.362	22.412	1.00	68.70
	508	CD	LYS	67	13.879	12.767	23.199	1.00	68.70
	509	CE	LYS	67	12.818	13.407	22.338	1.00	68.70
	510	NZ	LYS	67	11.597	13.688	23.149	1.00	68.70
5	511	C	LYS	67	17.734	10.114	24.092	1.00	55.49
	512	O	LYS	67	17.209	9.054	24.446	1.00	55.49
	513	N	CYS	68	18.749	10.658	24.759	1.00	60.89
	514	CA	CYS	68	19.179	10.011	25.992	1.00	60.89
	515	C	CYS	68	19.028	10.988	27.145	1.00	60.89
10	516	O	CYS	68	18.795	12.193	26.946	1.00	60.89
	517	CB	CYS	68	20.594	9.418	25.897	1.00	63.38
	518	SG	CYS	68	22.069	10.482	25.959	1.00	63.38
	519	N	GLN	69	19.113	10.457	28.355	1.00	61.40
	520	CA	GLN	69	18.943	11.268	29.546	1.00	61.40
15	521	CB	GLN	69	17.495	11.161	29.998	1.00	108.41
	522	CG	GLN	69	17.207	11.587	31.426	1.00	108.41
	523	CD	GLN	69	16.245	12.754	31.486	1.00	108.41
	524	OE1	GLN	69	15.641	13.126	30.493	1.00	108.41
	525	NE2	GLN	69	16.097	13.333	32.665	1.00	108.41
20	526	C	GLN	69	19.858	10.792	30.642	1.00	61.40
	527	O	GLN	69	19.859	9.609	31.005	1.00	61.40
	528	N	HIS	70	20.653	11.729	31.139	1.00	103.97
	529	CA	HIS	70	21.594	11.480	32.217	1.00	103.97
	530	CB	HIS	70	23.011	11.824	31.761	1.00	140.89
25	531	CG	HIS	70	24.032	11.697	32.844	1.00	140.89
	532	CD2	HIS	70	24.744	12.638	33.503	1.00	140.89
	533	ND1	HIS	70	24.407	10.485	33.376	1.00	140.89
	534	CE1	HIS	70	25.311	10.685	34.319	1.00	140.89
	535	NE2	HIS	70	25.534	11.984	34.416	1.00	140.89
30	536	C	HIS	70	21.186	12.373	33.396	1.00	103.97
	537	O	HIS	70	20.184	13.088	33.319	1.00	103.97
	538	N	GLN	71	21.968	12.364	34.470	1.00	101.70
	539	CA	GLN	71	21.646	13.163	35.640	1.00	101.70
	540	CB	GLN	71	22.512	12.706	36.820	1.00	136.43
35	541	CG	GLN	71	21.739	11.968	37.924	1.00	136.43
	542	CD	GLN	71	22.639	11.194	38.876	1.00	136.43
	543	OE1	GLN	71	23.660	11.696	39.322	1.00	136.43
	544	NE2	GLN	71	22.242	9.966	39.206	1.00	136.43
	545	C	GLN	71	21.782	14.663	35.407	1.00	101.70
40	546	O	GLN	71	21.838	15.441	36.361	1.00	101.70
	547	N	GLN	72	21.778	15.065	34.137	1.00	141.76
	548	CA	GLN	72	21.905	16.470	33.755	1.00	141.76
	549	CB	GLN	72	22.748	16.587	32.494	1.00	141.59
	550	CG	GLN	72	24.182	16.131	32.710	1.00	141.59
45	551	CD	GLN	72	25.045	16.307	31.482	1.00	141.59
	552	OE1	GLN	72	24.616	16.858	30.472	1.00	141.59
	553	NE2	GLN	72	26.285	15.841	31.570	1.00	141.59
	554	C	GLN	72	20.578	17.187	33.541	1.00	141.76
	555	O	GLN	72	20.531	18.246	32.918	1.00	141.76
50	556	N	VAL	73	19.509	16.598	34.067	1.00	141.76
	557	CA	VAL	73	18.150	17.144	33.996	1.00	141.76
	558	CB	VAL	73	17.945	18.230	35.093	1.00	113.45
	559	CG1	VAL	73	16.471	18.593	35.215	1.00	113.45
	560	CG2	VAL	73	18.475	17.718	36.424	1.00	113.45
55	561	C	VAL	73	17.677	17.707	32.644	1.00	141.76
	562	O	VAL	73	16.643	18.376	32.568	1.00	141.76
	563	N	ASN	74	18.433	17.441	31.583	1.00	110.03
	564	CA	ASN	74	18.056	17.906	30.249	1.00	110.03
	565	CB	ASN	74	18.782	19.208	29.880	1.00	123.79
60	566	CG	ASN	74	18.013	20.459	30.295	1.00	123.79
	567	OD1	ASN	74	16.818	20.402	30.597	1.00	123.79
	568	ND2	ASN	74	18.698	21.598	30.291	1.00	123.79
	569	C	ASN	74	18.382	16.840	29.212	1.00	110.03
	570	O	ASN	74	19.531	16.412	29.094	1.00	110.03

	571	N	GLU	75	17.367	16.416	28.460	1.00	64.12
	572	CA	GLU	75	17.552	15.399	27.433	1.00	64.12
	573	CB	GLU	75	16.190	14.961	26.882	1.00	93.37
	574	CG	GLU	75	15.332	14.330	27.971	1.00	93.37
5	575	CD	GLU	75	13.963	13.868	27.511	1.00	93.37
	576	OE1	GLU	75	13.583	14.146	26.355	1.00	93.37
	577	OE2	GLU	75	13.264	13.227	28.327	1.00	93.37
	578	C	GLU	75	18.454	15.910	26.319	1.00	64.12
	579	O	GLU	75	18.591	17.118	26.120	1.00	64.12
10	580	N	SER	76	19.090	14.984	25.611	1.00	56.18
	581	CA	SER	76	19.980	15.362	24.518	1.00	56.18
	582	CB	SER	76	20.944	14.217	24.188	1.00	74.86
	583	OG	SER	76	20.235	13.084	23.720	1.00	74.86
	584	C	SER	76	19.189	15.720	23.263	1.00	56.18
15	585	O	SER	76	17.968	15.559	23.199	1.00	56.18
	586	N	GLU	77	19.896	16.237	22.271	1.00	67.41
	587	CA	GLU	77	19.250	16.561	21.021	1.00	67.41
	588	CB	GLU	77	20.205	17.326	20.096	1.00	96.50
	589	CG	GLU	77	20.530	18.734	20.563	1.00	96.50
20	590	CD	GLU	77	19.281	19.545	20.859	1.00	96.50
	591	OE1	GLU	77	18.406	19.638	19.973	1.00	96.50
	592	OE2	GLU	77	19.173	20.089	21.978	1.00	96.50
	593	C	GLU	77	18.903	15.205	20.416	1.00	67.41
	594	O	GLU	77	19.605	14.210	20.646	1.00	67.41
25	595	N	PRO	78	17.605	15.136	19.660	1.00	64.74
	596	CD	PRO	78	16.712	16.106	19.495	1.00	62.17
	597	CA	PRO	78	17.447	13.852	19.067	1.00	64.74
	598	CB	PRO	78	16.047	14.101	18.514	1.00	62.17
	599	CG	PRO	78	15.527	15.197	19.372	1.00	62.17
30	600	C	PRO	78	18.421	13.473	17.959	1.00	64.74
	601	O	PRO	78	19.118	14.321	17.404	1.00	64.74
	602	N	VAL	79	18.469	12.183	17.670	1.00	45.82
	603	CA	VAL	79	19.274	11.638	16.593	1.00	45.82
	604	CB	VAL	79	20.455	10.798	17.123	1.00	63.76
35	605	CG1	VAL	79	21.165	10.108	15.972	1.00	63.76
	606	CG2	VAL	79	21.437	11.702	17.841	1.00	63.76
	607	C	VAL	79	18.266	10.745	15.857	1.00	45.82
	608	O	VAL	79	17.396	10.128	16.485	1.00	45.82
	609	N	TYR	80	18.347	10.697	14.533	1.00	52.05
40	610	CA	TYR	80	17.396	9.886	13.790	1.00	52.05
	611	CB	TYR	80	16.612	10.760	12.810	1.00	70.93
	612	CG	TYR	80	15.767	11.787	13.520	1.00	70.93
	613	CD1	TYR	80	16.329	12.975	13.998	1.00	70.93
	614	CE1	TYR	80	15.573	13.882	14.744	1.00	70.93
45	615	CD2	TYR	80	14.422	11.533	13.798	1.00	70.93
	616	CE2	TYR	80	13.656	12.427	14.543	1.00	70.93
	617	CZ	TYR	80	14.237	13.598	15.017	1.00	70.93
	618	OH	TYR	80	13.493	14.459	15.798	1.00	70.93
	619	C	TYR	80	18.016	8.711	13.074	1.00	52.05
50	620	O	TYR	80	18.975	8.859	12.320	1.00	52.05
	621	N	LEU	81	17.464	7.532	13.332	1.00	46.77
	622	CA	LEU	81	17.960	6.319	12.702	1.00	46.77
	623	CB	LEU	81	18.213	5.249	13.767	1.00	49.82
	624	CG	LEU	81	19.042	4.032	13.338	1.00	49.82
55	625	CD1	LEU	81	20.515	4.427	13.231	1.00	49.82
	626	CD2	LEU	81	18.884	2.907	14.354	1.00	49.82
	627	C	LEU	81	16.935	5.811	11.659	1.00	46.77
	628	O	LEU	81	15.720	5.865	11.881	1.00	46.77
	629	N	GLU	82	17.434	5.337	10.523	1.00	44.84
60	630	CA	GLU	82	16.568	4.816	9.487	1.00	44.84
	631	CB	GLU	82	16.372	5.863	8.395	1.00	75.78
	632	CG	GLU	82	15.459	5.412	7.277	1.00	75.78
	633	CD	GLU	82	14.890	6.571	6.490	1.00	75.78
	634	OE1	GLU	82	15.573	7.613	6.387	1.00	75.78

	635	OE2	GLU	82	13.764	6.437	5.968	1.00	75.78
	636	C	GLU	82	17.124	3.526	8.900	1.00	44.84
	637	O	GLU	82	18.256	3.478	8.434	1.00	44.84
	638	N	VAL	83	16.308	2.482	8.915	1.00	58.13
5	639	CA	VAL	83	16.715	1.177	8.410	1.00	58.13
	640	CB	VAL	83	16.204	0.070	9.358	1.00	48.46
	641	CG1	VAL	83	16.693	-1.285	8.909	1.00	48.46
	642	CG2	VAL	83	16.668	0.369	10.783	1.00	48.46
	643	C	VAL	83	16.212	0.919	6.986	1.00	58.13
10	644	O	VAL	83	15.033	1.088	6.697	1.00	58.13
	645	N	PHE	84	17.118	0.509	6.103	1.00	54.77
	646	CA	PHE	84	16.772	0.235	4.720	1.00	54.77
	647	CB	PHE	84	17.572	1.115	3.750	1.00	54.95
	648	CG	PHE	84	17.424	2.584	3.986	1.00	54.95
15	649	CD1	PHE	84	18.222	3.227	4.937	1.00	54.95
	650	CD2	PHE	84	16.503	3.336	3.246	1.00	54.95
	651	CE1	PHE	84	18.111	4.600	5.143	1.00	54.95
	652	CE2	PHE	84	16.378	4.708	3.438	1.00	54.95
	653	CZ	PHE	84	17.185	5.349	4.388	1.00	54.95
	654	C	PHE	84	17.031	-1.194	4.305	1.00	54.77
20	655	O	PHE	84	17.743	-1.947	4.980	1.00	54.77
	656	N	SER	85	16.474	-1.527	3.148	1.00	50.72
	657	CA	SER	85	16.625	-2.831	2.519	1.00	50.72
	658	CB	SER	85	15.392	-3.696	2.776	1.00	85.41
	659	OG	SER	85	15.578	-4.996	2.253	1.00	85.41
25	660	C	SER	85	16.737	-2.509	1.031	1.00	50.72
	661	O	SER	85	15.741	-2.166	0.397	1.00	50.72
	662	N	ASP	86	17.933	-2.595	0.470	1.00	46.74
	663	CA	ASP	86	18.122	-2.283	-0.939	1.00	46.74
	664	CB	ASP	86	18.070	-0.766	-1.139	1.00	57.20
30	665	CG	ASP	86	17.810	-0.345	-2.581	1.00	57.20
	666	OD1	ASP	86	18.547	-0.781	-3.500	1.00	57.20
	667	OD2	ASP	86	16.866	0.442	-2.795	1.00	57.20
	668	C	ASP	86	19.499	-2.821	-1.277	1.00	46.74
	669	O	ASP	86	20.166	-3.402	-0.429	1.00	46.74
35	670	N	TRP	87	19.936	-2.615	-2.505	1.00	48.74
	671	CA	TRP	87	21.241	-3.073	-2.935	1.00	48.74
	672	CB	TRP	87	21.226	-3.366	-4.440	1.00	51.62
	673	CG	TRP	87	20.649	-4.704	-4.804	1.00	51.62
	674	CD2	TRP	87	19.258	-5.039	-4.934	1.00	51.62
40	675	CE2	TRP	87	19.191	-6.406	-5.285	1.00	51.62
	676	CE3	TRP	87	18.064	-4.316	-4.793	1.00	51.62
	677	CD1	TRP	87	21.344	-5.846	-5.072	1.00	51.62
	678	NE1	TRP	87	20.479	-6.872	-5.361	1.00	51.62
	679	CZ2	TRP	87	17.966	-7.069	-5.500	1.00	51.62
45	680	CZ3	TRP	87	16.849	-4.974	-5.006	1.00	51.62
	681	CH2	TRP	87	16.813	-6.337	-5.357	1.00	51.62
	682	C	TRP	87	22.285	-2.011	-2.634	1.00	48.74
	683	O	TRP	87	23.440	-2.327	-2.297	1.00	48.74
50	684	N	LEU	88	21.889	-0.752	-2.793	1.00	48.62
	685	CA	LEU	88	22.774	0.361	-2.517	1.00	48.62
	686	CB	LEU	88	23.101	1.159	-3.775	1.00	41.58
	687	CG	LEU	88	24.163	0.628	-4.731	1.00	41.58
	688	CD1	LEU	88	24.506	1.715	-5.724	1.00	41.58
	689	CD2	LEU	88	25.415	0.208	-3.975	1.00	41.58
55	690	C	LEU	88	22.130	1.290	-1.503	1.00	48.62
	691	O	LEU	88	20.909	1.448	-1.458	1.00	48.62
	692	N	LEU	89	22.974	1.895	-0.683	1.00	46.32
	693	CA	LEU	89	22.532	2.823	0.336	1.00	46.32
	694	CB	LEU	89	22.342	2.098	1.671	1.00	41.30
60	695	CG	LEU	89	22.014	2.940	2.913	1.00	41.30
	696	CD1	LEU	89	20.786	3.782	2.656	1.00	41.30
	697	CD2	LEU	89	21.787	2.032	4.113	1.00	41.30
	698	C	LEU	89	23.636	3.863	0.459	1.00	46.32

	699	O	LEU	89	24.821	3.509	0.602	1.00	46.32
	700	N	LEU	90	23.259	5.134	0.353	1.00	43.08
	701	CA	LEU	90	24.233	6.196	0.489	1.00	43.08
	702	CB	LEU	90	23.818	7.418	-0.318	1.00	46.82
5	703	CG	LEU	90	24.810	8.588	-0.299	1.00	46.82
	704	CD1	LEU	90	26.217	8.116	-0.656	1.00	46.82
	705	CD2	LEU	90	24.344	9.655	-1.270	1.00	46.82
	706	C	LEU	90	24.229	6.528	1.975	1.00	43.08
	707	O	LEU	90	23.177	6.760	2.571	1.00	43.08
10	708	N	GLN	91	25.404	6.493	2.588	1.00	44.37
	709	CA	GLN	91	25.484	6.817	4.000	1.00	44.37
	710	CB	GLN	91	26.177	5.695	4.753	1.00	39.09
	711	CG	GLN	91	25.435	4.377	4.730	1.00	39.09
	712	CD	GLN	91	26.190	3.286	5.468	1.00	39.09
15	713	OE1	GLN	91	27.337	2.992	5.162	1.00	39.09
	714	NE2	GLN	91	25.535	2.678	6.433	1.00	39.09
	715	C	GLN	91	26.261	8.121	4.136	1.00	44.37
	716	O	GLN	91	27.172	8.390	3.357	1.00	44.37
	717	N	ALA	92	25.860	8.948	5.091	1.00	44.40
20	718	CA	ALA	92	26.534	10.217	5.309	1.00	44.40
	719	CB	ALA	92	25.618	11.365	4.952	1.00	35.90
	720	C	ALA	92	26.921	10.332	6.767	1.00	44.40
	721	O	ALA	92	26.223	9.806	7.631	1.00	44.40
	722	N	SER	93	28.025	11.019	7.041	1.00	39.65
25	723	CA	SER	93	28.435	11.214	8.419	1.00	39.65
	724	CB	SER	93	29.821	11.866	8.493	1.00	42.29
	725	OG	SER	93	29.947	12.998	7.649	1.00	42.29
	726	C	SER	93	27.373	12.092	9.062	1.00	39.65
	727	O	SER	93	27.048	11.939	10.239	1.00	39.65
30	728	N	ALA	94	26.801	13.006	8.291	1.00	49.05
	729	CA	ALA	94	25.759	13.865	8.848	1.00	49.05
	730	CB	ALA	94	26.397	15.014	9.617	1.00	25.45
	731	C	ALA	94	24.815	14.416	7.775	1.00	49.05
	732	O	ALA	94	25.238	14.702	6.668	1.00	49.05
35	733	N	GLU	95	23.542	14.563	8.099	1.00	54.30
	734	CA	GLU	95	22.598	15.115	7.126	1.00	54.30
	735	CB	GLU	95	21.200	14.552	7.355	1.00	64.16
	736	CG	GLU	95	21.107	13.088	6.999	1.00	64.16
	737	CD	GLU	95	19.770	12.488	7.345	1.00	64.16
40	738	OE1	GLU	95	19.563	11.286	7.063	1.00	64.16
	739	OE2	GLU	95	18.926	13.218	7.899	1.00	64.16
	740	C	GLU	95	22.594	16.636	7.253	1.00	54.30
	741	O	GLU	95	22.044	17.332	6.405	1.00	54.30
	742	N	VAL	96	23.234	17.127	8.317	1.00	54.64
45	743	CA	VAL	96	23.366	18.550	8.595	1.00	54.64
	744	CB	VAL	96	22.414	19.000	9.707	1.00	44.67
	745	CG1	VAL	96	22.662	20.472	10.030	1.00	44.67
	746	CG2	VAL	96	20.957	18.784	9.274	1.00	44.67
	747	C	VAL	96	24.800	18.787	9.049	1.00	54.64
50	748	O	VAL	96	25.161	18.494	10.194	1.00	54.64
	749	N	VAL	97	25.613	19.306	8.134	1.00	48.96
	750	CA	VAL	97	27.023	19.592	8.365	1.00	48.96
	751	CB	VAL	97	27.866	19.209	7.133	1.00	46.14
	752	CG1	VAL	97	29.339	19.450	7.407	1.00	46.14
55	753	CG2	VAL	97	27.628	17.773	6.764	1.00	46.14
	754	C	VAL	97	27.257	21.078	8.619	1.00	48.96
	755	O	VAL	97	26.654	21.934	7.956	1.00	48.96
	756	N	MET	98	28.148	21.385	9.560	1.00	48.67
	757	CA	MET	98	28.479	22.770	9.866	1.00	48.67
60	758	CB	MET	98	28.895	22.920	11.329	1.00	88.16
	759	CG	MET	98	27.724	22.792	12.290	1.00	88.16
	760	SD	MET	98	28.143	23.133	14.001	1.00	88.16
	761	CE	MET	98	28.281	21.471	14.634	1.00	88.16
	762	C	MET	98	29.592	23.222	8.937	1.00	48.67

	763	O	MET	98	30.487	22.451	8.603	1.00	48.67
	764	N	GLU	99	29.516	24.467	8.488	1.00	51.28
	765	CA	GLU	99	30.518	25.003	7.579	1.00	51.28
	766	CB	GLU	99	30.227	26.488	7.339	1.00	66.75
5	767	CG	GLU	99	31.195	27.175	6.403	1.00	66.75
	768	CD	GLU	99	30.842	28.632	6.164	1.00	66.75
	769	OE1	GLU	99	30.515	29.334	7.146	1.00	66.75
	770	OE2	GLU	99	30.901	29.072	4.994	1.00	66.75
	771	C	GLU	99	31.939	24.801	8.133	1.00	51.28
10	772	O	GLU	99	32.182	25.000	9.318	1.00	51.28
	773	N	GLY	100	32.874	24.401	7.280	1.00	56.63
	774	CA	GLY	100	34.233	24.185	7.748	1.00	56.63
	775	C	GLY	100	34.534	22.752	8.172	1.00	56.63
	776	O	GLY	100	35.670	22.300	8.074	1.00	56.63
15	777	N	GLN	101	33.519	22.037	8.654	1.00	64.74
	778	CA	GLN	101	33.683	20.645	9.065	1.00	64.74
	779	CB	GLN	101	32.550	20.236	10.003	1.00	77.71
	780	CG	GLN	101	32.559	20.959	11.325	1.00	77.71
	781	CD	GLN	101	33.844	20.719	12.090	1.00	77.71
20	782	OE1	GLN	101	34.912	21.200	11.702	1.00	77.71
	783	NE2	GLN	101	33.751	19.957	13.179	1.00	77.71
	784	C	GLN	101	33.695	19.702	7.855	1.00	64.74
	785	O	GLN	101	33.327	20.083	6.745	1.00	64.74
	786	N	PRO	102	34.132	18.452	8.055	1.00	53.53
25	787	CD	PRO	102	34.809	17.877	9.236	1.00	44.31
	788	CA	PRO	102	34.163	17.510	6.936	1.00	53.53
	789	CB	PRO	102	35.317	16.590	7.311	1.00	44.31
	790	CG	PRO	102	35.097	16.438	8.790	1.00	44.31
	791	C	PRO	102	32.841	16.752	6.795	1.00	53.53
30	792	O	PRO	102	32.064	16.635	7.739	1.00	53.53
	793	N	LEU	103	32.604	16.242	5.596	1.00	42.44
	794	CA	LEU	103	31.403	15.480	5.300	1.00	42.44
	795	CB	LEU	103	30.500	16.243	4.317	1.00	43.14
	796	CG	LEU	103	29.332	15.406	3.768	1.00	43.14
35	797	CD1	LEU	103	28.454	14.974	4.920	1.00	43.14
	798	CD2	LEU	103	28.522	16.193	2.768	1.00	43.14
	799	C	LEU	103	31.845	14.169	4.673	1.00	42.44
	800	O	LEU	103	32.569	14.163	3.679	1.00	42.44
	801	N	PHE	104	31.429	13.052	5.246	1.00	40.42
40	802	CA	PHE	104	31.825	11.772	4.659	1.00	40.42
	803	CB	PHE	104	32.503	10.860	5.701	1.00	57.95
	804	CG	PHE	104	33.631	11.515	6.453	1.00	57.95
	805	CD1	PHE	104	33.383	12.232	7.625	1.00	57.95
	806	CD2	PHE	104	34.943	11.411	6.003	1.00	57.95
45	807	CE1	PHE	104	34.436	12.836	8.341	1.00	57.95
	808	CE2	PHE	104	35.999	12.011	6.714	1.00	57.95
	809	CZ	PHE	104	35.741	12.721	7.880	1.00	57.95
	810	C	PHE	104	30.635	11.025	4.045	1.00	40.42
	811	O	PHE	104	29.571	10.908	4.661	1.00	40.42
50	812	N	LEU	105	30.837	10.528	2.833	1.00	44.12
	813	CA	LEU	105	29.810	9.765	2.144	1.00	44.12
	814	CB	LEU	105	29.383	10.445	0.840	1.00	40.26
	815	CG	LEU	105	28.872	11.866	0.989	1.00	40.26
	816	CD1	LEU	105	28.555	12.435	-0.367	1.00	40.26
55	817	CD2	LEU	105	27.668	11.857	1.899	1.00	40.26
	818	C	LEU	105	30.382	8.393	1.829	1.00	44.12
	819	O	LEU	105	31.587	8.227	1.639	1.00	44.12
	820	N	ARG	106	29.497	7.416	1.745	1.00	45.34
	821	CA	ARG	106	29.912	6.057	1.484	1.00	45.34
60	822	CB	ARG	106	30.135	5.384	2.829	1.00	57.54
	823	CG	ARG	106	30.591	3.964	2.800	1.00	57.54
	824	CD	ARG	106	30.297	3.378	4.162	1.00	57.54
	825	NE	ARG	106	30.888	2.066	4.356	1.00	57.54
	826	CZ	ARG	106	30.501	1.212	5.297	1.00	57.54

	827	NH1	ARG	106	29.516	1.530	6.128	1.00	57.54
	828	NH2	ARG	106	31.110	0.040	5.407	1.00	57.54
	829	C	ARG	106	28.800	5.359	0.710	1.00	45.34
	830	O	ARG	106	27.658	5.345	1.160	1.00	45.34
5	831	N	CYS	107	29.129	4.824	-0.465	1.00	48.19
	832	CA	CYS	107	28.156	4.098	-1.275	1.00	48.19
	833	C	CYS	107	28.337	2.663	-0.779	1.00	48.19
	834	O	CYS	107	29.268	1.948	-1.166	1.00	48.19
	835	CB	CYS	107	28.474	4.238	-2.769	1.00	54.03
10	836	SG	CYS	107	27.089	3.836	-3.893	1.00	54.03
	837	N	HIS	108	27.430	2.286	0.116	1.00	52.57
	838	CA	HIS	108	27.433	1.009	0.797	1.00	52.57
	839	CB	HIS	108	26.986	1.261	2.243	1.00	42.83
	840	CG	HIS	108	27.086	0.067	3.134	1.00	42.83
15	841	CD2	HIS	108	26.211	-0.448	4.029	1.00	42.83
	842	ND1	HIS	108	28.214	-0.725	3.196	1.00	42.83
	843	CE1	HIS	108	28.026	-1.677	4.092	1.00	42.83
	844	NE2	HIS	108	26.820	-1.531	4.613	1.00	42.83
	845	C	HIS	108	26.567	-0.048	0.136	1.00	52.57
20	846	O	HIS	108	25.398	0.192	-0.174	1.00	52.57
	847	N	GLY	109	27.144	-1.226	-0.072	1.00	46.92
	848	CA	GLY	109	26.413	-2.313	-0.703	1.00	46.92
	849	C	GLY	109	25.824	-3.310	0.273	1.00	46.92
	850	O	GLY	109	26.406	-3.596	1.309	1.00	46.92
25	851	N	TRP	110	24.657	-3.840	-0.063	1.00	39.32
	852	CA	TRP	110	23.983	-4.832	0.771	1.00	39.32
	853	CB	TRP	110	22.807	-5.430	-0.014	1.00	37.53
	854	CG	TRP	110	22.002	-6.428	0.744	1.00	37.53
	855	CD2	TRP	110	20.978	-6.153	1.710	1.00	37.53
30	856	CE2	TRP	110	20.507	-7.399	2.183	1.00	37.53
	857	CE3	TRP	110	20.414	-4.973	2.225	1.00	37.53
	858	CD1	TRP	110	22.105	-7.785	0.672	1.00	37.53
	859	NE1	TRP	110	21.212	-8.376	1.531	1.00	37.53
	860	CZ2	TRP	110	19.494	-7.508	3.152	1.00	37.53
35	861	CZ3	TRP	110	19.400	-5.078	3.195	1.00	37.53
	862	CH2	TRP	110	18.954	-6.344	3.645	1.00	37.53
	863	C	TRP	110	24.991	-5.918	1.134	1.00	39.32
	864	O	TRP	110	25.816	-6.297	0.309	1.00	39.32
	865	N	ARG	111	24.938	-6.405	2.369	1.00	45.97
40	866	CA	ARG	111	25.876	-7.447	2.818	1.00	45.97
	867	CB	ARG	111	25.607	-8.754	2.093	1.00	58.00
	868	CG	ARG	111	24.357	-9.430	2.525	1.00	58.00
	869	CD	ARG	111	24.273	-10.832	1.934	1.00	58.00
	870	NE	ARG	111	23.403	-11.623	2.786	1.00	58.00
45	871	CZ	ARG	111	23.773	-12.728	3.406	1.00	58.00
	872	NH1	ARG	111	25.005	-13.203	3.260	1.00	58.00
	873	NH2	ARG	111	22.918	-13.322	4.218	1.00	58.00
	874	C	ARG	111	27.337	-7.099	2.583	1.00	45.97
	875	O	ARG	111	28.184	-7.996	2.501	1.00	45.97
50	876	N	ASN	112	27.645	-5.817	2.438	1.00	52.35
	877	CA	ASN	112	29.017	-5.420	2.172	1.00	52.35
	878	CB	ASN	112	29.923	-5.796	3.341	1.00	76.11
	879	CG	ASN	112	29.974	-4.718	4.374	1.00	76.11
	880	OD1	ASN	112	30.488	-3.629	4.117	1.00	76.11
55	881	ND2	ASN	112	29.427	-4.997	5.553	1.00	52.35
	882	C	ASN	112	29.581	-6.010	0.883	1.00	52.35
	883	O	ASN	112	30.778	-6.304	0.792	1.00	52.35
	884	N	TRP	113	28.719	-6.180	-0.110	1.00	53.59
	885	CA	TRP	113	29.177	-6.682	-1.386	1.00	53.59
60	886	CB	TRP	113	27.991	-6.922	-2.333	1.00	53.83
	887	CG	TRP	113	27.170	-8.138	-1.993	1.00	53.83
	888	CD2	TRP	113	25.778	-8.348	-2.273	1.00	53.83
	889	CE2	TRP	113	25.440	-9.634	-1.783	1.00	53.83
	890	CE3	TRP	113	24.779	-7.578	-2.895	1.00	53.83

	891	CD1	TRP	113	27.607	-9.273	-1.368	1.00	53.83
	892	NE1	TRP	113	26.578	-10.173	-1.236	1.00	53.83
	893	CZ2	TRP	113	24.144	-10.169	-1.888	1.00	53.83
	894	CZ3	TRP	113	23.490	-8.107	-3.002	1.00	53.83
5	895	CH2	TRP	113	23.186	-9.394	-2.500	1.00	53.83
	896	C	TRP	113	30.068	-5.583	-1.939	1.00	53.59
	897	O	TRP	113	29.892	-4.407	-1.605	1.00	53.59
	898	N	ASP	114	31.022	-5.950	-2.779	1.00	64.92
	899	CA	ASP	114	31.893	-4.950	-3.363	1.00	64.92
10	900	CB	ASP	114	33.105	-5.602	-4.020	1.00	80.11
	901	CG	ASP	114	33.906	-6.427	-3.046	1.00	80.11
	902	OD1	ASP	114	34.241	-5.892	-1.968	1.00	80.11
	903	OD2	ASP	114	34.195	-7.603	-3.355	1.00	80.11
	904	C	ASP	114	31.122	-4.148	-4.390	1.00	64.92
15	905	O	ASP	114	30.332	-4.691	-5.170	1.00	64.92
	906	N	VAL	115	31.343	-2.844	-4.375	1.00	69.99
	907	CA	VAL	115	30.680	-1.966	-5.309	1.00	69.99
	908	CB	VAL	115	29.938	-0.865	-4.556	1.00	39.79
	909	CG1	VAL	115	29.177	0.018	-5.530	1.00	39.79
20	910	CG2	VAL	115	28.996	-1.485	-3.555	1.00	39.79
	911	C	VAL	115	31.764	-1.376	-6.198	1.00	69.99
	912	O	VAL	115	32.797	-0.930	-5.701	1.00	69.99
	913	N	TYR	116	31.540	-1.392	-7.511	1.00	52.13
	914	CA	TYR	116	32.524	-0.869	-8.457	1.00	52.13
25	915	CB	TYR	116	33.016	-1.988	-9.377	1.00	78.35
	916	CG	TYR	116	33.716	-3.109	-8.650	1.00	78.35
	917	CD1	TYR	116	33.009	-4.214	-8.178	1.00	78.35
	918	CE1	TYR	116	33.658	-5.247	-7.492	1.00	78.35
	919	CD2	TYR	116	35.093	-3.057	-7.736	1.00	78.35
30	920	CE2	TYR	116	35.752	-4.077	-7.275	1.00	78.35
	921	CZ	TYR	116	35.030	-5.170	-6.600	1.00	78.35
	922	OH	TYR	116	35.684	-6.180	-9.292	1.00	52.13
	923	C	TYR	116	31.946	0.258	-9.242	1.00	52.13
	924	O	TYR	116	30.749	0.507	-10.063	1.00	52.62
35	925	N	LYS	117	32.795	0.933	-10.901	1.00	52.62
	926	CA	LYS	117	32.339	2.040	-12.102	1.00	75.37
	927	CB	LYS	117	31.535	1.523	-13.200	1.00	75.37
	928	CG	LYS	117	32.339	0.848	-14.444	1.00	75.37
	929	CD	LYS	117	31.480	0.605	-14.904	1.00	75.37
40	930	CE	LYS	117	30.804	1.907	-16.222	1.00	75.37
	931	NZ	LYS	117	30.085	1.861	-10.095	1.00	52.62
	932	C	LYS	117	31.454	2.990	-10.585	1.00	52.62
	933	O	LYS	117	30.414	3.447	-8.859	1.00	53.28
	934	N	VAL	118	31.854	3.283	-8.029	1.00	53.28
45	935	CA	VAL	118	31.052	4.171	-6.566	1.00	39.37
	936	CB	VAL	118	31.522	4.181	-5.793	1.00	39.37
	937	CG1	VAL	118	30.807	5.300	-5.907	1.00	39.37
	938	CG2	VAL	118	31.216	2.841	-8.519	1.00	53.28
	939	C	VAL	118	31.048	5.611	-8.772	1.00	53.28
50	940	O	VAL	118	32.100	6.193	-8.663	1.00	50.90
	941	N	ILE	119	29.849	6.172	-9.072	1.00	50.90
	942	CA	ILE	119	29.704	7.555	-10.483	1.00	47.00
	943	CB	ILE	119	29.099	7.691	-10.821	1.00	47.00
	944	CG2	ILE	119	28.899	9.175	-11.507	1.00	47.00
55	945	CG1	ILE	119	30.023	7.033	-12.911	1.00	47.00
	946	CD1	ILE	119	29.506	7.082	-8.090	1.00	50.90
	947	C	ILE	119	28.760	8.211	-7.703	1.00	50.90
	948	O	ILE	119	27.767	7.606	-7.661	1.00	46.78
	949	N	TYR	120	29.087	9.429	-6.742	1.00	46.78
60	950	CA	TYR	120	28.228	10.172	-5.568	1.00	47.71
	951	CB	TYR	120	29.018	10.751	-4.589	1.00	47.71
	952	CG	TYR	120	29.508	9.727	-4.734	1.00	47.71
	953	CD1	TYR	120	30.764	9.150	-3.842	1.00	47.71
	954	CE1	TYR	120	31.225	8.210			

	955	CD2	TYR	120	28.716	9.332	-3.518	1.00	47.71
	956	CE2	TYR	120	29.167	8.376	-2.610	1.00	47.71
	957	CZ	TYR	120	30.427	7.820	-2.781	1.00	47.71
	958	OH	TYR	120	30.894	6.859	-1.911	1.00	47.71
5	959	C	TYR	120	27.559	11.319	-7.483	1.00	46.78
	960	O	TYR	120	28.166	11.972	-8.330	1.00	46.78
	961	N	TYR	121	26.306	11.572	-7.152	1.00	39.53
	962	CA	TYR	121	25.578	12.651	-7.807	1.00	39.53
	963	CB	TYR	121	24.378	12.092	-8.584	1.00	51.28
10	964	CG	TYR	121	24.767	11.242	-9.758	1.00	51.28
	965	CD1	TYR	121	25.075	9.897	-9.598	1.00	51.28
	966	CE1	TYR	121	25.525	9.131	-10.673	1.00	51.28
	967	CD2	TYR	121	24.909	11.802	-11.025	1.00	51.28
	968	CE2	TYR	121	25.359	11.046	-12.106	1.00	51.28
15	969	CZ	TYR	121	25.669	9.712	-11.920	1.00	51.28
	970	OH	TYR	121	26.158	8.978	-12.979	1.00	51.28
	971	C	TYR	121	25.079	13.703	-6.834	1.00	39.53
	972	O	TYR	121	24.692	13.392	-5.711	1.00	39.53
	973	N	LYS	122	25.104	14.955	-7.263	1.00	48.43
20	974	CA	LYS	122	24.584	16.022	-6.422	1.00	48.43
	975	CB	LYS	122	25.704	16.886	-5.851	1.00	57.69
	976	CG	LYS	122	25.215	17.619	-4.630	1.00	57.69
	977	CD	LYS	122	25.990	18.882	-4.345	1.00	57.69
	978	CE	LYS	122	25.543	19.987	-5.251	1.00	57.69
25	979	NZ	LYS	122	26.178	21.258	-4.865	1.00	57.69
	980	C	LYS	122	23.658	16.871	-7.296	1.00	48.43
	981	O	LYS	122	24.108	17.523	-8.231	1.00	48.43
	982	N	ASP	123	22.368	16.861	-6.983	1.00	47.40
	983	CA	ASP	123	21.384	17.609	-7.783	1.00	47.40
30	984	CB	ASP	123	21.625	19.122	-7.687	1.00	49.57
	985	CG	ASP	123	21.713	19.611	-6.269	1.00	49.57
	986	OD1	ASP	123	20.803	19.311	-5.468	1.00	49.57
	987	OD2	ASP	123	22.699	20.301	-5.953	1.00	49.57
	988	C	ASP	123	21.565	17.197	-9.241	1.00	47.40
35	989	O	ASP	123	21.856	18.044	-10.095	1.00	47.40
	990	N	GLY	124	21.433	15.904	-9.521	1.00	52.66
	991	CA	GLY	124	21.593	15.430	-10.888	1.00	52.66
	992	C	GLY	124	23.017	15.363	-11.421	1.00	52.66
	993	O	GLY	124	23.398	14.382	-12.041	1.00	52.66
40	994	N	GLU	125	23.807	16.408	-11.204	1.00	53.89
	995	CA	GLU	125	25.198	16.447	-11.672	1.00	53.89
	996	CB	GLU	125	25.787	17.841	-11.427	1.00	115.76
	997	CG	GLU	125	25.113	18.952	-12.208	1.00	115.76
	998	CD	GLU	125	25.418	18.876	-13.689	1.00	115.76
45	999	OE1	GLU	125	26.615	18.910	-14.044	1.00	115.76
	1000	OE2	GLU	125	24.469	18.784	-14.498	1.00	115.76
	1001	C	GLU	125	26.085	15.412	-10.974	1.00	53.89
	1002	O	GLU	125	25.912	15.130	-9.790	1.00	53.89
	1003	N	ALA	126	27.033	14.847	-11.709	1.00	51.23
50	1004	CA	ALA	126	27.954	13.880	-11.125	1.00	51.23
	1005	CB	ALA	126	28.557	12.996	-12.218	1.00	49.62
	1006	C	ALA	126	29.051	14.673	-10.422	1.00	51.23
	1007	O	ALA	126	29.659	15.551	-11.020	1.00	51.23
	1008	N	LEU	127	29.302	14.373	-9.157	1.00	63.08
55	1009	CA	LEU	127	30.332	15.088	-8.409	1.00	63.08
	1010	CB	LEU	127	30.641	14.370	-7.104	1.00	50.82
	1011	CG	LEU	127	29.663	14.719	-6.003	1.00	50.82
	1012	CD1	LEU	127	30.265	14.281	-4.689	1.00	50.82
	1013	CD2	LEU	127	29.403	16.221	-6.004	1.00	50.82
60	1014	C	LEU	127	31.643	15.322	-9.142	1.00	63.08
	1015	O	LEU	127	32.233	14.384	-9.688	1.00	63.08
	1016	N	LYS	128	32.096	16.574	-9.132	1.00	120.62
	1017	CA	LYS	128	33.343	16.933	-9.780	1.00	120.62
	1018	CB	LYS	128	33.360	18.423	-10.120	1.00	105.58

	1019	CG	LYS	128	32.187	18.879	-10.946	1.00	105.58
	1020	CD	LYS	128	32.494	20.181	-11.667	1.00	105.58
	1021	CE	LYS	128	31.295	20.661	-12.465	1.00	105.58
	1022	NZ	LYS	128	30.167	21.011	-11.563	1.00	120.62
5	1023	C	LYS	128	34.535	16.589	-8.883	1.00	120.62
	1024	O	LYS	128	35.604	16.232	-9.381	1.00	102.50
	1025	N	TYR	129	34.353	16.714	-7.568	1.00	102.50
	1026	CA	TYR	129	35.415	16.387	-6.613	1.00	91.38
	1027	CB	TYR	129	34.823	16.167	-5.216	1.00	91.38
10	1028	CG	TYR	129	34.316	17.406	-4.528	1.00	91.38
	1029	CD1	TYR	129	32.980	17.523	-4.148	1.00	91.38
	1030	CE1	TYR	129	32.519	18.664	-3.477	1.00	91.38
	1031	CD2	TYR	129	35.187	18.455	-4.224	1.00	91.38
	1032	CE2	TYR	129	34.741	19.598	-3.557	1.00	91.38
15	1033	CZ	TYR	129	33.408	19.699	-3.185	1.00	91.38
	1034	OH	TYR	129	32.960	20.831	-2.533	1.00	102.50
	1035	C	TYR	129	36.133	15.099	-7.024	1.00	102.50
	1036	O	TYR	129	35.553	14.244	-7.692	1.00	95.53
	1037	N	TRP	130	37.394	14.948	-6.636	1.00	95.53
20	1038	CA	TRP	130	38.102	13.709	-6.940	1.00	77.30
	1039	CB	TRP	130	39.605	13.916	-7.127	1.00	77.30
	1040	CG	TRP	130	40.317	12.599	-7.015	1.00	77.30
	1041	CD2	TRP	130	40.414	11.594	-8.027	1.00	77.30
	1042	CE2	TRP	130	41.001	10.447	-7.440	1.00	77.30
25	1043	CE3	TRP	130	40.046	11.536	-9.379	1.00	77.30
	1044	CD1	TRP	130	40.853	12.046	-5.881	1.00	77.30
	1045	NE1	TRP	130	41.262	10.752	-6.124	1.00	77.30
	1046	CZ2	TRP	130	41.229	9.269	-8.149	1.00	77.30
	1047	CZ3	TRP	130	40.278	10.365	-10.083	1.00	77.30
30	1048	CH2	TRP	130	40.862	9.250	-9.469	1.00	95.53
	1049	C	TRP	130	37.903	12.742	-5.784	1.00	95.53
	1050	O	TRP	130	38.038	13.124	-4.620	1.00	71.08
	1051	N	TYR	131	37.589	11.488	-6.091	1.00	71.08
	1052	CA	TYR	131	37.397	10.505	-5.034	1.00	66.47
35	1053	CB	TYR	131	35.934	10.495	-4.565	1.00	66.47
	1054	CG	TYR	131	34.894	10.405	-5.657	1.00	66.47
	1055	CD1	TYR	131	34.370	9.178	-6.055	1.00	66.47
	1056	CE1	TYR	131	33.355	9.111	-7.009	1.00	66.47
	1057	CD2	TYR	131	34.387	11.562	-6.246	1.00	66.47
40	1058	CE2	TYR	131	33.375	11.506	-7.201	1.00	66.47
	1059	CZ	TYR	131	32.857	10.283	-7.572	1.00	66.47
	1060	OH	TYR	131	31.819	10.246	-8.477	1.00	71.08
	1061	C	TYR	131	37.838	9.098	-5.384	1.00	71.08
	1062	O	TYR	131	38.058	8.768	-6.554	1.00	130.21
45	1063	N	GLU	132	37.970	8.277	-4.345	1.00	130.21
	1064	CA	GLU	132	38.389	6.884	-4.467	1.00	141.76
	1065	CB	GLU	132	39.252	6.520	-3.266	1.00	141.76
	1066	CG	GLU	132	38.484	6.649	-1.959	1.00	141.76
	1067	CD	GLU	132	39.311	7.221	-0.824	1.00	141.76
50	1068	OE1	GLU	132	40.544	7.379	-0.985	1.00	141.76
	1069	OE2	GLU	132	38.717	7.507	0.239	1.00	130.21
	1070	C	GLU	132	37.135	6.013	-4.479	1.00	130.21
	1071	O	GLU	132	36.031	6.503	-4.234	1.00	122.18
	1072	N	ASN	133	37.307	4.724	-4.745	1.00	122.18
55	1073	CA	ASN	133	36.182	3.803	-5.090	1.00	141.76
	1074	CB	ASN	133	36.698	2.392	-5.502	1.00	141.76
	1075	CG	ASN	133	35.592	1.777	-5.522	1.00	141.76
	1076	OD1	ASN	133	34.412	0.200	-5.831	1.00	141.76
	1077	ND2	ASN	133	35.980	3.806	-3.505	1.00	122.18
60	1078	C	ASN	133	35.348	3.627	-2.406	1.00	122.18
	1079	O	ASN	133	35.879	4.032	-3.681	1.00	110.94
	1080	N	HIS	134	34.044	4.052	-2.630	1.00	110.94
	1081	CA	HIS	134	33.013	2.627	-2.355	1.00	116.53
	1082	CB	HIS	134	32.503				

	1083	CG	HIS	134	33.300	1.858	-1.341	1.00	116.53
	1084	CD2	HIS	134	33.153	1.742	-0.001	1.00	116.53
	1085	ND1	HIS	134	34.341	1.029	-1.687	1.00	116.53
	1086	CE1	HIS	134	34.797	0.425	-0.605	1.00	116.53
5	1087	NE2	HIS	134	34.091	0.837	0.431	1.00	116.53
	1088	C	HIS	134	33.169	4.773	-1.283	1.00	110.94
	1089	O	HIS	134	32.312	4.627	-0.408	1.00	110.94
	1090	N	ASN	135	34.245	5.532	-1.105	1.00	107.95
	1091	CA	ASN	135	34.430	6.296	0.125	1.00	107.95
10	1092	CB	ASN	135	35.464	5.654	1.057	1.00	141.21
	1093	CG	ASN	135	35.389	6.207	2.490	1.00	141.21
	1094	OD1	ASN	135	34.536	7.044	2.801	1.00	141.21
	1095	ND2	ASN	135	36.271	5.735	3.358	1.00	141.21
	1096	C	ASN	135	34.900	7.680	-0.310	1.00	107.95
15	1097	O	ASN	135	35.952	7.836	-0.925	1.00	107.95
	1098	N	ILE	136	34.095	8.685	-0.005	1.00	65.75
	1099	CA	ILE	136	34.421	10.048	-0.387	1.00	65.75
	1100	CB	ILE	136	33.401	10.550	-1.433	1.00	65.18
	1101	CG2	ILE	136	32.002	.306	-0.943	1.00	65.18
20	1102	CG1	ILE	136	33.587	12.030	-1.717	1.00	65.18
	1103	CD1	ILE	136	32.601	12.535	-2.780	1.00	65.18
	1104	C	ILE	136	34.457	10.983	0.826	1.00	65.75
	1105	O	ILE	136	33.593	10.924	1.706	1.00	65.75
	1106	N	SER	137	35.475	11.838	0.863	1.00	51.67
25	1107	CA	SER	137	35.646	12.785	1.957	1.00	51.67
	1108	CB	SER	137	36.944	12.470	2.714	1.00	87.54
	1109	OG	SER	137	37.068	13.249	3.889	1.00	87.54
	1110	C	SER	137	35.678	14.225	1.449	1.00	51.67
	1111	O	SER	137	36.522	14.593	0.629	1.00	51.67
30	1112	N	ILE	138	34.729	15.021	1.924	1.00	63.18
	1113	CA	ILE	138	34.634	16.431	1.559	1.00	63.18
	1114	CB	ILE	138	33.178	16.801	1.239	1.00	64.58
	1115	CG2	ILE	138	33.030	18.301	1.103	1.00	64.58
	1116	CG1	ILE	138	32.754	16.080	-0.043	1.00	64.58
35	1117	CD1	ILE	138	31.285	16.134	-0.328	1.00	64.58
	1118	C	ILE	138	35.119	17.126	2.815	1.00	63.18
	1119	O	ILE	138	34.379	17.271	3.786	1.00	63.18
	1120	N	THR	139	36.384	17.525	2.783	1.00	80.92
	1121	CA	THR	139	37.063	18.140	3.920	1.00	80.92
40	1122	CB	THR	139	38.557	18.282	3.609	1.00	76.51
	1123	OG1	THR	139	38.721	19.040	2.403	1.00	76.51
	1124	CG2	THR	139	39.189	16.909	3.432	1.00	76.51
	1125	C	THR	139	36.576	19.468	4.498	1.00	80.92
	1126	O	THR	139	36.484	19.612	5.721	1.00	80.92
45	1127	N	ASN	140	36.277	20.441	3.644	1.00	57.80
	1128	CA	ASN	140	35.837	21.738	4.151	1.00	57.80
	1129	CB	ASN	140	36.840	22.821	3.731	1.00	95.08
	1130	CG	ASN	140	37.066	23.863	4.812	1.00	95.08
	1131	OD1	ASN	140	36.122	24.315	5.458	1.00	95.08
50	1132	ND2	ASN	140	38.320	24.259	5.005	1.00	95.08
	1133	C	ASN	140	34.438	22.108	3.657	1.00	57.80
	1134	O	ASN	140	34.300	22.924	2.752	1.00	57.80
	1135	N	ALA	141	33.413	21.512	4.265	1.00	63.45
	1136	CA	ALA	141	32.031	21.765	3.871	1.00	63.45
55	1137	CB	ALA	141	31.060	21.206	4.914	1.00	40.09
	1138	C	ALA	141	31.740	23.242	3.642	1.00	63.45
	1139	O	ALA	141	32.185	24.106	4.399	1.00	63.45
	1140	N	THR	142	30.971	23.505	2.588	1.00	60.40
	1141	CA	THR	142	30.573	24.847	2.192	1.00	60.40
60	1142	CB	THR	142	31.247	25.210	0.871	1.00	65.36
	1143	OG1	THR	142	32.580	25.646	1.137	1.00	65.36
	1144	CG2	THR	142	30.489	26.292	0.144	1.00	65.36
	1145	C	THR	142	29.062	24.871	2.017	1.00	60.40
	1146	O	THR	142	28.432	23.815	1.955	1.00	60.40

	1147	N	VAL	143	28.471	26.061	1.956	1.00	51.83
	1148	CA	VAL	143	27.031	26.150	1.762	1.00	51.83
	1149	CB	VAL	143	26.547	27.626	1.744	1.00	51.35
	1150	CG1	VAL	143	27.058	28.335	0.507	1.00	51.35
5	1151	CG2	VAL	143	25.019	27.673	1.807	1.00	51.35
	1152	C	VAL	143	26.667	25.448	0.434	1.00	51.83
	1153	O	VAL	143	25.584	24.884	0.292	1.00	51.83
	1154	N	GLU	144	27.599	25.466	-0.513	1.00	54.88
	1155	CA	GLU	144	27.411	24.836	-1.812	1.00	54.88
10	1156	CB	GLU	144	28.554	25.200	-2.749	1.00	66.83
	1157	CG	GLU	144	28.639	26.639	-3.146	1.00	66.83
	1158	CD	GLU	144	29.941	26.929	-3.860	1.00	66.83
	1159	OE1	GLU	144	30.280	26.169	-4.799	1.00	66.83
	1160	OE2	GLU	144	30.624	27.908	-3.478	1.00	66.83
15	1161	C	GLU	144	27.348	23.308	-1.754	1.00	54.88
	1162	O	GLU	144	26.862	22.675	-2.685	1.00	54.88
	1163	N	ASP	145	27.869	22.707	-0.692	1.00	47.71
	1164	CA	ASP	145	27.840	21.258	-0.607	1.00	47.71
	1165	CB	ASP	145	28.902	20.746	0.360	1.00	46.72
20	1166	CG	ASP	145	30.292	21.045	-0.116	1.00	46.72
	1167	OD1	ASP	145	30.613	20.700	-1.268	1.00	46.72
	1168	OD2	ASP	145	31.077	21.629	0.667	1.00	46.72
	1169	C	ASP	145	26.463	20.785	-0.200	1.00	47.71
	1170	O	ASP	145	26.227	19.592	-0.055	1.00	47.71
25	1171	N	SER	146	25.549	21.727	-0.007	1.00	42.81
	1172	CA	SER	146	24.175	21.355	0.314	1.00	42.81
	1173	CB	SER	146	23.363	22.573	0.750	1.00	49.76
	1174	OG	SER	146	23.841	23.139	1.955	1.00	49.76
	1175	C	SER	146	23.583	20.794	-0.993	1.00	42.81
30	1176	O	SER	146	24.014	21.160	-2.091	1.00	42.81
	1177	N	GLY	147	22.611	19.905	-0.879	1.00	56.97
	1178	CA	GLY	147	22.008	19.334	-2.064	1.00	56.97
	1179	C	GLY	147	21.419	17.975	-1.766	1.00	56.97
	1180	O	GLY	147	21.382	17.546	-0.612	1.00	56.97
35	1181	N	THR	148	20.937	17.294	-2.797	1.00	35.67
	1182	CA	THR	148	20.371	15.968	-2.594	1.00	35.67
	1183	CB	THR	148	18.945	15.784	-3.251	1.00	41.21
	1184	OG1	THR	148	19.077	15.127	-4.522	1.00	41.21
	1185	CG2	THR	148	18.251	17.118	-3.427	1.00	41.21
40	1186	C	THR	148	21.386	15.106	-3.297	1.00	35.67
	1187	O	THR	148	21.853	15.447	-4.382	1.00	35.67
	1188	N	TYR	149	21.743	13.998	-2.668	1.00	37.71
	1189	CA	TYR	149	22.753	13.118	-3.233	1.00	37.71
	1190	CB	TYR	149	23.988	13.045	-2.317	1.00	40.71
45	1191	CG	TYR	149	24.803	14.300	-2.117	1.00	40.71
	1192	CD1	TYR	149	24.289	15.396	-1.442	1.00	40.71
	1193	CE1	TYR	149	25.081	16.544	-1.214	1.00	40.71
	1194	CD2	TYR	149	26.117	14.366	-2.568	1.00	40.71
	1195	CE2	TYR	149	26.907	15.494	-2.357	1.00	40.71
50	1196	CZ	TYR	149	26.389	16.581	-1.680	1.00	40.71
	1197	OH	TYR	149	27.168	17.712	-1.506	1.00	40.71
	1198	C	TYR	149	22.234	11.701	-3.349	1.00	37.71
	1199	O	TYR	149	21.256	11.316	-2.690	1.00	37.71
	1200	N	TYR	150	22.918	10.930	-4.183	1.00	32.88
55	1201	CA	TYR	150	22.629	9.526	-4.333	1.00	32.88
	1202	CB	TYR	150	21.325	9.288	-5.123	1.00	48.85
	1203	CG	TYR	150	21.384	9.537	-6.605	1.00	48.85
	1204	CD1	TYR	150	21.813	8.534	-7.483	1.00	48.85
	1205	CE1	TYR	150	21.854	8.748	-8.853	1.00	48.85
60	1206	CD2	TYR	150	20.997	10.765	-7.138	1.00	48.85
	1207	CE2	TYR	150	21.038	10.990	-8.502	1.00	48.85
	1208	CZ	TYR	150	21.470	9.979	-9.353	1.00	48.85
	1209	OH	TYR	150	21.566	10.223	-10.700	1.00	48.85
	1210	C	TYR	150	23.853	9.009	-5.047	1.00	32.88

Line	Serial	Atom	Res	ResNum	X	Y	Z	Occ	B
	1211	O	TYR	150	24.668	9.802	-5.513	1.00	32.88
	1212	N	CYS	151	24.018	7.699	-5.108	1.00	43.72
	1213	CA	CYS	151	25.173	7.151	-5.793	1.00	43.72
	1214	C	CYS	151	24.734	5.984	-6.660	1.00	43.72
5	1215	O	CYS	151	23.634	5.457	-6.488	1.00	43.72
	1216	CB	CYS	151	26.229	6.672	-4.779	1.00	45.51
	1217	SG	CYS	151	25.716	5.340	-3.631	1.00	45.51
	1218	N	THR	152	25.605	5.601	-7.588	1.00	49.22
	1219	CA	THR	152	25.366	4.470	-8.467	1.00	49.22
10	1220	CB	THR	152	25.033	4.892	-9.940	1.00	42.84
	1221	OG1	THR	152	26.153	5.566	-10.535	1.00	42.84
	1222	CG2	THR	152	23.823	5.794	-9.968	1.00	42.84
	1223	C	THR	152	26.647	3.655	-8.467	1.00	49.22
	1224	O	THR	152	27.752	4.192	-8.290	1.00	49.22
15	1225	N	GLY	153	26.501	2.352	-8.638	1.00	49.54
	1226	CA	GLY	153	27.664	1.499	-8.669	1.00	49.54
	1227	C	GLY	153	27.298	0.134	-9.203	1.00	49.54
	1228	O	GLY	153	26.118	-0.243	-9.243	1.00	49.54
	1229	N	LYS	154	28.314	-0.610	-9.618	1.00	50.10
20	1230	CA	LYS	154	28.108	-1.946	-10.141	1.00	50.10
	1231	CB	LYS	154	29.078	-2.209	-11.297	1.00	64.36
	1232	CG	LYS	154	28.956	-3.599	-11.885	1.00	64.36
	1233	CD	LYS	154	30.078	-3.925	-12.851	1.00	64.36
	1234	CE	LYS	154	30.006	-5.382	-13.286	1.00	64.36
25	1235	NZ	LYS	154	31.019	-5.728	-14.324	1.00	64.36
	1236	C	LYS	154	28.310	-2.994	-9.048	1.00	50.10
	1237	O	LYS	154	29.402	-3.123	-8.497	1.00	50.10
	1238	N	VAL	155	27.236	-3.709	-8.714	1.00	62.56
	1239	CA	VAL	155	27.295	-4.784	-7.727	1.00	62.56
30	1240	CB	VAL	155	26.139	-4.722	-6.732	1.00	41.01
	1241	CG1	VAL	155	26.266	-5.872	-5.742	1.00	41.01
	1242	CG2	VAL	155	26.132	-3.391	-6.009	1:00	41.01
	1243	C	VAL	155	27.163	-6.063	-8.546	1.00	62.56
	1244	O	VAL	155	26.211	-6.224	-9.312	1.00	62.56
35	1245	N	TRP	156	28.110	-6.975	-8.380	1.00	74.40
	1246	CA	TRP	156	28.104	-8.205	-9.159	1.00	74.40
	1247	CB	TRP	156	26.846	-9.049	-8.887	1.00	64.29
	1248	CG	TRP	156	26.728	-9.536	-7.464	1.00	64.29
	1249	CD2	TRP	156	27.569	-10.497	-6.808	1.00	64.29
40	1250	CE2	TRP	156	27.114	-10.605	-5.472	1.00	64.29
	1251	CE3	TRP	156	28.661	-11.276	-7.218	1.00	64.29
	1252	CD1	TRP	156	25.826	-9.119	-6.528	1.00	64.29
	1253	NE1	TRP	156	26.052	-9.753	-5.330	1.00	64.29
	1254	CZ2	TRP	156	27.717	-11.464	-4.537	1.00	64.29
45	1255	CZ3	TRP	156	29.260	-12.130	-6.290	1.00	64.29
	1256	CH2	TRP	156	28.783	-12.215	-4.961	1.00	64.29
	1257	C	TRP	156	28.162	-7.814	-10.639	1.00	74.40
	1258	O	TRP	156	29.121	-7.178	-11.088	1.00	74.40
	1259	N	GLN	157	27.128	-8.163	-11.397	1.00	71.89
50	1260	CA	GLN	157	27.132	-7.841	-12.823	1.00	71.89
	1261	CB	GLN	157	26.876	-9.105	-13.650	1.00	111.42
	1262	CG	GLN	157	28.041	-10.072	-13.672	1.00	111.42
	1263	CD	GLN	157	29.351	-9.380	-13.965	1.00	111.42
	1264	OE1	GLN	157	29.504	-8.683	-14.969	1.00	111.42
	1265	NE2	GLN	157	30.312	-9.570	-13.081	1.00	111.42
55	1266	C	GLN	157	26.192	-6.731	-13.292	1.00	71.89
	1267	O	GLN	157	26.153	-6.418	-14.476	1.00	71.89
	1268	N	LEU	158	25.437	-6.124	-12.385	1.00	61.40
	1269	CA	LEU	158	24.522	-5.061	-12.789	1.00	61.40
	1270	CB	LEU	158	23.078	-5.463	-12.469	1.00	60.41
60	1271	CG	LEU	158	22.575	-6.756	-13.113	1.00	60.41
	1272	CD1	LEU	158	21.104	-6.948	-12.777	1.00	60.41
	1273	CD2	LEU	158	22.778	-6.677	-14.605	1.00	60.41
	1274	C	LEU	158	24.822	-3.703	-12.149	1.00	61.40

	1275	O	LEU	158	25.619	-3.596	-11.213	1.00	61.40
	1276	N	ASP	159	24.167	-2.668	-12.662	1.00	56.42
	1277	CA	ASP	159	24.338	-1.322	-12.140	1.00	56.42
	1278	CB	ASP	159	24.465	-0.311	-13.276	1.00	74.24
5	1279	CG	ASP	159	25.653	-0.586	-14.170	1.00	74.24
	1280	OD1	ASP	159	26.794	-0.666	-13.663	1.00	74.24
	1281	OD2	ASP	159	25.444	-0.721	-15.392	1.00	74.24
	1282	C	ASP	159	23.135	-0.972	-11.282	1.00	56.42
	1283	O	ASP	159	21.992	-1.211	-11.680	1.00	56.42
10	1284	N	TYR	160	23.390	-0.419	-10.098	1.00	43.45
	1285	CA	TYR	160	22.303	-0.038	-9.214	1.00	43.45
	1286	CB	TYR	160	22.309	-0.884	-7.936	1.00	50.12
	1287	CG	TYR	160	22.158	-2.369	-8.182	1.00	50.12
	1288	CD1	TYR	160	23.210	-3.115	-8.705	1.00	50.12
15	1289	CE1	TYR	160	23.076	-4.483	-8.933	1.00	50.12
	1290	CD2	TYR	160	20.961	-3.026	-7.896	1.00	50.12
	1291	CE2	TYR	160	20.814	-4.392	-8.121	1.00	50.12
	1292	CZ	TYR	160	21.875	-5.113	-8.637	1.00	50.12
	1293	OH	TYR	160	21.760	-6.467	-8.840	1.00	50.12
20	1294	C	TYR	160	22.384	1.437	-8.868	1.00	43.45
	1295	O	TYR	160	23.341	2.125	-9.219	1.00	43.45
	1296	N	GLU	161	21.370	1.922	-8.175	1.00	46.75
	1297	CA	GLU	161	21.304	3.318	-7.810	1.00	46.75
	1298	CB	GLU	161	20.454	4.057	-8.847	1.00	65.60
25	1299	CG	GLU	161	19.930	5.421	-8.439	1.00	65.60
	1300	CD	GLU	161	19.318	6.190	-9.614	1.00	65.60
	1301	OE1	GLU	161	18.653	7.226	-9.377	1.00	65.60
	1302	OE2	GLU	161	19.517	5.765	-10.777	1.00	65.60
	1303	C	GLU	161	20.687	3.385	-6.432	1.00	46.75
30	1304	O	GLU	161	19.707	2.702	-6.148	1.00	46.75
	1305	N	SER	162	21.270	4.190	-5.559	1.00	41.55
	1306	CA	SER	162	20.743	4.297	-4.202	1.00	41.55
	1307	CB	SER	162	21.841	4.761	-3.241	1.00	41.77
	1308	OG	SER	162	22.155	6.124	-3.467	1.00	41.77
35	1309	C	SER	162	19.622	5.311	-4.170	1.00	41.55
	1310	O	SER	162	19.458	6.079	-5.103	1.00	41.55
	1311	N	GLU	163	18.856	5.294	-3.088	1.00	45.18
	1312	CA	GLU	163	17.794	6.261	-2.881	1.00	45.18
	1313	CB	GLU	163	16.998	5.907	-1.632	1.00	80.94
40	1314	CG	GLU	163	16.137	4.687	-1.787	1.00	80.94
	1315	CD	GLU	163	14.993	4.941	-2.730	1.00	80.94
	1316	OE1	GLU	163	14.163	5.812	-2.407	1.00	80.94
	1317	OE2	GLU	163	14.922	4.285	-3.794	1.00	80.94
	1318	C	GLU	163	18.535	7.576	-2.653	1.00	45.18
45	1319	O	GLU	163	19.687	7.581	-2.236	1.00	45.18
	1320	N	PRO	164	17.893	8.709	-2.928	1.00	47.28
	1321	CD	PRO	164	16.592	8.936	-3.576	1.00	31.71
	1322	CA	PRO	164	18.598	9.970	-2.712	1.00	47.28
	1323	CB	PRO	164	17.888	10.913	-3.677	1.00	31.71
50	1324	CG	PRO	164	16.472	10.450	-3.551	1.00	31.71
	1325	C	PRO	164	18.525	10.444	-1.256	1.00	47.28
	1326	O	PRO	164	17.624	10.084	-0.497	1.00	47.28
	1327	N	LEU	165	19.480	11.263	-0.868	1.00	31.92
	1328	CA	LEU	165	19.513	11.769	0.499	1.00	31.92
55	1329	CB	LEU	165	20.705	11.139	1.228	1.00	52.60
	1330	CG	LEU	165	21.098	11.756	2.561	1.00	52.60
	1331	CD1	LEU	165	19.980	11.527	3.565	1.00	52.60
	1332	CD2	LEU	165	22.404	11.139	3.029	1.00	52.60
	1333	C	LEU	165	19.697	13.275	0.454	1.00	31.92
60	1334	O	LEU	165	20.401	13.775	-0.416	1.00	31.92
	1335	N	ASN	166	19.084	14.007	1.366	1.00	38.25
	1336	CA	ASN	166	19.297	15.450	1.345	1.00	38.25
	1337	CB	ASN	166	17.969	16.186	1.543	1.00	38.79
	1338	CG	ASN	166	17.056	16.079	0.309	1.00	38.79

Line	Serial	Atom	Residue	ResSeq	X	Y	Z	Occ	B
	1339	OD1	ASN	166	17.546	15.847	-0.801	1.00	38.79
	1340	ND2	ASN	166	15.748	16.259	0.490	1.00	38.79
	1341	C	ASN	166	20.341	15.889	2.398	1.00	38.25
	1342	O	ASN	166	20.282	15.480	3.561	1.00	38.25
5	1343	N	ILE	167	21.309	16.695	1.978	1.00	41.84
	1344	CA	ILE	167	22.326	17.187	2.894	1.00	41.84
	1345	CB	ILE	167	23.732	16.672	2.516	1.00	52.89
	1346	CG2	ILE	167	24.814	17.546	3.159	1.00	52.89
	1347	CG1	ILE	167	23.884	15.227	2.997	1.00	52.89
10	1348	CD1	ILE	167	25.008	14.493	2.326	1.00	52.89
	1349	C	ILE	167	22.356	18.698	2.934	1.00	41.84
	1350	O	ILE	167	22.535	19.347	1.905	1.00	41.84
	1351	N	THR	168	22.194	19.250	4.132	1.00	49.92
	1352	CA	THR	168	22.213	20.694	4.336	1.00	49.92
15	1353	CB	THR	168	20.999	21.151	5.122	1.00	52.27
	1354	OG1	THR	168	19.818	20.706	4.465	1.00	52.27
	1355	CG2	THR	168	20.977	22.658	5.238	1.00	52.27
	1356	C	THR	168	23.434	21.157	5.126	1.00	49.92
	1357	O	THR	168	23.768	20.577	6.156	1.00	49.92
20	1358	N	VAL	169	24.078	22.216	4.649	1.00	52.96
	1359	CA	VAL	169	25.230	22.791	5.331	1.00	52.96
	1360	CB	VAL	169	26.359	23.106	4.346	1.00	44.29
	1361	CG1	VAL	169	27.578	23.646	5.112	1.00	44.29
	1362	CG2	VAL	169	26.710	21.865	3.560	1.00	44.29
25	1363	C	VAL	169	24.837	24.102	6.037	1.00	52.96
	1364	O	VAL	169	24.456	25.058	5.373	1.00	52.96
	1365	N	ILE	170	24.920	24.138	7.372	1.00	52.65
	1366	CA	ILE	170	24.585	25.345	8.146	1.00	52.65
	1367	CB	ILE	170	23.700	25.033	9.380	1.00	54.27
30	1368	CG2	ILE	170	22.411	24.342	8.945	1.00	54.27
	1369	CG1	ILE	170	24.473	24.181	10.390	1.00	54.27
	1370	CD1	ILE	170	23.644	23.798	11.619	1.00	54.27
	1371	C	ILE	170	25.841	26.060	8.636	1.00	52.65
	1372	O	ILE	170	26.931	25.488	8.620	1.00	52.65
35	1373	N	LYS	171	25.697	27.308	9.075	1.00	92.13
	1374	CA	LYS	171	26.849	28.070	9.551	1.00	92.13
	1375	CB	LYS	171	26.566	29.574	9.470	1.00	112.78
	1376	CG	LYS	171	27.788	30.436	9.745	1.00	112.78
	1377	CD	LYS	171	27.599	31.881	9.293	1.00	112.78
40	1378	CE	LYS	171	27.658	32.008	7.772	1.00	112.78
	1379	NZ	LYS	171	27.643	33.430	7.310	1.00	112.78
	1380	C	LYS	171	27.244	27.674	10.974	1.00	92.13
	1381	O	LYS	171	26.388	27.384	11.812	1.00	92.13
	1382	N	ALA	172	28.551	27.662	11.230	1.00	124.64
45	1383	CA	ALA	172	29.108	27.282	12.529	1.00	124.64
	1384	CB	ALA	172	30.617	27.553	12.537	1.00	104.18
	1385	C	ALA	172	28.457	27.910	13.772	1.00	124.64
	1386	O	ALA	172	28.071	27.191	14.695	1.00	124.64
	1387	N	PRO	173	28.337	29.254	13.819	1.00	141.76
50	1388	CD	PRO	173	28.819	30.230	12.825	1.00	113.27
	1389	CA	PRO	173	27.730	29.953	14.963	1.00	141.76
	1390	CB	PRO	173	27.492	31.354	14.415	1.00	113.27
	1391	CG	PRO	173	28.701	31.556	13.575	1.00	113.27
	1392	C	PRO	173	26.461	29.332	15.553	1.00	141.76
55	1393	O	PRO	173	25.733	28.603	14.876	1.00	141.76
	1394	N	ARG	174	26.219	29.644	16.826	1.00	135.93
	1395	CA	ARG	174	25.070	29.155	17.592	1.00	135.93
	1396	CB	ARG	174	24.358	30.340	18.256	1.00	141.76
	1397	CG	ARG	174	25.304	31.216	19.065	1.00	141.76
60	1398	CD	ARG	174	24.573	32.197	19.965	1.00	141.76
	1399	NE	ARG	174	25.519	32.986	20.755	1.00	141.76
	1400	CZ	ARG	174	25.178	33.813	21.741	1.00	141.76
	1401	NH1	ARG	174	23.901	33.970	22.071	1.00	141.76
	1402	NH2	ARG	174	26.115	34.484	22.400	1.00	141.76

	1403	C	ARG	174	24.068	28.322	16.796	1.00	135.93
	1404	O	ARG	174	24.026	27.095	16.923	1.00	135.93
	1405	C1	NAG	21A	25.553	-8.090	14.864	1.00	113.42
	1406	C2	NAG	21A	26.103	-8.923	13.694	1.00	113.42
5	1407	N2	NAG	21A	25.455	-8.533	12.455	1.00	113.42
	1408	C7	NAG	21A	26.186	-8.153	11.409	1.00	113.42
	1409	O7	NAG	21A	27.417	-8.115	11.428	1.00	113.42
	1410	C8	NAG	21A	25.436	-7.756	10.148	1.00	113.42
	1411	C3	NAG	21A	25.876	-10.419	13.955	1.00	113.42
10	1412	O3	NAG	21A	26.513	-11.185	12.940	1.00	113.42
	1413	C4	NAG	21A	26.441	-10.817	15.323	1.00	113.42
	1414	O4	NAG	21A	26.084	-12.164	15.616	1.00	113.42
	1415	C5	NAG	21A	25.905	-9.887	16.423	1.00	113.42
	1416	O5	NAG	21A	26.175	-8.502	16.092	1.00	113.42
15	1417	C6	NAG	21A	26.569	-10.164	17.760	1.00	113.42
	1418	O6	NAG	21A	26.198	-9.199	18.732	1.00	113.42
	1419	C1	NAG	42A	9.440	5.012	15.315	1.00	74.70
	1420	C2	NAG	42A	8.867	3.648	14.939	1.00	74.70
	1421	N2	NAG	42A	9.316	2.609	15.844	1.00	74.70
20	1422	C7	NAG	42A	8.618	2.342	16.941	1.00	74.70
	1423	O7	NAG	42A	7.605	2.973	17.251	1.00	74.70
	1424	C8	NAG	42A	9.129	1.223	17.840	1.00	74.70
	1425	C3	NAG	42A	9.294	3.312	13.516	1.00	74.70
	1426	O3	NAG	42A	8.752	2.058	13.131	1.00	74.70
25	1427	C4	NAG	42A	8.835	4.399	12.538	1.00	74.70
	1428	O4	NAG	42A	9.469	4.168	11.266	1.00	74.70
	1429	C5	NAG	42A	9.262	5.795	13.046	1.00	74.70
	1430	O5	NAG	42A	8.894	6.001	14.433	1.00	74.70
	1431	C6	NAG	42A	8.596	6.900	12.259	1.00	74.70
30	1432	O6	NAG	42A	9.556	7.808	11.744	1.00	81.02
	1433	C1	NAG	42B	8.771	3.603	10.203	1.00	81.02
	1434	C2	NAG	42B	9.620	3.832	8.945	1.00	81.02
	1435	N2	NAG	42B	9.736	5.248	8.651	1.00	81.02
	1436	C7	NAG	42B	10.935	5.828	8.641	1.00	81.02
35	1437	O7	NAG	42B	11.980	5.214	8.866	1.00	81.02
	1438	C8	NAG	42B	10.986	7.317	8.327	1.00	81.02
	1439	C3	NAG	42B	9.064	3.068	7.750	1.00	81.02
	1440	O3	NAG	42B	9.888	3.298	6.616	1.00	81.02
	1441	C4	NAG	42B	9.103	1.604	8.138	1.00	81.02
40	1442	O4	NAG	42B	8.834	0.730	7.000	1.00	81.02
	1443	C5	NAG	42B	8.162	1.393	9.341	1.00	81.02
	1444	O5	NAG	42B	8.628	2.187	10.472	1.00	81.02
	1445	C6	NAG	42B	8.140	-0.057	9.812	1.00	81.02
	1446	O6	NAG	42B	7.263	-0.235	10.916	1.00	81.02
45	1447	C1	MAN	42C	7.548	0.362	6.612	1.00	121.66
	1448	C2	MAN	42C	7.465	0.370	5.065	1.00	121.66
	1449	O2	MAN	42C	8.504	1.176	4.523	1.00	121.66
	1450	C3	MAN	42C	7.571	-1.048	4.480	1.00	121.66
	1451	O3	MAN	42C	8.850	-1.599	4.759	1.00	121.66
50	1452	C4	MAN	42C	6.480	-1.965	5.048	1.00	121.66
	1453	O4	MAN	42C	5.296	-1.845	4.272	1.00	121.66
	1454	C5	MAN	42C	6.167	-1.621	6.510	1.00	121.66
	1455	O5	MAN	42C	7.300	-0.964	7.127	1.00	121.66
	1456	C6	MAN	42C	5.858	-2.862	7.336	1.00	121.66
55	1457	O6	MAN	42C	5.372	-3.923	6.522	1.00	69.14
	1458	C1	NAG	166A	14.879	16.481	-0.659	1.00	69.14
	1459	C2	NAG	166A	13.401	16.282	-0.279	1.00	69.14
	1460	N2	NAG	166A	13.208	14.952	0.269	1.00	69.14
	1461	C7	NAG	166A	12.951	14.790	1.565	1.00	69.14
60	1462	O7	NAG	166A	12.855	15.734	2.356	1.00	69.14
	1463	C8	NAG	166A	12.765	13.364	2.065	1.00	69.14
	1484	C3	NAG	166A	12.515	16.472	-1.519	1.00	69.14
	1465	O3	NAG	166A	11.139	16.439	-1.147	1.00	69.14
	1466	C4	NAG	166A	12.831	17.806	-2.209	1.00	69.14

1467	O4	NAG	166A	12.124	17.873	-3.464	1.00	69.14
1468	C5	NAG	166A	14.346	17.962	-2.463	1.00	69.14
1469	O5	NAG	166A	15.072	17.789	-1.224	1.00	69.14
1470	C6	NAG	166A	14.736	19.321	-3.074	1.00	69.14
1471	O6	NAG	166A	15.449	20.162	-2.169	1.00	69.14
1472	C1	NAG	166B	11.515	19.084	-3.754	1.00	88.70
1473	C2	NAG	166B	11.108	19.132	-5.235	1.00	88.70
1474	N2	NAG	166B	12.288	19.054	-6.081	1.00	88.70
1475	C7	NAG	166B	12.566	17.929	-6.736	1.00	88.70
1476	O7	NAG	166B	11.857	16.927	-6.667	1.00	88.70
1477	C8	NAG	166B	13.816	17.904	-7.601	1.00	88.70
1478	C3	NAG	166B	10.337	20.432	-5.516	1.00	88.70
1479	O3	NAG	166B	9.844	20.426	-6.848	1.00	88.70
1480	C4	NAG	166B	9.165	20.603	-4.535	1.00	88.70
1481	O4	NAG	166B	8.572	21.908	-4.731	1.00	88.70
1482	C5	NAG	166B	9.688	20.469	-3.089	1.00	88.70
1483	O5	NAG	166B	10.358	19.203	-2.919	1.00	88.70
1484	??	NAG	166B	8.612	20.538	-2.021	1.00	88.70
1485	O6	NAG	166B	9.186	20.529	-0.721	1.00	140.?3
1486	C1	MAN	166C	7.210	22.047	-4.475	1.00	140.?3
1487	C2	MAN	166C	6.971	23.248	-3.529	1.00	140.23
1488	O2	MAN	166C	8.186	23.629	-2.897	1.00	140.23
1489	C3	MAN	166C	6.384	24.444	-4.292	1.00	140.23
1490	O3	MAN	166C	7.294	24.880	-5.294	1.00	140.23
1491	C4	MAN	166C	5.054	24.047	-4.942	1.00	140.23
1492	O4	MAN	166C	4.019	24.073	-3.966	1.00	140.23
1493	C5	MAN	166C	5.141	22.640	-5.572	1.00	140.23
1494	O5	MAN	166C	6.527	22.236	-5.734	1.00	140.23
1495	C6	MAN	166C	4.497	22.590	-6.946	1.00	140.23
1496	O6	MAN	166C	3.935	21.313	-7.207	1.00	140.23
1497	OH2	WAT	1000	17.505	20.612	-1.007	1.00	68.91
1498	OH2	WAT	1001	8.876	15.888	-2.154	1.00	68.91
1499	OH2	WAT	1002	24.042	8.073	7.063	1.00	68.91
1500	OH2	WAT	1003	18.824	3.262	-1.304	1.00	68.91
1501	OH2	WAT	1004	30.337	-6.784	-6.997	1.00	68.91
1502	OH2	WAT	1005	23.648	-7.978	-9.801	1.00	68.91
1503	OH2	WAT	1006	15.659	-8.042	14.310	1.00	68.91
1504	OH2	WAT	1007	20.414	5.554	-0.296	1.00	68.91
1505	OH2	WAT	1008	25.967	2.758	12.004	1.00	68.91
1506	OH2	WAT	1009	15.148	17.603	2.679	1.00	68.91
1507	OH2	WAT	1010	20.894	14.371	-7.289	1.00	68.91
1508	OH2	WAT	1011	29.583	-2.803	0.523	1.00	68.91
1509	OH2	WAT	1012	23.414	-6.190	4.824	1.00	68.91
1510	OH2	WAT	1013	15.450	4.228	29.002	1.00	68.91
1511	OH2	WAT	1014	20.819	19.173	25.674	1.00	68.91
1512	OH2	WAT	1015	26.533	-12.922	-8.874	1.00	68.91
1513	OH2	WAT	1016	20.297	0.066	-4.940	1.00	68.91
1514	OH2	WAT	1017	12.264	10.290	21.606	1.00	68.91
1515	OH2	WAT	1018	10.662	12.690	26.479	1.00	68.91
1516	OH2	WAT	1019	30.520	28.860	10.139	1.00	68.91
1517	OH2	WAT	1020	10.314	0.397	3.316	1.00	68.91
1518	OH2	WAT	1021	29.439	18.571	-2.756	1.00	68.91
1519	OH2	WAT	1022	35.124	0.026	-10.508	1.00	68.91
1520	OH2	WAT	1023	26.056	0.085	8.311	1.00	68.91
1521	OH2	WAT	1024	29.558	14.948	9.236	1.00	68.91
1522	OH2	WAT	1025	28.174	4.087	-11.726	1.00	68.91
1523	OH2	WAT	1026	9.612	1.088	0.709	1.00	68.91
1524	OH2	WAT	1027	28.026	4.309	20.417	1.00	68.91
1525	OH2	WAT	1028	25.503	9.375	10.445	1.00	68.91
1526	OH2	WAT	1029	16.927	10.725	-7.396	1.00	68.91
1527	OH2	WAT	1030	32.003	6.822	32.047	1.00	68.91
1528	OH2	WAT	1031	12.4??	0.452	21.294	1.00	68.91
1529	OH2	WAT	1032	15.327	0.065	19.129	1.00	68.91
1530	OH2	WAT	1033	11.536	8.204	33.994	1.00	68.91

	1531	OH2	WAT	1034	18.003	7.978	-6.726	1.00	68.91
	1532	OH2	WAT	1035	34.477	2.731	-7.719	1.00	68.91
	1533	OH2	WAT	1036	25.373	34.820	8.269	1.00	68.91
	1534	OH2	WAT	1037	14.026	16.389	25.301	1.00	68.91
5	1535	OH2	WAT	1038	30.733	30.153	16.022	1.00	68.91
	1536	OH2	WAT	1039	25.276	21.121	-10.191	1.00	68.91
	1537	OH2	WAT	1040	16.971	8.768	-11.221	1.00	68.91
	1538	OH2	WAT	1041	26.997	12.580	36.282	1.00	68.91
	1539	OH2	WAT	1042	5.954	6.575	17.557	1.00	68.91
10	1540	OH2	WAT	1043	26.429	-14.196	14.154	1.00	68.91
	1541	OH2	WAT	1044	41.801	6.111	-5.021	1.00	68.91
	1542	OH2	WAT	1045	16.712	8.152	1.031	1.00	68.91
	1543	OH2	WAT	1046	10.222	17.172	0.994	1.00	68.91
	1544	OH2	WAT	1047	26.531	8.260	28.436	1.00	68.91
15	1545	OH2	WAT	1048	17.529	12.929	2.834	1.00	68.91
	1546	OH2	WAT	1049	31.571	12.227	-10.072	1.00	68.91
	1547	OH2	WAT	1050	22.536	1.995	35.016	1.00	68.91
	1548	OH2	WAT	1051	26.121	6.724	-12.642	1.00	68.91
	1549	OH2	WAT	1052	14.788	0.096	2.327	1.00	68.91
20	1550	OH2	WAT	1053	36.387	12.151	-8.959	1.00	68.91
	1551	OH2	WAT	1054	30.213	-9.146	-4.152	1.00	68.91
	1552	OH2	WAT	1055	33.615	21.863	-0.263	1.00	68.91
	1553	OH2	WAT	1056	10.283	-4.295	32.761	1.00	68.91
	1554	OH2	WAT	1057	28.514	0.501	-14.456	1.00	68.91
25	1555	OH2	WAT	1058	16.608	-5.089	16.354	1.00	68.91
	1556	OH2	WAT	1059	32.212	-2.748	2.548	1.00	68.91
	1557	OH2	WAT	1060	28.253	-14.928	-6.193	1.00	68.91
	1558	OH2	WAT	1061	22.375	14.011	20.937	1.00	68.91
	1559	OH2	WAT	1062	17.962	-4.643	18.605	1.00	68.91
30	1560	OH2	WAT	1063	33.412	17.614	12.726	1.00	68.91
	1561	OH2	WAT	1064	14.403	13.829	5.224	1.00	68.91
	1562	OH2	WAT	1065	22.334	16.845	22.648	1.00	68.91
	1563	OH2	WAT	1066	3.946	-0.489	7.854	1.00	68.91
	1564	OH2	WAT	1067	19.383	17.873	5.189	1.00	68.91
35	1565	OH2	WAT	1068	15.472	16.647	23.054	1.00	68.91
	1566	OH2	WAT	1069	29.541	28.573	2.954	1.00	68.91
	1567	OH2	WAT	1070	22.439	9.086	32.823	1.00	68.91
	1568	OH2	WAT	1071	12.994	2.582	4.613	1.00	68.91
	1569	OH2	WAT	1072	8.173	-4.098	4.759	1.00	68.91
40	1570	OH2	WAT	1073	6.843	21.529	-8.563	1.00	68.91
	1571	OH2	WAT	1074	6.493	8.743	13.308	1.00	68.91
	1572	OH2	WAT	1075	38.018	4.521	-0.320	1.00	68.91
	1573	OH2	WAT	1076	24.471	-3.010	18.115	1.00	68.91
	1574	OH2	WAT	1077	25.888	-4.454	10.596	1.00	68.91
45	1575	OH2	WAT	1078	14.459	7.299	-5.712	1.00	68.91
	1576	OH2	WAT	1079	29.390	19.413	11.601	1.00	68.91
	1577	OH2	WAT	1080	20.808	23.774	28.950	1.00	68.91
	1578	OH2	WAT	1081	30.321	32.666	4.517	1.00	68.91
	1579	OH2	WAT	1082	18.638	14.702	5.513	1.00	68.91
50	1580	OH2	WAT	1083	10.393	2.751	24.212	1.00	68.91
	1581	OH2	WAT	1084	34.357	8.750	4.350	1.00	68.91
	1582	OH2	WAT	1085	38.981	27.376	6.226	1.00	68.91
	1583	OH2	WAT	1086	13.633	-5.771	10.421	1.00	68.91
	1584	OH2	WAT	1087	30.187	-0.118	1.986	1.00	68.91
55	1585	OH2	WAT	1088	19.984	12.423	13.551	1.00	68.91
	1586	OH2	WAT	1089	33.138	0.672	3.694	1.00	68.91
	1587	OH2	WAT	1090	22.605	13.264	0.581	1.00	68.91
	1588	OH2	WAT	1091	14.668	10.306	8.575	1.00	68.91
	1589	OH2	WAT	1092	21.896	16.105	11.480	1.00	68.91
60	1590	OH2	WAT	1093	26.996	0.604	11.132	1.00	68.91
	1591	OH2	WAT	1094	31.571	7.546	16.430	1.00	68.91
	1592	OH2	WAT	1095	30.193	3.267	-18.033	1.00	68.91
	1593	OH2	WAT	1096	30.112	6.862	20.521	1.00	68.91
	1594	OH2	WAT	1097	25.159	32.416	11.157	1.00	68.91

	1595	OH2	WAT	1098	25.354	-13.410	18.368	1.00	68.91
	1596	OH2	WAT	1099	20.969	-1.882	24.389	1.00	68.91
	1597	OH2	WAT	1100	32.515	-1.311	-2.770	1.00	68.91
	1598	OH2	WAT	1101	30.357	10.302	-14.689	1.00	68.91
5	1599	OH2	WAT	1102	30.517	8.184	27.857	1.00	68.91
	1600	OH2	WAT	1103	13.656	-2.654	31.941	1.00	68.91
	1601	OH2	WAT	1104	15.222	19.539	18.640	1.00	68.91
	1602	OH2	WAT	1105	34.184	25.830	5.139	1.00	68.91
	1603	OH2	WAT	1106	27.056	25.512	13.333	1.00	68.91
10	1604	OH2	WAT	1107	33.492	6.985	-2.929	1.00	68.91
	1605	OH2	WAT	1108	12.951	8.497	11.009	1.00	68.91
	1606	OH2	WAT	1109	23.498	11.331	13.153	1.00	68.91
	1607	OH2	WAT	1110	29.557	-10.045	18.238	1.00	68.91
	1608	OH2	WAT	1111	29.239	18.077	-10.203	1.00	68.91
15	1609	OH2	WAT	1112	20.316	12.553	-11.333	1.00	68.91
	1610	OH2	WAT	1113	27.872	2.853	33.575	1.00	68.91
	1611	OH2	WAT	1114	21.439	20.739	-11.349	1.00	68.91
	1612	OH2	WAT	1115	34.052	2.985	36.842	1.00	68.91
	1613	OH2	WAT	1116	11.123	-3.141	18.133	1.00	68.91
20	1614	OH2	WAT	1117	10.985	13.263	12.061	1.00	68.91
	1615	OH2	WAT	1118	33.767	28.659	-2.115	1.00	68.91
	1616	OH2	WAT	1119	23.247	24.523	18.586	1.00	68.91
	1617	OH2	WAT	1120	31.382	23.627	14.310	1.00	68.91
	1618	OH2	WAT	1121	12.025	-1.649	0.565	1.00	68.91
25	1619	OH2	WAT	1122	9.969	2.385	20.835	1.00	68.91
	1620	OH2	WAT	1123	20.360	-3.059	-13.904	1.00	68.91

As used herein, an atomic coordinate, also referred to herein as a structure coordinate or coordinate, is a mathematical coordinate derived from mathematical equations related to the patterns obtained on diffraction of X-rays by the atoms of a protein crystal. The diffraction data are typically used to calculate an electron density map, such as that

5   shown in Fig. 1, which is used to establish the positions of the individual atoms within the unit cell of the crystal. A model that substantially represents the atomic coordinates specified in Table 1 includes not only models that literally represent the coordinates but also models representing a coordinate transformation of such atomic coordinates, for example, by changing the spatial orientation of the coordinates.

10   Additional embodiments of the present invention include 3-D models of extracellular domains of FcεRIα proteins that substantially represent the atomic coordinates specified in Table 5, Table 6, Table 7 or Table 8, each of which is at the end of the Examples section. Similarly, a model that substantially represents the atomic coordinates specified in Table 5, Table 6, Table 7 or Table 8 includes not only models that literally represent the coordinates but also models representing a coordinate

15   that literally represent the coordinates but also models representing a coordinate transformation of such atomic coordinates.

The present invention also includes a 3-D model that is a modification of a 3-D model that substantially represents the atomic coordinates specified in Table 5, Table 6, Table 7 or Table 8. As used herein, a modification, also referred to herein as a model

20   modification, is a model that represents a protein that binds to a Fc domain of an antibody. A model modification includes, but is not limited to: a refinement of the model that substantially represents the atomic coordinates specified in Table 1, Table 5, Table 6, Table 7 or Table 8; a model representing any fragment of a protein having the atomic coordinates specified in Table 1, Table 5, Table 6, Table 7 or Table 8 that binds

25   to a Fc domain of an antibody; a model based on other FcεRIα protein crystals, such as a model based on one or more of the crystals disclosed in the Examples; a model produced using homology modeling techniques to, for example, incorporate all or any part of the amino acid sequence of another FcR into a 3-D model of the extracellular domain of the model substantially representing the atomic coordinates specified in Table 1, Table 5,

30   Table 6, Table 7 or Table 8 or incorporate all or any part of the amino acid sequence of a FcεRIα protein into a 3-D model of another FcR; and a modification representing a FcR

with an altered function, which preferably can be used to design a mutein with an improved function compared to an unmodified protein. As used herein, the term unmodified protein refers to a protein that has not been intentionally subjected to either random or site-directed (i.e., targeted) mutagenesis.

A model of the present invention can be represented in a variety of forms including, but not limited to, listing the coordinates of all atoms comprising the model, providing a physical 3-D model, imaging the model on a computer screen, providing a picture of said model, and deriving a set of coordinates based of a picture of the model, for example by extracting coordinates from a picture or placing a similar immunoglobulin domain into the 3-D model of human $FceRI\alpha_{1-176}$ protein form M1, $FceRI\alpha_{1-176}$ protein form M2, $FceRI\alpha_{1-172}$ protein form T1, $FceRI\alpha_{1-172}$ protein form T2, or $FceRI\alpha_{1-172}$ protein form H1 and deriving a model of the similar domain. Physical 3-D models are tangible and include, but are not limited to, stick models and space-filling models. The phrase "imaging the model on a computer screen" refers to the ability to express (or represent) and manipulate the model on a computer screen using appropriate computer hardware and software technology known to those skilled in the art. Such technology is available from a variety of sources including, for example, Evans and Sutherland, Salt Lake City, Utah, Biosym Technologies, San Diego, CA, Tripos, Inc., and Molecular Simulations Inc. The phrase "providing a picture of the model" refers to the ability to generate a "hard copy" of the model. Hard copies include both motion and still pictures. Computer screen images and pictures of the model can be visualized in a number of formats including, but not limited to, electron density maps, ribbon diagrams, space-filling representations, α carbon traces, topology diagrams, lists of interatomic vectors, phi/psi/chi angle representations of the coordinates, and contact maps, examples of some of which are in the Figs. Representations of the model can include the entire model or portions thereof.

In one embodiment, a model of the present invention identifies the solvent accessibility of amino acid residues of the corresponding protein. The solvent accessibilities of the amino acids in human $FceRI\alpha_{1-176}$ protein (form M1) are indicated in Table 2.

Table 2. PhFcεRIα$_{1-176}$, Form M1, residue exposure

```
>>>> Surface plot for:
>>>>      structure file= fcr10_gen.mtf
>>>>      coordinate set= fcr10b.pdb
```

resid	resname	access	access-main	access-side
4	LYS	18.7522	5.5920	29.2803
5	PRO	0.5301	0.7105	0.2895
6	LYS	14.4465	0.5227	25.5856
7	VAL	1.6658	2.9151	0.0000
8	SER	10.6765	1.6199	28.7895
9	LEU	3.3901	4.3765	2.4038
10	ASN	12.4750	0.9379	24.0120
11	PRO	9.1378	0.189ö	21.0688
12	PRO	10.7886	2.5914	21.7181
13	TRP	2.8040	0.1461	3.8672
14	ASN	2.8382	0.0019	5.6746
15	ARG	0.8717	0.0047	1.3672
16	ILE	0.8262	0.0000	1.6524
17	PHE	0.2251	0.0002	0.3536
18	LYS	10.3275	2.1781	16.8470
19	GLY	5.9941	5.9941	0.0000
20	GLU	3.4574	0.0003	6.2230
21	ASN	5.5027	3.1911	7.8142
22	VAL	0.4139	0.5396	0.2464
23	THR	5.3412	0.0611	12.3812
24	LEU	0.1383	0.0000	0.2767
25	THR	6.9459	0.0105	16.1931
26	CYS	0.2279	0.2962	0.0913
27	ASN	6.3601	2.3608	10.3594
28	GLY	15.2937	15.2937	0.0000
29	ASN·	12.5836	3.3134	21.8538
30	ASN	2.9321	4.7397	1.1246
31	PHE	10.9538	0.4808	16.9384
32	PHE	16.8929	5.7840	23.2409
33	GLU	19.4108	11.1422	26.0256
34	VAL	10.7289	4.6702	18.8072
35	SER	2.4235	2.0900	3.0905
36	SER	13.8183	6.2435	28.9679
37	THR	0.2048	0.0825	0.3679
38	LYS	11.0359	0.0996	19.7850
39	TRP	0.0222	0.0000	0.0311
40	PHE	3.1821	0.0194	4.9894
41	HIS	3.3786	0.3964	5.3667
42	ASN	6.4876	7.0690	5.9062
43	GLY	10.7019	10.7019	0.0000
44	SER	11.7545	1.4355	32.3926
45	LEU	12.7619	7.2235	18.3003
46	SER	5.1618	3.6359	8.2137
47	GLU	18.9113	6.7955	28.6039
48	GLU	5.1912	1.8435	7.8693
49	THR	10.4814	0.7172	23.5005
50	ASN	12.2883	1.2937	23.2828

	51	SER	7.5408	0.9771	20.6683
	52	SER	5.9824	1.1729	15.6016
	53	LEU	2.7948	0.0000	5.5895
	54	ASN	11.0365	4.8824	17.1907
5	55	ILE	1.4787	1.1377	1.8197
	56	VAL	10.1929	3.7822	18.7406
	57	ASN	10.0544	0.9161	19.1928
	58	ALA	0.4355	0.5444	0.0000
	59	LYS	12.3709	0.0000	22.2676
10	60	PHE	3.8585	0.0995	6.0065
	61	GLU	8.4358	0.0765	15.1232
	62	ASP	3.5771	0.0000	7.1543
	63	SER	0.1109	0.0000	0.3328
	64	GLY	1.4454	1.4454	0.0000
15	65	GLU	3.8623	0.1172	6.8583
	66	TYR	0.6305	0.0000	0.9458
	67	LYS	5.0231	0.0000	9.0416
	68	CYS	0.0000	0.0000	0.0000
	69	GLN	4.0004	0.1217	7.1034
20	70	HIS	1.6360	1.2124	1.9183
	71	GLN	12.0520	6.5738	16.4346
	72	GLN	6.9718	4.8885	8.6385
	73	VAL	18.2550	4.0583	37.1841
	74	ASN	11.7258	0.8064	22.6451
25	75	GLU	8.0572	4.5805	10.8386
	76	SER	1.1935	1.7903	0.0000
	77	GLU	11.7837	0.3001	20.9705
	78	PRO	6.8729	3.9043	10.8310
	79	VAL	4.7487	0.8978	9.8832
30	80	TYR	10.6722	1.0753	15.4707
	81	LEU	0.6889	1.0101	0.3678
	82	GLU	6.0039	0.0005	10.8066
	83	VAL	1.1805	2.0660	0.0000
	84	PHE	3.1391	0.5957	4.5925
35	85	SER	11.3103	7.0817	19.7676
	86	ASP	5.0469	1.8059	8.2880
	87	TRP	8.7876	0.0000	12.3027
	88	LEU	0.2129	0.4258	0.0000
	89	LEU	0.4967	0.0525	0.9408
40	90	LEU	0.0300	0.0599	0.0000
	91	GLN	0.1846	0.0000	0.3323
	92	ALA	0.1116	0.1271	0.0495
	93	SER	6.6376	5.5213	8.8700
	94	ALA	6.8725	1.3918	28.7952
45	95	GLU	7.3784	1.6594	11.9535
	96	VAL	11.5981	3.7388	22.0772
	97	VAL	0.8323	0.7102	0.9951
	98	MET	11.2704	0.4727	22.0682
	99	GLU	9.0020	2.3489	14.3246
50	100	GLY	8.7203	8.7203	0.0000
	101	GLN	10.5632	0.0000	19.0137
	102	PRO	7.5364	2.1046	14.7788
	103	LEU	0.0101	0.0065	0.0136
	104	PHE	7.5886	0.0000	11.9250
55	105	LEU	0.0013	0.0000	0.0026
	106	ARG	5.0182	0.0005	7.8855

	107	CYS	0.1269	0.1901	0.0004
	108	HIS	0.9132	0.3845	1.2657
	109	GLY	0.5179	0.5179	0.0000
	110	TRP	4.5690	0.0000	6.3966
5	111	ARG	16.0050	8.4847	20.3023
	112	ASN	12.3469	5.3472	19.3466
	113	TRP	5.4418	2.5536	6.5971
	114	ASP	12.2436	2.6722	21.8150
	115	VAL	1.0913	1.1789	0.9745
10	116	TYR	9.9588	0.0536	14.9114
	117	LYS	15.8288	6.4497	23.3321
	118	VAL	2.4049	3.9634	0.3269
	119	ILE	7.4508	0.0000	14.9016
	120	TYR	0.0000	0.0000	0.0000
15	121	TYR	3.5355	0.0193	5.2936
	122	LYS	4.6755	0.3398	8.1440
	123	ASP	10.1763	6.7061	13.6465
	124	GLY	13.3789	13.3789	0.0000
	125	GLU	13.2240	0.9044	23.0796
20	126	ALA	9.8218	3.5091	35.0725
	127	LEU	2.8644	3.0445	2.6843
	128	LYS	20.0249	8.2304	29.4606
	129	TYR	9.3305	2.8367	12.5774
	130	TRP	16.4879	6.2307	20.5908
25	131	TYR	3.4405	3.5735	3.3740
	132	GLU	11.9086	2.0563	19.7905
	133	ASN	9.2765	4.2727	14.2802
	134	HIS	7.6393	0.0000	12.7321
	135	ASN	8.0044	0.1229	15.8860
30	136	ILE	0.3804	0.3402	0.4205
	137	SER	9.9436	6.1883	17.4541
	138	ILE	0.9720	0.9189	1.0252
	139	THR	14.4684	2.3046	30.6869
	140	ASN	12.6642	3.2729	22.0554
35	141	ALA	0.2430	0.2930	0.0431
	142	THR	6.7751	0.0000	15.8087
	143	VAL	14.3987	1.2997	31.8640
	144	GLU	14.4366	2.9912	23.5929
	145	ASP	0.6429	0.0018	1.2841
40	146	SER	5.5523	1.9108	12.8352
	147	GLY	4.1321	4.1321	0.0000
	148	THR	4.1370	0.0488	9.5879
	149	TYR	0.0265	0.0000	0.0398
	150	TYR	3.8147	0.0000	5.7220
45	151	CYS	0.0000	0.0000	0.0000
	152	THR	3.7177	0.0000	8.6747
	153	GLY	0.4224	0.4224	0.0000
	154	LYS	6.3203	0.0000	11.3765
	155	VAL	0.0418	0.0267	0.0620
50	156	TRP	11.9658	3.7888	15.2367
	157	GLN	15.4277	4.3561	24.2849
	158	LEU	14.1140	0.4176	27.8104
	159	ASP	13.2798	6.7381	19.8215
	160	TYR	4.2173	2.1486	5.2517
55	161	GLU	11.5466	4.1966	17.4267
	162	SER	0.5960	0.8940	0.0000

	163	GLU	10.5746	0.2964	18.7972
	164	PRO	11.0115	3.8863	20.5117
	165.	LEU	1.6740	0.6758	2.6721
	166	ASN	5.2259	2.2692	8.1825
5	167	ILE	0.2968	0.5937	0.0000
	168	THR	9.8239	0.0262	22.8875
	169	VAL	1.6748	2.6882	0.3236
	170	ILE	10.3926	1.8982	18.8869
	171	LYS	15.1729	2.4981	25.3128
10	172	ALA	11.6822	3.6722	43.7220
	173	PRO	13.4157	5.3766	24.1346
	174	ARG	25.5533	20.1410	28.6460
	21A	NAG	17.8283	0.0000	17.8283
	42A	NAG	10.6799	0.0000	10.6799
15	42B	NAG	8.9040	0.0000	8.9040
	42C	MAN	17.4386	0.0000	17.4386
	166A	NAG	16.8280	0.0000	16.8280
	166B	NAG	16.9174	0.0000	16.9174
	166C	MAN	21.1827	0.0000	21.1827

The solvent accessibilities of the amino acids in human FcεRIα protein forms T1, T2, M2 and M1 are indicated in Tables 9, 10, 11, and 12 respectively, each of which is at the end of the Examples section.

Residues that are solvent accessible are important as they represent amino acids that are on the external surface of the protein and, as such, may be involved in binding of a FcR to an antibody and as such be useful in designing proteins with an enhanced binding activity or in identifying compounds that inhibit such binding. In addition, solvent accessible residues can represent targets for modification to produce a FcR with improved function. Such analysis also identifies residues in the interior, or core, of the protein. Such residues can also be targeted to produce proteins with improved functions, such as enhanced stability. A model of the present invention also provides additional information that is not available from other sources. For example, a model can identify the crystal contacts between crystals and predict the location of the IgE binding domain, including those amino acids that actually form contacts with a Fc domain of an IgE antibody, such as those in the binding face of the FcεRIα protein. A model can also identify the amino acids in the interface between domain 1 and domain 2 (i.e., the D1D2 interface), as well as those in the cleft formed between the two domains.

One embodiment of the present invention is a model that represents a protein that binds to a Fc domain of an IgE antibody with an affinity that is at least equivalent to the affinity of the extracellular domain of human FcεRIα for any one of the following IgE antibodies: a human IgE antibody, a canine IgE antibody, a feline IgE antibody, an equine IgE antibody, a rat IgE antibody, and a murine IgE antibody. Such a model can represent an extracellular domain of a human FcεRIα protein, a canine FcεRIα protein, a feline FcεRIα protein, an equine FcεRIα protein, a murine FcεRIα protein, and a rat FcεRIα protein. Such a model can also represent a protein with altered substrate specificity, preferably designed based on a model of the present invention. WO 98/23964, *ibid.*, reports the ability of an isolated human FcεRIα protein to bind to canine, feline and equine IgE antibodies. Models of the present invention can be used to design a FcR with increased affinity for an antibody of a species other than self, such as, but not limited to, a human FcεRIα with increased affinity for a canine, feline or equine IgE antibody.

The present invention includes a model that represents a FcR that binds to an antibody of its respective class (i.e., IgE, IgG, IgM, IgA or IgD antibody class). Also included is a model that represents a FcR designed to bind to an antibody of a class other than the class to which the protein naturally binds. Such a model of the present

5   invention can be produced, for example, by incorporating all or any part of the amino acid sequence of the other FcR into a 3-D model of the extracellular domain of a human FcɛRIα protein. Such an embodiment includes any model that specifically incorporates any Ig domains that are placed in an orientation (packing interfaces and bend angles) that is based on the structure of the FcɛRIα. A preferred model of the present invention

10   represents a FcR that binds to an IgE antibody or to an IgG antibody. In one embodiment, a model of the present invention is a 3-D model of an extracellular antibody binding domain of a FcR other than human FcɛRIα, such as of a FcR that binds to an IgG antibody. Such proteins and models thereof can be designed by homology modeling by, for example, altering the substrate specificity of a FcɛRIα protein such that

15   the altered protein binds an IgG antibody.

A preferred modified model of the present invention is a model that has a 3-D structure comprising atomic coordinates that have a root mean square deviation of protein backbone atoms of less than 10 angstrom when superimposed, using backbone atoms, on the 3-D model substantially represented by the atomic coordinates specified in

20   Table 1, Table 5, Table 6, Table 7 or Table 8, and more particularly atomic coordinates specified in Table 1. Preferably such a model has a 3-D structure comprising atomic coordinates that have a root mean square deviation of protein backbone atoms of less than 8 angstroms, preferably less than 7 angstroms, preferably less than 6 angstroms, preferably less than 5 angstroms, preferably less than 4 angstroms, preferably less than 3

25   angstroms, preferably less than 2 angstroms, and preferably less than 1 angstroms, when superimposed, using backbon3 atoms, on the 3-D model substantially represented by the atomic coordinates specified in Table 1, Table 5, Table 6, Table 7, or Table 8, and more particularly atomic coordinates specified in Table 1. In this embodiment, such a model represents a FcR that binds to an antibody. The backbone atoms are those atoms that

30   form the backbone, or 3-D folding pattern, of the model. As such, backbone atoms are the base residues of amino acids, i.e., nitrogen, carbon, the alpha carbon and oxygen.

Also preferred is a model modification having an amino acid sequence that shares at least about 30%, preferably at least about 40%, more preferably at least about 45%, more preferably at least about 50%, more preferably at least about 60% and even more preferably at least about 80% amino acid sequence homology, with a human FcεRIα

5 protein, as determined using the program ALIGN with default parameters, optimal global alignment of two sequences with no short-cuts. It is to be noted that, using the same program and parameters, the extracellular domain of a human FcεRIα protein (i.e., soluble human FcεRIα protein) shares about 48% identity with feline and rat soluble FcεRIα proteins, about 49% with a murine soluble FcεRIα protein, about 50% identity with a canine soluble FcεRIα protein, and about 60% identity with an equine soluble

10 FcεRIα protein. A preferred model of the present invention represents an IgE binding domain, i.e., a region that binds to an IgE antibody.

One embodiment of the present invention is a 3-D model of a human FcεRIα protein produced by a method that includes the steps of: (a) crystallizing an extracellular

15 domain of a human FcεRIα protein, such as, but not limited to a protein having amino acid sequence SEQ ID NO:2 or SEQ ID NO:4; (b) collecting X-ray diffraction data from the crystallized protein; and (c) determining the model from the X-ray diffraction data, preferably in combination with an amino acid sequence of the protein. A protein for crystal formation can be produced using a variety of techniques well known to those

20 skilled in the art. As disclosed herein, a human FcεRIα protein to be crystallized is preferably produced in recombinant insect cells transformed with a gene encoding an extracellular domain of a human FcεRIα protein, such as a baculovirus genetically engineered to produce the protein. The purity of the FcεRIα protein must be sufficient to permit the production of crystals that can be analyzed by X-ray crystallography to a

25 resolution that permits determination of a 3-D model of the protein. Preferably the resolution is at least about 4 angstroms (i.e., 4 angstroms or better), more preferably at least about 3.5 angstroms, more preferably at least about 3 angstroms, more preferably at least about 2.5 angstroms, more preferably at least about 2 angstroms and even more preferably at least about 1.5 angstroms. Methods to obtain such purity levels are well

30 known to those skilled in the art.

As disclosed herein, a preferred method to crystallize a FcεRIα protein is by vapor distillation. Particularly preferred methods are disclosed in the Examples. It should be appreciated that the present invention also includes other methods known to those skilled in the art by which the protein can be crystallized.

3-D models of some proteins have been determined; see, for example, Blundell et al., *Protein Crystallography*, Academic Press, London, 1976. However, as discussed herein, elucidation of the crystal structure of the extracellular domain of the human FcεRIα was difficult. In one embodiment, crystal structure determination includes obtaining high-resolution data using synchrotron radiation. Such data can be collected, for example, at the Stanford Synchrotron Source Laboratory, Palo Alto, CA, or the Advanced Photon Source at Argonne National Laboratories, Argonne, IL. Additional locations to collect such data include, but are not limited to, Brookhaven, NY, and Japan. In one embodiment, diffraction data from native and heavy-atom treated crystals provide an initial image of the protein structure which is refined into an electron density map. Details regarding data collection and interpretation are provided in the Examples section.

One embodiment of the present invention is a method to produce a 3-D model of a FcεRIα protein that includes positioning amino acid representations (i.e., representing amino acids) of the protein at substantially the coordinates listed in Table 1, Table 5, Table 6, Table 7, or Table 8. That is, knowledge of the coordinates of the protein permits one skilled in the art to produce a model of the protein using those coordinates. Such a model, or any model which is essentially represented by a simple coordinate transformation of the coordinates specified in Table 1, Table 5, Table 6, Table 7, or Table 8, can be represented in a variety of methods as heretofore disclosed and is included in the present invention.

In another embodiment, a model of the present invention can be refined to obtain an improved model, which is an example of a model modification, also referred to as a modified model. Refining methods can include, but are not limited to, further data collection and analysis; data collection from frozen crystals; introduction of solvent molecules to the structure; clarification of secondary structure; and analyses of crystallized complexes between a FcR and an antibody or inhibitory compound. An

additional model refinement method includes analyzing a 3-D model to predict amino acid residues that if replaced are likely to yield proteins with at least one improved function, effecting at least one such replacement, determining whether the activity of the modified protein agrees with the prediction, and refining the model as necessary.

5   Methods to determine whether the modification agrees with prediction include producing the modified protein and performing assays with that modified protein to determine if the protein does indeed exhibit the improved function(s), such as desired activity, stability and solubility properties. Assays to measure such functions are well known in the art; examples of several such assays are disclosed herein.

10   Another embodiment of the present invention is a modified 3-D model that represents a FcR other than a human FcεRIα protein represented by the 3-D model the coordinates of which are listed in Table 1, Table 5, Table 6, Table 7, or Table 8. Preferably the amino acid sequence of the protein to be modeled is known. In such a case, the modified model can be produced using the technique of homology modeling,

15   preferably by incorporating (e.g., grafting, overlaying or replacing) all or any portion of the amino acid sequence of the other FcR into the 3-D model of the human FcεRIα protein to produce the modified model which comprises the other FcR. General techniques for homology modeling, also referred to as molecular replacement, have been disclosed in, for example, Greer, 1990, *Proteins: Structure, Function, and Genetics 7*,

20   317-334; Havel et al., 1991, *J. Mol. Biol. 217*, 1-7; Schiffer et al., 1990, *Proteins: Structure, Function, and Genetics 8*, 30-43; and Lattman, 1985, *Methods Enzymol 115*, 55-77. However, such technology has not been applied to FcRs since, until the present invention, no 3-D model of any FcR was available. Thus, the present invention now allows the solving of the structures of a number of other natural and mutated forms of

25   FcRs or any other protein with significant amino acid homology, especially to the functional Ig domains of the human FcεRIα protein.

In one embodiment, a model of a FcR, such as, but not limited to a FcεRIα protein, is produced by extracting the 3-D coordinates from a published figure or building a 3-D model with atoms from other Ig domains wherein the Ig domains are

30   oriented as predicted for a human FcεRIα$_{1-176}$ protein or a FcεRIα$_{1-172}$ protein. For example, a model of the present invention can be produced by orienting two known Ig

domains into a bent confirmation similar to that of the two domains of the human FcεRIα protein. Such a model is referred to as a model in which domain 1 and domain 2 are oriented in a manner as specified by the structural coordinates listed in Table 1, Table 5, Table 6, Table 7, or Table 8. This model can then be used in further molecular

5 replacement methods. Such methods can include the steps of (a) orienting the model by three rotations; and (b) translating the model in one to three directions to produce additional model modifications.

Suitable FcRs for which a 3-D model can be determined using homology modeling include any mammalian FcR, such as a protein that binds to IgE, IgG, IgM,

10 IgA or IgD antibodies. Preferred is a protein that binds to an IgE antibody or an IgG antibody. Preferred FcRs that bind to IgE include human, canine, feline, equine, murine and rat FcεRIα proteins. The present invention also includes the use of other Ig domains to produce models of the present invention.

One embodiment of the present invention is a 3-D model of a FcR having an

15 improved function compared to an unmodified protein as well as a method to produce such a modified model. Such an improved function includes, but is not limited to, enhanced activity, enhanced stability and enhanced solubility. Such a modified model can be produced by replacing at least one amino acid based on information derived from analyzing the 3-D model of a FcεRIα protein, such as the model of a human FcεRIα$_{1-176}$

20 protein or a FcεRIα$_{1-172}$ protein, such that the replacement leads to a protein with an improved function. As used herein, a replacement refers to an (i.e., one or more) amino acid substitution, insertion, deletion, inversion and/or derivatization (e.g., acetylation, glycosylation, phosphorylation, PEG modification, biotinylation, and covalent attachment of other ligands or other compounds to the protein. In one embodiment,

25 synthetic chemical methods are used to produce either a fragment or the entire protein to, for example, introduce non-natural amino acids or other chemical compounds into the structure of a FcR. For example, based on a structure of the present invention, one can design synthetic peptides or larger proteins that could be linked to produce an intact protein with IgE binding activity, the structure allowing one to design the start and stop

30 points for these peptides, e.g., at surface accessible loops. In accordance with the present invention, an amino acid that is substituted or inserted can be a natural amino

acid or an unnatural amino acid, including a derivitized amino acid. Methods to identify regions in the protein that, if changed, yield a protein with an improved function are disclosed below.

The present invention includes use of a 3-D model of the present invention to identify a compound that inhibits binding between a FcR and an antibody. The advantages of using a 3-D model to identify inhibitory compounds are multi-fold in that the model depicts the site at which a Fc domain of an antibody binds to its FcR, i.e., the antibody-binding domain, also referred to as the antibody binding site. As such, a large number of potential inhibitory compounds can be initially analyzed without having to perform in vitro or in vivo laboratory studies. As used herein, methods to identify inhibitory compounds include, but are not limited to, designing inhibitory compounds based on the 3-D model of a FcR, probing such a 3-D model with compounds that are potential inhibitors in order to identify those compounds that are actually inhibitory of the binding of an antibody to its FcR, screening a compound data base using such a 3-D model to identify compounds that inhibit such binding, and combinations thereof. Methods to use 3-D models to design, probe for, or screen for suitable inhibitory compounds are known to those skilled in the art. In particular, there are a number of computer programs that enable such methods. See, for example, PCT Publication No. WO 95/35367, by Wilson et al., published December 28, 1995.

An inhibitory compound can be any natural or synthetic compound that inhibits the binding of an antibody to a FcR. Examples include, but are not limited to, inorganic compounds, oligonucleotides, proteins, peptides, antibodies, antibody fragments, mimetics of peptides or antibodies (such as, mimetics of antibody or receptor binding sites), and other organic compounds. Compounds can inhibit binding in either a competitive or non-competitive manner and can either interact at the binding site or allosterically. An inhibitory compound should be capable of physically and structurally associating with a FcR and/or an antibody such that the compound can inhibit binding between the two entitites. As such, an inhibitory compound is preferably small and is of a structure that effectively prevents or disrupts binding. Inhibitory compounds can be identified in one or multiple steps. For example, a compound initially identified that inhibits binding between an antibody and FcR to some extent can be used as a lead to

design, probe or screen for a compound with improved characteristics, such as greater efficacy, safety, solubility, etc. A preferred inhibitory compound is a compound that is efficacious when administered to an animal in an amount that results in a serum concentration of from about 1 nanomolar (nM) to 100 micromolar (μM), with a

5   concentration of from about 10 nM to 10 μM being more preferred.

One embodiment of the present invention is a method to identify a compound that inhibits the binding between an IgE antibody and a FcεRIα protein. Such a method includes the step of using a 3-D model substantially representing the atomic coordinates specified in Table 1, Table 5, Table 6, Table 7, or Table 8 to identify such a compound.

10   Included in the present invention are inhibitory compounds that interact directly with the IgE binding domain or the receptor binding domain of the IgE antibody as well as compounds that interact indirectly with an FcεRIα protein, such as compounds that interact with the D1D2 interface, with the cleft between D1 and D2, with a region not consisting of a N-linked glycosylation site, with a region suggested by a combination of

15   3-D model and mutagenesis analysis to indirectly affect antibody binding, a region suggested by homology with other FcεRIα proteins of other species, a region suggested by homology with other FcRs. In a preferred embodiment, an inhibitory compound interacts with at least one of the following regions of a model representing a FcεRIα protein: a A'B loop of D1, a EF loop of D1, a BC loop of D2, a C strand of D2, a CC'

20   loop of D2, a C'E loop of D2, a F strand of domain D2, a FG loop of D2, and a tryptophan-containing hydrophobic ridge. It is to be noted that the A'B and EF loops of D1 are immediately adjacent to the IgE binding domain in D2 and as such are predicted, for the first time, by the model to be good targets for inhibitory compounds. In a preferred embodiment, an inhibitory compound of the present invention interacts with at

25   least one amino acid that is a crystal contact as predicted by the atomic coordinates listed in Table 1, Table 5, Table 6, Table 7 or Table 8. Inhibitory compounds of the present invention preferably interact with at least one of the following amino acid residues: amino acid 87, 110, 113, 115, 117, 118, 120, 121, 122, 123, 128, 129, 131, 149, 153, 154, 155, 156, 157, 158, and 159 of SEQ ID NO:2 or SEQ ID NO:4, as well as any

30   surface residue within about 10 angstroms of any of the listed amino acids. More

preferred is an inhibitory compound that interacts with at least one amino acid that is a crystal contact predicted to also be part of the IgE binding domain. Particularly preferred are amino acids 87, 117, 121, 123, 128, 159 of SEQ ID NO:2 or SEQ ID NO:4 as well as any surface residue within about 10 angstroms of amino acids 87, 117, 121,

5   123, 128, 159 of SEQ ID NO:2 or SEQ ID NO:4. In one embodiment, an inhibitory compound of the present invention is a peptide corresponding to at least a portion of any of the identified regions or a derivative thereof, such as a peptide mimetic or other compound that mimics that peptide. Preferred is a peptide corresponding to at least a portion of the FG loop of D2, or a derivative thereof, such as a peptide mimetic or other

10   compound that mimics that peptide.

One embodiment of a method to identify a compound that inhibits the binding between an IgE antibody and a FcεRIα protein includes the steps of: (a) generating a model substantially representing the atomic coordinates listed in Table 1, Table 5, Table 6, Table 7, or Table 8, or a model of an IgE binding domain thereof, on a

15   computer screen; (b) generating the spacial structure of a compound to be tested; and (c) testing to determine if the compound interacts with said IgE binding domain, wherein such an interaction indicates that the compound is capable of inhibiting the binding of an IgE antibody to a FcεRIα protein. In a preferred embodiment, step (a) includes the step of identifying one or more amino acid(s) in the IgE binding domain of the model that

20   interact directly with the Fc domain of an IgE antibody when the Fc domain binds to the IgE binding domain. Preferably a compound to be tested will interact directly with one or more of those amino acid(s). Preferred amino acids with which an inhibitory compound should interact are disclosed herein.

The present invention also includes inhibitory compounds isolated in accordance

25   with the methods disclosed herein. Methods to produce such compounds in quantities sufficient for use, for example, as protective agents (e.g., preventatives or therapeutics) are known to those skilled in the art. It should also be appreciated that it is within the scope of the present invention to expand the use of models of the present invention to produce models of any suitable FcRs (i.e., model modifications) and to identify

30   compounds that inhibit the binding of antibodies to such FcRs.

The present invention also includes use of a 3-D model of the present invention to rationally design and construct modified forms of FcRs that have one or more improved functions, such as, but not limited to, increased activity, increased stability and increased solubility compared to an unmodified FcR. Muteins of the present invention include full-length proteins as well as fragments (i.e., truncated versions) of such

5   proteins.

One embodiment of the present invention is a FcR that comprises a mutein that binds to a Fc domain of an antibody. Such a mutein has an improved function compared to a protein comprising SEQ ID NO:2 or SEQ ID NO:4. Examples of such an improved

10   function include, but are not limited to, increased stability, increased affinity for an Fc domain of an antibody, altered substrate specificity, and increased solubility. Such a mutein can be produced by a method that includes the steps of: (a) analyzing a 3-D model substantially representing the atomic coordinates specified in Table 1, Table 5, Table 6, Table 7, or Table 8 to identify at least one amino acid of the protein represented

15   by the model which if replaced by a specified amino acid would effect the improved function of the protein; and (b) replacing the identified amino acid(s) to produce a mutein having the improved function. Knowledge of the coordinates allows one to target specific residues, e.g. in the hydrophobic core or on the surface, to generate an accessible set of variants that can then be selected for a particular property, e.g. high

20   stability, high affinity, altered substrate specificity, or other desirable properties (i.e., improved functions). Without the coordinates, one would have to analyze an extraordinarily large number of variants, e.g., on the order of ~10^{11} possibilities. The structure, in contrast, allows one to pick the most relevant residues for selecting a desired property by, for example, phage display or other methods. In a preferred

25   embodiment, replacement of one or more amino acids does not substantially disrupt the 3-D structure of the protein; i.e., the modified protein, or mutein, is still capable of binding to the Fc domain of an antibody. A preferred mutein is a FcR that binds to a Fc domain of an IgE antibody, although the invention also covers muteins binding to other classes of antibodies.

30   In one embodiment, a mutein of the present invention has increased stability compared to its unmodified counterpart. As used herein, increased stability refers to the

ability of a mutein to be more resistant, for example, to higher or lower temperature, to more acidic or basic pH, to higher or lower salt concentrations, to oxidation and/or reduction, to deamidation, to other forms of chemical degradation and to proteolytic degradation compared to unmodified FcR. Increased stability can also refer to the ability

5   of a mutein of the present invention to be stable for a longer period of time either during storage (i.e., to have a longer shelf life) or during use (i.e., to have a longer half-life under reaction conditions) than does an unmodified protein. Muteins of the present invention can also exhibit a decreased entropy of unfolding, thereby stabilizing the proteins. Increased stability can be measured using a variety of methods known to those

10 skilled in the art; examples include, but are not limited to, determination of melting temperature, thermal denaturation, pressure denaturation, enthalpy of unfolding, free energy of the protein, or stability in the presence of a chaotropic agents such as urea, guanidinium chloride, guanidinium thiocyanate, etc. A preferred mutein of the present invention has a melting temperature substantially higher than that of an unmodified FcR.

15 Preferably the melting temperature of a mutein is at least about 1°C higher, and more preferably at least about 10°C higher than the melting temperature of the corresponding unmodified protein. Also preferred is a mutein having binding activity over a pH range that is at least about 1 pH unit higher and/or lower than the active pH range of the corresponding unmodified protein.

20   Another embodiment of the present invention is a mutein that exhibits increased affinity for a Fc domain of an antibody compared to its unmodified counterpart. As used herein, a mutein having increased affinity is a FcR that exhibits a higher affinity constant (K_A) or lower dissociation constant (K_D) than its unmodified counterpart. Such a higher affinity constant can be achieved by increasing the association rate (k_a) between the

25 mutein and the Fc domain and/or decreasing the dissociation rate (k_d) between the mutein and the Fc domain. A preferred mutein of the present invention has a K_A for a Fc domain of at least about 3×10^9 liters/mole (M^{-1}), which is equivalent to a K_D of less than or equal to about 3.3×10^{-10} moles/liter (M). More preferred is a mutein having a K_A for a Fc domain of at least about 2×10^{10} M^{-1}, and even more preferably of at least

30 about 1×10^{11} M^{-1}. Also preferred is a mutein having a k_a for a Fc domain of at least about 1×10^5 liters/mole-second as well as a mutein having a k_d for a Fc domain of less

than or equal to 3×10^{-5}/second. More preferred is a mutein having a k_a for a Fc domain of at least about 3×10^5 liters/mole-second, and even more preferably of 1×10^6 liters/mole-second. Also preferred are muteins having a k_d for a Fc domain of less than or equal to 1×10^{-5}/second or even more preferably less than or equal to 3×10^{-4}/second.

A preferred Fc domain is that of an IgE antibody. Methods to measure such binding constants is well known to those skilled in the art; see, for example, Cook et al., 1997, *ibid.*, which reports the following values for the binding of human FceRIα protein to human IgE: k_{a1} of 3.5 ($\pm$0.9) $\times 10^5$ M^{-1}s^{-1}; k_{a2} of 8.6 ($\pm$3.5) $\times 10^4$ M^{-1}s^{-1}; k_{d1} of 1.2 ($\pm$0.1) $\times 10^{-2}$ s^{-1}; k_{d2} of 3.2 ($\pm$0.8) $\times 10^{-5}$ s^{-1}; K_{A1} of 2.0 $\times 10^7$ M^{-1}; K_{A2} of 2.9 $\times 10^9$ M^{-1}.

Another embodiment of the present invention is a mutein that exhibits altered substrate specificity compared to its unmodified counterpart. A mutein exhibiting altered substrate specificity is a mutein that binds with increased affinity to a Fc domain of an antibody class or antibody species of a different type than that normally bound by its unmodified counterpart. In one embodiment, a mutein of a human FceRIα protein with altered substrate specificity is a FcR that binds with increased affinity to a IgE antibody of another mammal, such as, but not limited to, a canine, feline, equine, murine, or rat IgE antibody. In another embodiment, a mutein of a human FceRIα protein with altered substrate specificity is a FcR that binds with increased affinity to an antibody of another class, such as IgG, IgM, IgA, or IgD, with IgG being preferred. Such a mutein can also show altered species substrate specificity. Methods to determine whether a mutein exhibits altered substrate specificity are well known to those skilled in the art.

Yet another embodiment of the present invention is a mutein that exhibits increased solubility compared to its unmodified counterpart. Such a protein is less likely to form aggregates. Methods to determine whether a mutein exhibits increased solubility are well known to those skilled in the art.

As disclosed herein, the 3-D model representing a FceRIα protein is advantageous in determining strategies for producing muteins having an improved function, e.g., for identifying targets to modify in order to obtain muteins having improved functions. Examples of targets are as follows. A key feature of the human FceRIα$_{1-176}$ protein or the FceRIα$_{1-172}$ protein is the crystal contacts in five space groups,

a subset of which are predicted to interact directly with a Fc domain of an IgE antibody. Such contacts are included in the IgE binding domain which is unique for human FcεRIα in that the domain includes a tryptophan-containing hydrophobic ridge positioned on the top face of the crystal structure (i.e., amino acids W87, W110, W113, and W156 of SEQ ID NO:2 or SEQ ID NO:4) and an FG loop comprising amino acids from 155 to 158 of SEQ ID NO:2 or SEQ ID NO:4 that protrudes above the interface in an unusual manner. Another key feature is the interface between domain 1 and domain 2 (i.e., the D1D2 interface) which includes amino acids 12, 13, 14, 15, 16, 17, 18, 20, 84, 85 and 86 in D1 and 87, 88, 89, 90, 91, 92, 93, 95, 104, 106, 108, 110, 111, 161, 163, 164, and 165 in D2 of SEQ ID NO:2 or SEQ ID NO:4. Also importa... are the two domains themselves: D1 includes amino acids 1 through 86 of SEQ ID NO:2 or SEQ ID NO:4; and D2 includes amino acids 87 through 176 of SEQ ID NO:2 or amino acids 87 through 172 of SEQ ID NO:4. Another important feature is the cleft between D1 and D2, which can be identified using the coordinates. Other areas of interest include the hydrophobic core which can be identified using the coordinates, the A'B loop of D1, which includes amino acids 18 and 19, the EF loop of D1, which includes amino acids 59-63, the BC loop of D2, which includes amino acids 110-114, the C strand of D2, which includes amino acids 114-123, the CC' loop of D2, which includes amino acids 123-125, the C'E loop of D2, which includes amino acids 127-134, in the different confirmations observed in the five crystal forms, and the F strand of D2, which includes amino acids 147-155 of SEQ ID NO:2 or SEQ ID NO:4. Yet another striking feature is the finding that the amino and carboxyl termini of the human FcεRIα$_{1-176}$ protein are only 10 angstroms apart.

In accordance with the present invention, a mutein having an improved function can be produced by a method that includes replacing at least one amino acid based on information derived from analyzing a 3-D model of the present invention to produce the mutein having the improved function. Knowledge of the structure of the extracellular domain of a human FcεRIα protein crystal, for example, permits the rational design and construction of modified forms of the protein by permitting the prediction and production of substitutions, insertions, deletions, inversions and/or derivatizations that effect an improved function. That is, analysis of 3-D models of the present invention

provide information as to which amino acid residues are important and, as such, which amino acids can be changed without harming the protein. In making amino acid replacements, it is preferred to use amino acid replacements that have similar numbers of atoms and that allow conservation of salt bridges, hydrophobic interactions and

5   hydrogen bonds unless the goal is to purposefully change such interactions. The 3-D structure of the human FcεRIα protein suggests that large deletions may not be desirable, particularly due to the relation between the various domains of the protein and the observation that most of the structure is well ordered in the crystal. An exception to this is the non-constrained loops of D1, which apparently could be deleted or shortened

10 without harming the protein's function. These loops span amino acids 31-35 and 70-74 of SEQ ID NO:2 or SEQ ID NO:4.

It is to be appreciated that although one amino acid replacement capable of improving the function of a protein can substantially improve that function, more than one amino acid replacement can result in cumulative changes depending on the number

15 and location of the replacements. For example, although one amino acid replacement capable of substantially increasing the stability of a protein can increase the melting temperature of that modified protein by about 1°C, about 5 to about 6 replacements may increase the melting temperature of the resultant protein by about 10°C.

In accordance with the present invention, the 3-D model of the human FcεRIα

20 protein has been analyzed, using techniques known to those skilled in the art, to determine the accessibility of the amino acids represented within the model to solvent. Such information is provided in, for example, Table 2, Table 9, Table 10, Table 11, and Table 12.

A number of methods can be used to produce muteins of the present invention.

25 One method includes the steps of: (a) analyzing a 3-D model substantially representing the coordinates specified in Table 1, Table 5, Table 6, Table 7, or Table 8 to identify at least one amino acid of the modeled protein which if replaced by a specified amino acid would effect an improved function; and (b) replacing the identified amino acid(s) to produce a mutein having that improved function. In one embodiment, a method to

30 produce a mutein includes the steps of (a) comparing a key region of a model of a human FcεRIα protein with the amino acid sequence of a FcR having an improved function

compared to the unmodified FcεRIα protein in order to identify at least one amino acid segment of the FcR with the improved function that if incorporated into the FcεRIα protein represented by the model would give the FcεRIα protein the improved function; and (b) incorporating the segment into the FcεRIα protein, thereby providing a mutein with the improved function. In another embodiment, a method to produce a protein includes the steps of: (a) using a model representing a human FcεRIα protein to identify a 3-D arrangement of residues that can be randomized by mutagenesis to allow the construction of a library of molecules from which a improved function can be selected; and (b) identifying at least one member of the mutagenized library having the improved function. In one example, a mutein is produced by a method that includes the steps of: (a) effecting random mutagenesis of nucleic acid molecules encoding a target of a FcεRIα protein as identified by analyzing a model of that protein, such as an IgE binding domain; (b) cloning such mutagenized nucleic acid molecules into a phage display library, wherein said phage display library expresses the target; and (c) identifying at least one member of the library that expresses a target with an improved function, such as an antibody binding domain exhibiting increased affinity for an antibody. As stated above, the model allows the use of this technique in a straightforward manner that could not be accomplished in the absence of the model. It is to be also noted that these methods can also be used with other models of the present invention to produce muteins of the present invention.

The present invention includes a number of methods, based on analysis of a 3-D model of the present invention, to replace (i.e., add, delete, substitute, invert, derivatize) at least one amino acid residue in the protein represented by the model in order to produce a mutein of the present invention. Such methods include, but are not limited to: (a) replacing at least one amino acid in at least one non-constrained loop of domain 1 in an area proximal to the FcεRI gamma chain putative binding site; (b) joining an amino-terminal amino acid residue to a carboxyl-terminal amino acid residue of an extracellular domain of a FcεRIα protein; (c) replacing at least one amino acid site with an amino acid suitable for derivatization; (d) replacing at least one pair of amino acids of the protein with a cysteine pair to enable the formation of a disulfide bond that stabilizes the protein; (e) removing at least a portion of the region between the B strand and C strand

of domain 1; (f) removing at least a portion of the region between the C strand and E strand of domain 1; (g) replacing at least one amino acid in the IgE binding domain in order to increase the affinity between an IgE antibody and the protein; (h) replacing at least one amino acid of the protein with an amino acid such that the replacement

5   decreases the entropy of unfolding of the protein; (i) replacing at least one asparagine or glutamine of the protein with an amino acid that is less susceptible to deamidation than is the amino acid to be replaced; (j) replacing at least one methionine, histidine or tryptophan with an amino acid that is less susceptible to an oxidation or reduction reaction than is the amino acid to be replaced; (k) replacing at least one arginine of the

10   protein with an amino acid that is less susceptible to dicarbonyl compound modification than is the amino acid to be replaced; (l) replacing at least one amino acid of the protein susceptible to reaction with a reducing sugar sufficient to reduce protein function with an amino acid less susceptible to that reaction; (m) replacing at least one amino acid of the protein with an amino acid capable of increasing the stability of the inner core of the

15   protein; (n) replacing at least one amino acid of the protein with at least one N-linked glycosylation site; (o) replacing at least one N-linked glycosylation site of the protein with at least one amino acid that does not comprise an N-linked glycosylation site; and (p) replacing at least one amino acid of the protein with an amino acid that reduces aggregation of the protein.

20   Amino acid replacements can be carried out using recombinant DNA techniques known to those skilled in the art, including site-directed mutagenesis (e.g., oligonucleotide mutagenesis, random mutagenesis, polymerase chain reaction (PCR)-aided mutagenesis, gapped-circle site-directed mutagenesis) or chemical synthetic methods of a nucleic acid molecule encoding the desired protein, such as, but not limited

25   to a human FcεRIα protein, followed by expression of the mutated gene in a suitable expression system, preferably an insect, mammalian, bacterial, yeast, insect, or mammalian expression system. See, for example, Sambrook et al., *ibid.*

One embodiment of the present invention is a mutein in which at least one amino acid in at least one non-constrained loop of a FcεRIα protein is replaced in order to

30   improve a function of the protein. Finding that the human FcεRIα protein had such loops was surprising, and it is believed, without being bound by theory, that a mutein in

which at least a portion of at least one such loop is replaced, would at least exhibit enhanced stability. In a preferred embodiment, at least a portion of one or more of such loops is (are) deleted. Preferred loops to replace are in domain 1 (i.e., spanning amino acids 31-35 and 70-74 of SEQ ID NO:2 or SEQ ID NO:4), preferably in an area

5   proximal to the FcεRI gamma chain putative binding site, i.e., the site on the FcεRIα protein to which the gamma chain of the high affinity Fc epsilon receptor is thought to bind. In a preferred embodiment, one or more amino acids is replaced to make loops shorter, but including 1 or 2 hydrophobic residues to pack toward the protein interior and at least one hydrophilic residue to maintain solubility.

10   Another embodiment of the present invention is a mutein of the extracellular domain of a FcεRIα protein in which an N-terminal (amino-terminal) amino acid residue is joined, preferably covalently, to a C-terminal (carboxyl-terminal) amino acid residue in order to improve a function of the protein. Finding that the N-termini and C-termini of the human FcεRIα protein were only 10 angstroms apart was quite surprising.

15   Without being bound by theory, it is believed that such a mutein would at least exhibit enhanced stability. Furthermore, a covalent linker used to join the termini could also include a substance useful, for example, to anchor a mutein on a surface, as would be useful, for example, in a diagnostic assay, or to label the mutein. For a protein consisting of SEQ ID NO:2, a preferred N-terminal residue is an amino acid residue at

20   position 1, 2, or 3 of SEQ ID NO:2, and a preferred C-terminal residue is an amino acid residue at position 174, 175, or 176 of SEQ ID NO:2. Covalent linkage can be accomplished by methods known to those skilled in the art, such as, but not limited to, adding one or more N-terminal and C-terminal cysteines and crosslinking them with chemical compounds, adding additional residues in the coding sequence to allow the

25   formation of a disulfide bond, or adding one or more lysines and coupling them through a 10 angstrom linker, and including non-natural amino acid analogues by synthetic methods or by a combination of biosynthetic and organosynthetic methods. Examples of a substance to add to a covalent linker includes: ligands useful in allowing for the attachment of a mutein to a surface, such as biotin and related compounds, avidin and

30   related compounds, metal binding compounds, sugar binding compounds, immunoglobulin binding domains, and other tag domains; and detectable markers, such

as enzyme labels, physical labels, radioactive labels, fluorescent labels, chemiluminescent labels, and chromophoric labels. Examples include, but are not limited to, alkaline phosphatase, horseradish peroxidase, digoxygenin, luciferase, other light-generating enzymes and magnetic beads. It is also to be noted that ligands can

5 function as detectable markers.

Another embodiment of the present invention is a mutein in which at least one amino acid is replaced with an amino acid suitable for derivatization. Muteins in which at least one amino acid is replaced with an amino acid suitable for derivatization include proteins that are chemically modified (e.g., a lysine already existing on the protein is

10 modified) as well as those in which an amino acid residue is replaced with a different amino acid residue (e.g., a glycine with a lysine) as well as proteins to which a substance is added, preferably to the amino or carboxyl terminus of the protein. Examples of such substances include ligands and detectable markers as disclosed above. Preferable amino acids to replace include residues that are solvent exposed (e.g., those listed in Table 2,

15 Table 9, Table 10, Table 11, or Table 12), but that are preferably not within about 10 angstroms of the IgE binding domain. In one embodiment, a glycosylation site, or other solvent exposed site, is replaced with a charged or polar residue to increase solubility or create more stable muteins. Glycosylation sites in human FcεRIα protein include amino acids 21, 42, 50 74, 135, 140, and 166 of SEQ ID NO:2 or SEQ ID NO:4. A preferred

20 amino acid to use as a replacement, or to chemically modify directly, includes a cysteine or a lysine, with a cysteine being preferred. Compounds to use in chemical derivatizations are known to those skilled in the art; cysteines can, for example, be derivatized with maleimides.

Another embodiment of the present invention is a mutein in which a pair of

25 amino acids have been replaced with a cysteine pair in order to improve the function of the mutein, at least by increasing stability. Cysteine pairs can be substituted into a FcεRIα protein at any two residue positions identified with available programs and algorithms that would allow the formation of an undistorted disulfide bridge. In one embodiment, a serine and lysine near the termini of the protein is each replaced with a

30 cysteine. In another embodiment, cysteine pairs are replaced with other amino acids, such as serines to eliminate non-essential disulfide bonds.

Another embodiment of the present invention is a mutein in which at least one amino acid is replaced in the region between the B strand and C strand of domain 1 and/or the region between the C and E strand of domain 1. In a preferred embodiment, at least a portion of such a region is deleted.

5   Another embodiment of the present invention is a mutein in which at least one amino acid is replaced in the IgE binding domain in order to increase the affinity between an IgE antibody and the protein. Preferred residues to replace are in or near the IgE binding domain, or IgE binding site, as determined by analysis of the 3-D model. Such residues are preferably within about 10 angstroms of residues identified by

10   mutagenesis and further shown by model to be in an IgE binding site. Examples of such residues include amino acids 87, 110, 113, 115, 117, 118, 120, 121, 122, 123, 128, 129, 131, 149, 153, 154, 155, 156, 157, 158, and 159 of SEQ ID NO:2 or SEQ ID NO:4, and amino acids within 10 angstroms of such listed amino acids. In one embodiment, preferred amino acids to replace include amino acids 87, 115, 117, 118, 120-123, 128,

15   129, 131, 149, 153, 155 and 159 of SEQ ID NO:2 or SEQ ID NO:4 as well as any surface residue within about 10 angstroms of any of the listed amino acids, with amino acids 87, 117, 121, 123, 128, 159 of SEQ ID NO:2 or SEQ ID NO:4 as well as any surface residue within about 10 angstroms of amino acids 87, 117, 121, 123, 128, 159 of SEQ ID NO:2 or SEQ ID NO:4 being particularly preferred. It is to be noted that amino

20   acids 115, 118, 120, 131, 149 and 155 of SEQ ID NO:2 or SEQ ID NO:4 are buried, and that amino acids that are partially buried or glycine include residues 122, 129 and 153. Additional amino acid residues to target include those in the A'B loop of D1, and EF loop of D1. Note that these residues are not the same as those shown in mutation studies to affect IgE binding since some of those mutants have mutations in amino acids that are

25   internal to the protein; this finding can only be made by analysis of a model of the present invention.

Another embodiment of the present invention is a mutein in which at least one amino acid is replaced with an amino acid capable of increasing the stability of the inner core or surface of the protein. Preferred amino acids to replace are hydrophilic residues

30   located in the hydrophobic core of the protein and/or hydrophobic amino acids at the protein surface that are not within about 10 angstroms of the IgE binding domain

residues of D1 or D2. Preferred amino acids to replace into the hydrophobic core are hydrophobic residues such as, but not limited to, tryptophan, leucine, isoleucine, valine and alanine, as well as space filling amino acids, such as other aromatic amino acids. Preferred amino acids to replace onto the surface are polar amino acids, such as, but not

5 limited to, glutamic acid, glutamine, aspartic acid, asparagine, histidine and serine. Muteins having one or more such amino acid replacements would exhibit at least increased stability and/or reduced aggregation. Additional preferred amino acid replacements are those that introduce salt bridges at the protein surface to stabilize protein folds. It is noted that the cysteines at positions 26 and 68 of SEQ ID NO:2 or

10 SEQ ID NO:4 form a disulfide bond in domain 1 that is somewhat exposed to solvent, depending especially on the conformation of the D1 "30 loop" (i.e., amino acids 31-35 of SEQ ID NO:2 or SEQ ID NO:4). In one embodiment, changes in neighboring residues can be made in, for example, residues 1-5, 27-37, 49-52, or 69-75, to bury this disulfide from exposure to solvent. For example, phage display of receptors with

15 randomized mutations in the 30 loop, might be useful for selecting receptors that react less well with reducing reagents and have a more stable D1 core.

      Another embodiment of the present invention is a mutein in which at least one amino acid is replaced with an amino acid that decreases the entropy of unfolding of the protein. The entropy of unfolding of a protein can be measured and compared to that of

20 another protein using techniques known to those skilled in the art. A number of methods known to those skilled in the art can be used to reduce the number of protein conformations possible in the unfolded state, thereby improving the ability of the protein to fold correctly. One embodiment of the present invention for decreasing the entropy of unfolding includes replacing at least one amino acid of the protein with a specified

25 amino acid in order to maintain certain desirable phi and psi backbone conformation angles in the protein; see, for example, PCT International Publication No. WO 89/01520, by Drummond et al., published February 23, 1989. For example, a proline residue in a protein constrains the backbone conformation to certain restricted angles. Analysis of a 3-D model of a protein of the present invention permits the identification

30 of candidate replacement positions in the protein that have the conformation expected for a proline, but that do not have a proline in them. Such knowledge is used to

introduce prolines into such candidate replacement positions to "anchor" the resultant mutein in the desired conformation. The 3-D model also permits the identification of candidate replacement sites that if replaced with a proline do not substantially disrupt the 3-D structure of the resultant protein. Similarly, glycines in appropriate positions can be

5 replaced with an amino acid having a β carbon atom or a branched β carbon atom, preferably an alanine, in order to stabilize the backbone of the protein.

Another embodiment of the present invention is a mutein in which at least one asparagine or glutamine is replaced with an amino acid that is less susceptible to deamidation. Preferred amino acids to replace include solvent accessible asparagines

10 and glutamines.

Another embodiment of the present invention is a mutein in which at least one methionine, histidine or tryptophan is replaced with an amino acid that is less susceptible to an oxidation or reduction reaction. Preferred amino acids to replace include M98, H70, and H41. It would not be preferred to replace any of the tryptophans,

15 nor H108 or H134 of SEQ ID NO:2 or SEQ ID NO:4.

Another embodiment of the present invention is a mutein in which at least one arginine is replaced with an amino acid that is less susceptible to dicarbonyl compound modification. Although R174 could be changed, it would probably not be preferable to change amino acids at the D1D2 interface or near the IgE binding site, such as amino

20 acids 15, 106, or 111 of SEQ ID NO:2.

Another embodiment of the present invention is a mutein in which at least one amino acid that is susceptible to reaction with a reducing sugar sufficient to reduce protein function is replaced with an amino acid that is less susceptible to such a reaction. For example, lysines, glutamines and asparagines that could react with a sugar, such as

25 galactose, glucose or lactose can be replaced with non-reactive amino acids.

Another embodiment of the present invention is a mutein in which one or more N-linked glycosylation sites are added to or removed from the protein, preferably by substitution with an appropriate amino acid. A FcεRIα protein with additional N-linked glycosylation sites is more soluble. The ability to design a FcεRIα protein having fewer,

30 or no, N-linked glycosylation sites is also valuable as production of such a protein from production run to production run is likely to be more uniform. One embodiment is a

FcεRIα mutein with no N-linked glycosylation sites that is stable, active, and soluble. Such a protein has an advantage of being produced in *E. coli* at low cost. In one embodiment, one or more exposed hydrophobic amino acids are changed to charged residues that form salt bridges to stabilize the protein fold and make it soluble. It is to be

5   noted that the glycosylation sites that appear to be most often observed in the different crystal structures in the same conformation are the carbohydrate attached to positions 42 and 166 of SEQ ID NO:2 or SEQ ID NO:4. The carbohydrate attached to position 42 always appears to cover the phenylalanine at position 60 of SEQ ID NO:2 or SEQ ID NO:4. As such, one embodiment of the present invention is to remove the glycosylation

10   site at position 42, e.g., by substitution with a suitable amino acid. This embodiment has the additional advantage that the resultant mutein has an exposed phenylalanine at position 60, thereby leading to increased IgE binding activity.

Another embodiment of the present invention is a mutein in which at least one amino acid is replaced with an amino acid that reduces aggregation and increases

15   solubility of the protein, such as, for example, replacing one or more hydrophobic residues on the surface with one or more hydrophilic residues. Other examples of such amino acids to replace are disclosed herein.

Another embodiment of the present invention to enhance stability is the addition of polyethylene glycol (PEG) groups to a FcR protein, i.e., to produce a "pegylated" FcR

20   protein. In one embodiment, the PEG group(s) can substitute for carbohydrate group(s) due to removal of one or more N-glycosylation sites. Such PEG group(s) can be attached to easily modifiable residues, such as cysteines or lysines, on the surface of the protein, such residues identifiable by analysis of a 3-D model of the present invention.

Another embodiment of the present invention is a mutein that comprises a FcR

25   having a substance, such as a ligand or detectable marker, attached to an amino acid of the protein such that the substance does not substantially interfere with the antibody binding activity of the protein. The substance is attached in such a manner that the substance is also capable of performing its function, such as binding to a second member of a ligand pair or enabling detection of the protein. The FcR to which a substance is

30   attached can be either an unmodified protein or a mutein of the present invention. Suitable attachment sites can be identified using 3-D models of the present invention.

Preferred attachment sites include solvent exposed amino acids, such as those listed in Table 2, Table 9, Table 10, Table 11, or Table 12. Substances can be attached, or conjugated, to the protein using techniques known to those skilled in the art. It is to be appreciated that a preferred method to attach a substance to an amino acid is to modify

5 that amino acid to have a reactive attachment site, such as is present on cysteine and lysine amino acids. As such, an attachment site comprising a solvent exposed amino acid refers to the nature of the amino acid prior to any modification required for attachment. Examples of suitable substances to attach to a FcR include any compound capable of binding to or reacting with another substance, such as those described for

10 attachment to a covalent linker.

It is to be appreciated that muteins of the present invention can include amino acids which are not modified because they would negatively impact the function of the protein. Such amino acids can be identified using a 3-D model of the present invention.

It should also be appreciated that it is within the scope of the present invention to

15 expand the use of models of the present invention to produce models of and make modifications to any suitable FcRs or other Ig domain-containing proteins to produce muteins having a desired function.

The present invention also includes nucleic acid molecules that encode muteins of the present invention as well as recombinant molecules and recombinant cells that

20 include such nucleic acid molecules. Methods to produce such proteins are also disclosed herein.

The present invention includes an isolated $Fc\epsilon RI\alpha$ protein that consists of SEQ ID NO:2, i.e., $PhFc\epsilon RI\alpha_{1-176}$. Also included in the present invention is a protein consisting of an extracellular domain of a $Fc\epsilon RI\alpha$ protein that is structurally homologous

25 to an isolated $Fc\epsilon RI\alpha$ protein consisting of SEQ ID NO:2. As used herein, a protein that is structurally homologous to $PhFc\epsilon RI\alpha_{1-176}$ is a protein that (a) includes both D1 and D2 domains, (b) shares at least about 30%, and preferably at least about 40%, amino acid sequence identity with SEQ ID NO:2, as determined using a ALIGN with default parameters, optimal global alignment of two sequences with no short-cuts, (c) displays a

30 substantially equivalent affinity for an IgE antibody as does a complete extracellular domain of the corresponding $Fc\epsilon RI\alpha$ protein, and (d) produces crystals having sufficient

quality to enable structure determination. Examples of such proteins include a human FcεRIα protein having SEQ ID NO:4, i.e., PhFcεRIα$_{1-172}$ and a human FcεRIα protein having an amino acid sequence that spans from amino acid 3 through amino acid 174 of SEQ ID NO:2, i.e., PhFcεRIα$_{3-174}$. It is to be noted that these examples are provided to

5   clarify the definition of a structurally homologous FcεRIα protein and are not intended to limit the scope of such proteins. That is, a FcεRIα protein that is structurally homologous to PhFcεRIα$_{1-176}$ is any mammalian FcεRIα protein having the listed characteristics. Preferred are human, canine, feline, equine, murine and rat proteins that are structurally homologous to PhFcεRIα$_{1-176}$. Also included herein are nucleic acid

10   molecules to encode such proteins as well as recombinant molecules and recombinant cells that include such nucleic acid molecules. Methods to produce such proteins are also disclosed herein. Preferably such proteins are produced in insect cells.

The present invention also includes a FcεRIα protein consisting of SEQ ID NO:4 except that the isoleucine at position 170 has been replaced by a cysteine. Also included

15   in the present invention is a protein consisting of an extracellular domain of a FcεRIα protein that is structurally homologous to an isolated FcεRIα protein consisting of SEQ ID NO:4 except that the isoleucine at position 170 has been replaced by a cysteine.

The present invention also includes the following novel structures as identified by a 3-D model of the present invention: a crystal contact cluster, preferably involved in

20   IgE binding; a tryptophan-containing hydrophobic ridge; a FG loop in D2; a D1D2 interface; a cleft between D1 and D2; a domain 1; a domain 2; a hydrophobic core; a A'B loop of D1; a EF loop of D1; a BC loop of D2; a C strand of D2; a CC' loop of D2; a C'E loop of D2; and a strand of D2. Also included herein are nucleic acid molecules to encode such structures as well as recombinant molecules and recombinant cells that

25   include such nucleic acid molecules. Also included are methods to produce such structures and models thereof.

The present invention also includes isolated nucleic acid molecules encoding proteins of the present invention, including, but not limited to, proteins comprising unmodified extracellular domains of FcRs, novel structures within such proteins, and

30   muteins. As used herein, an isolated nucleic acid molecule encoding a protein is a nucleic acid molecule that has been removed from its natural milieu. As such, "isolated"

does not reflect the extent to which the nucleic acid molecule has been purified. An isolated nucleic acid molecule can be DNA, RNA, or derivatives of either DNA or RNA.

A nucleic acid molecule encoding a mutein of the present invention can be produced by mutation of parental protein genes (e.g., unmodified or previously modified protein-encoding genes, or portions thereof) using recombinant DNA techniques heretofore disclosed or by chemical synthesis. Resultant mutein nucleic acid molecules can be amplified using recombinant DNA techniques known to those skilled in the art, such as PCR amplification or cloning (see, for example, Sambrook et al., *ibid.*), or by chemical synthesis. A mutein can also be produced by chemical modification of a protein expressed by a nucleic acid molecule encoding an unmodified protein or mutein-encoding gene.

Proteins of the present invention can be produced in a variety of ways, including production and recovery of recombinant proteins and chemical synthesis. In one embodiment, a protein of the present invention is produced by culturing a cell capable of expressing the protein under conditions effective to produce the protein, and recovering the protein. A preferred cell to culture is a recombinant cell that is capable of expressing the protein, the recombinant cell being produced by transforming a host cell with one or more nucleic acid molecules of the present invention. Transformation of a nucleic acid molecule into a host cell can be accomplished by any method by which a nucleic acid molecule can be inserted into a cell. Transformation techniques include, but are not limited to, transfection, electroporation, microinjection, lipofection, adsorption, and protoplast fusion. A recombinant cell may remain unicellular or may grow into a tissue, organ or a multicellular organism. Transformed nucleic acid molecules of the present invention can remain extrachromosomal or can integrate into one or more sites within a chromosome of a host cell in such a manner that their ability to be expressed is retained.

Suitable host cells to transform include any cell that can be transformed. Host cells can be either untransformed cells or cells that are already transformed with at least one nucleic acid molecule. Host cells of the present invention can be endogenously (i.e., naturally) capable of producing a protein of the present invention, but such cells are not preferred. Host cells of the present invention can be any cell that when transformed with a nucleic acid molecule of the present invention are capable of producing a protein of the

present invention, including bacterial, yeast, other fungal, insect, animal, and plant cells. Preferred host cells include bacterial, yeast, insect and mammalian cells, and more preferred host cells include *Escherichia*, *Bacillus*, *Saccharomyces*, *Pichia*, *Trichoplusia*, *Spodoptera* and mammalian cells. Particularly preferred host cells are *Trichoplusia ni* cells, *Spodoptera frugiperda* cells, and Chinese hamster ovary cells.

A recombinant cell is preferably produced by transforming a host cell with a recombinant molecule comprising a nucleic acid molecule of the present invention operatively linked to an expression vector containing one or more transcription control sequences. The phrase operatively linked refers to insertion of a nucleic acid molecule into an expression vector in a manner such that the molecule is able to be expressed when transformed into a host cell. As used herein, an expression vector is a DNA or RNA vector that is capable of transforming a host cell, of replicating within the host cell, and of effecting expression of a specified nucleic acid molecule. Expression vectors can be either prokaryotic or eukaryotic, and are typically viruses or plasmids. Expression vectors of the present invention include any vectors that function (i.e., direct gene expression) in recombinant cells of the present invention, including in bacterial, yeast, other fungal, insect, animal, and plant cells. Preferred expression vectors of the present invention can direct gene expression in bacterial, yeast, insect and mammalian cells.

Nucleic acid molecules of the present invention can be operatively linked to expression vectors containing regulatory control sequences such as promoters, operators, repressors, enhancers, termination sequences, origins of replication, and other regulatory control sequences that are compatible with the host cell and that control the expression of the nucleic acid molecules. In particular, recombinant molecules of the present invention include transcription control sequences. Transcription control sequences are sequences which control the initiation, elongation, and termination of transcription. Particularly important transcription control sequences are those which control transcription initiation, such as promoter, enhancer, operator and repressor sequences. Suitable transcription control sequences include any transcription control sequence that can function in at least one of the recombinant cells of the present invention. A variety of such transcription control sequences are known to those skilled in the art. Preferred

transcription control sequences include those which function in bacterial, yeast, insect and mammalian cells.

It may be appreciated by one skilled in the art that use of recombinant DNA technologies can improve expression of transformed nucleic acid molecules by manipulating, for example, the number of copies of the nucleic acid molecules within a host cell, the efficiency with which those nucleic acid molecules are transcribed, the efficiency with which the resultant transcripts are translated, and the efficiency of post-translational modifications. Recombinant techniques useful for increasing the expression of nucleic acid molecules of the present invention include, but are not limited to, operatively linking nucleic acid molecules to high-copy number plasmids, integration of the nucleic acid molecules into one or more host cell chromosomes, addition of vector stability sequences to plasmids, substitutions or modifications of transcription control signals (e.g., promoters, operators, enhancers), substitutions or modifications of translational control signals (e.g., ribosome binding sites, Shine-Dalgarno sequences), modification of nucleic acid molecules of the present invention to correspond to the codon usage of the host cell, deletion of sequences that destabilize transcripts, and use of control signals that temporally separate recombinant cell growth from recombinant protein production during fermentation. The activity of an expressed recombinant protein of the present invention may be improved by fragmenting, modifying, or derivatizing nucleic acid molecules encoding such a protein.

In accordance with the present invention, recombinant cells can be used to produce proteins by culturing such cells under conditions effective to produce such a protein, and recovering the protein. Effective conditions to produce a protein include, but are not limited to, appropriate media, bioreactor, temperature, pH and oxygen conditions that permit protein production. An appropriate medium refers to any medium in which a cell of the present invention, when cultured, is capable of producing the protein. An effective medium is typically an aqueous medium comprising assimilable carbohydrate, nitrogen and phosphate sources, as well as appropriate salts, minerals, metals and other nutrients, such as vitamins. The medium may comprise complex nutrients or may be a defined minimal medium. Cells of the present invention can be cultured in conventional fermentation bioreactors, which include, but are not limited to,

batch, fed-batch, cell recycle, and continuous fermentors. Culturing can also be conducted in shake flasks, test tubes, microtiter dishes, and petri plates. Culturing is carried out at a temperature, pH and oxygen content appropriate for the recombinant cell. Such culturing conditions are well within the expertise of one of ordinary skill in the art.

5   Depending on the vector and host system used for production, resultant proteins may either remain within the recombinant cell; be secreted into the fermentation medium; be secreted into a space between two cellular membranes, such as the periplasmic space in *E. coli*; or be retained on the outer surface of a cell or viral membrane. The phrase "recovering the protein" refers simply to collecting the whole

10   fermentation medium containing the protein and need not imply additional steps of separation or purification. Proteins of the present invention can be purified using a variety of standard protein purification techniques, such as, but not limited to, affinity chromatography, ion exchange chromatography, filtration, electrophoresis, hydrophobic interaction chromatography, gel filtration chromatography, reverse phase

15   chromatography, chromatofocusing and differential solubilization.

     The present invention also includes isolated (i.e., removed from their natural milieu) antibodies that selectively bind to a FcR of the present invention (i.e., anti-FcR antibodies). As used herein, the term "selectively binds to" FcR refers to the ability of antibodies of the present invention to preferentially bind to specified proteins of the

20   present invention. Binding can be measured using a variety of methods standard in the art including enzyme immunoassays (e.g., ELISA), immunoblot assays, etc.; see, for example, Sambrook et al., *ibid.* Isolated antibodies of the present invention can include antibodies in a bodily fluid (such as, but not limited to, serum), or antibodies that have been purified to varying degrees. Antibodies of the present invention can be polyclonal

25   or monoclonal. Functional equivalents of such antibodies, such as antibody fragments and genetically-engineered antibodies (including single chain antibodies or chimeric antibodies that can bind to more than one epitope) are also included in the present invention. Antibodies can be produced using methods known to those skilled in the art.

     A preferred method to produce antibodies of the present invention includes

30   (a) administering to an animal an effective amount of a protein of the present invention to produce the antibodies and (b) recovering the antibodies. In another method,

antibodies of the present invention are produced recombinantly using techniques as heretofore disclosed to produce proteins of the present invention. Antibodies raised against defined proteins can be advantageous because such antibodies are not substantially contaminated with antibodies against other substances that might otherwise cause interference in a diagnostic assay or side effects if used in a therapeutic composition.

Antibodies of the present invention have a variety of potential uses that are within the scope of the present invention. Examples of such uses are disclosed in WO 98/27208, *ibid.*, see, for example, page 24.

A FcR of the present invention can include chimeric molecules comprising at least a portion of a FcR that binds to an antibody and a second molecule that enables the chimeric molecule to be bound to a substrate in such a manner that the antibody receptor portion binds to the antibody in at least as effective a manner as a FcR that is not bound to a substrate. An example of a suitable second molecule includes a portion of an immunoglobulin molecule or another ligand that has a suitable binding partner that can be immobilized on a substrate, e.g., biotin and avidin, or a metal-binding protein and a metal (e.g., His), or a sugar-binding protein and a sugar (e.g., maltose).

The present invention includes uses of proteins, antibodies and inhibitory compounds of the present invention for the diagnosis and treatment of allergy and the regulation of other immune responses in an animal.

One embodiment is a therapeutic composition comprising at least one of the following therapeutic compounds: an inhibitory compound of the present invention, a mutein of the present invention, or an antibody of the present invention. Also included is a method to protect an animal from allergy or other abnormal immune responses. Such a method includes the step of administering a therapeutic composition of the present invention to the animal. As used herein, the ability of a therapeutic composition of the present invention to protect an animal from allergy or other abnormal immune responses refers to the ability of that composition to, for example, treat, ameliorate or prevent allergy or other abnormal immune responses. General characteristics of therapeutic compositions and methods to produce and use such therapeutic compositions are disclosed, for example, in WO 98/27208, *ibid.*, see, for example, page 39-47. It is to

be noted that although the compositions and methods disclosed in WO 98/27208, *ibid.*, relate to feline FcεRIα proteins, they are also applicable to therapeutic compositions of the present invention. Therapeutic compositions of the present invention are advantageous because they can be derived from analysis of 3-D models of the present invention and have improved functions, such as efficacy and safety.

Another embodiment is a diagnostic reagent comprising a mutein of the present invention. As used herein, a diagnostic reagent is a composition that includes a mutein that is used to detect allergy or other abnormal immune responses in an animal. Also included in the present invention are methods, including *in vivo* methods and *in vitro* methods, to (a) detect allergy or other abnormal immune response, or susceptibility thereto, in an animal, comprising use of a diagnostic reagent comprising a mutein of the present invention and (b) to enhance the performance of an IgE binding assay, said method comprising incorporating into the assay a mutein of the present invention. General characteristics of diagnostic reagents and methods to produce and use such diagnostic reagents are disclosed, for example, in WO 98/27208, *ibid.*, see, for example, page 2-39. It is to be noted that although the reagents and methods disclosed in WO 98/27208, *ibid.*, relate to feline FcεRIα proteins, they are also applicable to diagnostic reagents, kits and detection methods of the present invention. Muteins of the present invention are advantageous in such applications because of their enhanced affinity for antibodies, altered specificity, enhanced solubility and/or enhanced stability, enabling for example use in otherwise adverse conditions and longer shelf-life.

The following examples are provided for the purposes of illustration and are not intended to limit the scope of the invention.

EXAMPLES

<u>Example 1</u>

This Example describes the production of a FceRIα nucleic acid molecule, a recombinant molecule, a recombinant cell, a recombinant virus, and a FceRIα protein of the present invention.

A number of human FceRIα proteins of variable lengths (i.e., 171, 172, and 176 amino acids) were produced in a variety of cell lines (i.e., Chinese hamster ovary cells, *Pichia pastoris* yeast, *Spodoptera frugiperda* (*Sf9*) insect cells and *Trichoplusia ni* (Hi-5) insect cells). Due to a number of factors, however, including protein length, solubility, and extent and variability of glycosylation, only one FceRIα protein was useful in producing a crystal of sufficient quality for the first determination of a model of an extracellular domain of a FceRIα protein. The production of this protein is disclosed below.

A nucleic acid molecule comprising the first 176 amino acids of the mature form of the human FceRIα protein, nucleic acid molecule and protein designated herein as nhFceRIα$_{1-528}$ and PhFceRIα$_{1-176}$, respectively, was produced as follows. An *EcoRI-HindIII* fragment from plasmid EdpC20 (Blank et al., *ibid.*) containing the human FceRIα signal sequence and residues 1-172 of the mature human FceRIα protein was ligated to two oligonucleotides coding for residues 172-176 of the mature protein and two stop codons. The two oligonucleotides, having nucleic acid sequences of 5' AGCTCCGCGT GAGAAGTAAT AAG 3' (SEQ ID NO:5) and 5' GATCCTTATT ACTTCTCACG CGG 3' (SEQ ID NO:6), had *HindIII* and *BamHI* overhangs when annealed together, which permitted the ligation of nhFceRIα$_{1-528}$ into *EcoRI* and *HindIII* cleaved baculovirus transfer vector pVL1392 (available from Pharmingen, San Diego, CA) to produce recombinant molecule pVL1392-nhFceRIα$_{1-528}$. The resultant construct was verified by DNA sequencing.

Recombinant virus was produced as follows. Recombinant molecule pVL1392-nhFceRIα$_{1-528}$ was co-transfected with a linear Baculogold baculovirus DNA (available from Pharmingen) into *S. frugiperda* Sf9 cells to form recombinant cell *Sf9*:pVL1392-nhFceRIα$_{1-528}$ which was cultured to produce recombinant virus, namely BV:pVL1392-nhFceRIα$_{1-528}$ using techniques known to those skilled in the art. Supernatants of

transfected $Sf9$:pVL1392-nhFcεRIα$_{1-528}$ cells were amplified once in TNM-FH medium

(available from Pharmingen), followed by a second amplification in serum-free medium

(SF-900, available from Gibco, Gaithersburg, MD) in a final volume of about 500

milliliters (ml). For $Sf9$:pVL1392-nhFcεRIα$_{1-528}$ cells grown in shaker flasks, TNM-FH

5   medium was supplemented with pluronic F-68 (available from Pharmingen). For each

virus stock used in protein production, the optimal amount of virus and harvest time

post-infection was determined by small scale tests in 50 ml shaker flasks.

Recombinant protein PhFcεRIα$_{1-176}$ was produced as follows. *Trichoplusia ni*

(Hi-5) cells were infected with recombinant virus BV:pVL1392-nhFcεRIα$_{1-528}$ that had

10   been produced as described above to produce recombinant cell Hi-5:pVL1392-

nhFcεRIα$_{1-528}$. Recombinant cell Hi-5:pVL1392-nhFcεRIα$_{1-528}$ was grown in shaker or

spinner flasks for production of PhFcεRIα$_{1-176}$. Typical yields of PhFcεRIα$_{1-176}$ were

about 2 to 12 milligrams per liter (mg/liter) of infected cells 2 to 4 days after infection.

Recombinant protein PhFcεRIα$_{1-176}$ was purified as follows. Supernatants from

15   1.5 to 5 liters of recombinant Hi-5:pVL1392-nhFcεRIα$_{1-528}$ cells were collected, filtered

through 0.2 micron filters, and loaded directly onto a Mab15-1 (Sechi et al., 1996, *J.*

Biol. Chem. 271, 19256-19263) monoclonal antibody column. Supernatants were

recirculated over the column at least twice, followed by buffer (100 millimolar (mM)

Na, K phosphate, pH 7) washes of about 300 ml, until the absorbance at 280 nanometers

20   (nm) of the eluant returned to zero. PhFcεRIα$_{1-176}$ was eluted by two urea washes: 100 ml

of 5 molar (M) urea in 100 mM phosphate, pH 7.0; then 100 ml of 7 M urea in 100 mM

phosphate, pH 7.0; followed by extensive regeneration with 100 mM Na, K phosphate,

pH 7.0. The urea eluants were pool~~ concentrated to about 25 to 40 ml with an Amicon

stirring concentrator, and dialyzed 4 times against 2 liters of 50 mM Tris, pH 7.5. The

25   purity of PhFcεRIα$_{1-176}$ was verified by SDS-PAGE. Purified PhFcεRIα$_{1-176}$ was stored

at 4°C in the presence of 0.05% sodium azide. Final yield of PhFcεRIα$_{1-176}$ was about

50% based on an absorption coefficient of 2.6 mg^{-1}ml for the purified protein and the

initial total protein estimated using ELISA assays with the initial cell supernatants.

An inhibition-ELISA assay was used to quantitate PhFcεRIα$_{1-176}$ expression and

30   yields in initial transfected supernatants, subsequent viral amplifications and large scale

protein preparations. In this assay, the binding of Mab15-1 antibody to the plated

PhFcεRIα$_{1-176}$ protein was monitored using a goat anti-mouse-alkaline phosphatase antibody (A-2429, available from Sigma, St. Louis, MO). Unknown samples were used to compete for antibody binding and compared with a standard curve generated in parallel. Fifty microliters (ml or mL) of purified PhFcεRIα$_{1-176}$ was incubated in

5   microtiter plates overnight at 4°C at a concentration of 1 mg/ml in phosphate-buffered saline. Plates were rinsed with wash buffer containing 20 mM Hepes, pH 7.5, 100 mM NaCl, 0.1% Tween-20 (Hepes/NaCl buffer) and blocked with Hepes/NaCl buffer containing 1% Carnation dry milk. Standard inhibitor samples ranging from 0.1-50 mg/ml of PhFcεRIα$_{1-176}$ in two-fold dilution series were incubated with Mab15-1 (0.1

10   mg/ml final concentration) and added in duplicate to wells coated with PhFcεRIα$_{1-176}$. Standard controls included wells without overnight incubation with PhFcεRIα$_{1-176}$, and addition of Mab15-1 without inhibiting PhFcεRIα$_{1-176}$. Secondary antibody in a 1:5000 dilution was incubated after washing for 12 hour at room temperature. Plates were washed and developed using the AP reagent p-nitrophenyl phosphate (PNPP, available

15   from Sigma 104-105). Microplates were read using a Molecular Devices SpectraMax Plus reader at 405 nm.

Example 2

This Example describes the production of a FcεRIα protein crystal of the present invention.

20   Purified PhFcεRIα$_{1-176}$, produced as described in Example 1, was concentrated to a final concentration of 20 mg/ml in 20 mM Tris pH 7.5. Crystallization was carried out using the hanging drop method, with a precipitant composed of 100 mM Tris, pH 8.5, 200 mM NaOAc, and 18-24% PEG 4000. Crystals were obtained in 2 to 10 days amidst significant amounts of protein precipitate. At lower PEG concentrations, a different

25   crystal form was observed. The crystals used in the structure determination typically grow as clusters of 3 to 20 crystals that could be separated manually. The crystals belong to the monoclinic space group C2, with cell dimensions of 88.6 x 69.6 x 49.3 angstroms, alpha=gamma=90 degrees, beta=116.7 degrees, with one receptor molecule per asymmetric unit. Such crystals diffracted to a resolution of about 2.4 angstroms.

30   Crystals were harvested into harvest buffer containing 35% PEG 4000, 100 mM Tris pH 8.5. It is to be noted that the inventors produced and tested several hundred crystals

using the various other proteins described in Example 1, before successfully obtaining the crystal described immediately above.

Example 3

        This Example describes the production of additional FcεRIα protein crystals of

5   the present invention.

        Nucleic acid molecule nhFcεRIα$_{1-516}$, encoding the first 172 amino acids of the human FcεRIα protein was expressed in *T. ni* Hi-5 cells to produce PhFcεRIα$_{1-172}$ in a manner similar to that described for the production of PhFcεRIα$_{1-176}$ in Example 1. Purified PhFcεR$^{I\sim}$$_{1-172}$ was concentrated to a final concentration of 20 mg/ml in 20 mM

10   Tris pH 7.5. Crystallization was carried out using the hanging drop method, with a precipitant composed of 0.1-0.2 M NaAcetate, 0.1M Na Citrate, pH 5.6, 18-24% PEG, and HECAMEG detergent at it's Critical Micelle concentration (19.5 mM). Crystals were obtained in 2 to 10 days amidst significant amounts of protein precipitate. The crystals belong to the monoclinic space group P6122 with unit cell dimensions of 58 x

15   58 x 226 angstroms, alpha=beta=90 degrees; gamma=120 degrees, with one receptor molecule per asymmetric unit. Such crystals diffracted to a resolution of about 3.2 angstroms.

        Using a different protocol, purified PhFcεRIα$_{1-176}$, produced as described in Example 1, was concentrated to a final concentration of 10 mg/ml in 20 mM Tris pH

20   7.5. Crystallization was carried out using the hanging drop method, with a precipitant composed of 100 mM Tris, pH 7.5, 0-20% isopropanol, and 18-24% PEG 4000. Crystals were obtained in 2 to 10 days amidst significant amounts of protein precipitate. The crystals belong to the monoclinic space group C2, with cell dimensions of 136.02 x 75.01 x 79.28 angstroms, alpha=gamma=90 degrees; beta=117.8 degrees. Such crystals

25   diffracted to a resolution of about 3.0 angstroms.

Example 4

        This Example describes the production of a three-dimensional model of the present invention.

        For data collection, crystals, produced as described in Example 2, were mounted

30   in nylon loops (available from Hampton-Research, Laguna Niguel, CA) and rapidly cooled in liquid nitrogen after a short (about 30 second) soak in harvest buffer

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supplemented with 14% glycerol. Heavy atom soaks with K_2PtBr_4 and K_3AuCl_3 were
done in harvest buffer with 5 mM Pt for 48 hours and 1 mM Au for 18 days. Data were
collected at the Stanford Synchrotron Radiation Laboratories (SSRL) 7-1 beamline and
at the Dupont-Northwestern-Dow undulator beamline at the Advanced Photon Source at
5   Argonne National Laboratories. The statistics for these data are shown in Table 3.

Table 3. Crystallographic data and model refinement

	Native	SeM	Pt
Resolution	2.4Å	3.0Å	4.0Å
Wavelength/Energy (Å/keV)	1.08/11.48	1.02/12.12	1.05/11.76
Completeness , % (Last Shell)	96.9 (92.5)	99.9 (100.0)	96.3 (69.9)
Ave. Redundancy (Last Shell)	3.9 (3.4)	7.6 (7.3)	6.2 (2.7)
Rmerge, % (last shell)	5.7 (22.6)	10.1 (39.8)	5.1 (7.0)
<I/sI> (last shell)	23.8 (4.5)	19.0 (3.9)	35.2 (15.9)
DF/F (Resolution)	-	0.218 (20-3Å)	0.093 (20-4Å)
No. of sites	-	1	1
Phasing Power acentric/centric	-	1.50/1.93	0.41/0.61
Rcullis acentric/centric	-	0.66/0.70	0.94/0.97

Overall Figure of Merit   =   0.487
FOM after DM =   0.673

Refinement Statistics: 500-2.4Å

# Reflections (free)	=	10247 (880)
Rfactor/Rfree, %	=	24.2/27.1
#atoms	=	1620
#waters	=	126
RMSD bonds	=	0.0077Å
RMSD angles	=	1.53°
Ave. B	=	65.7Å²

$R_{merge} = S|I_i - <I>|/S|I|$, where I_i is the intensity of and individual reflection and $<I>$ is the average intensity of that reflection.

$R_{cryst} = S|F_p| - |F_c|/S|F_p|$, where F_c is the calculated and F_p is the observed structure factor amplitude.

Phasing Power = F_{hcalc}/E, where F_{hcalc} = the heavy atom structure factor amplitude and E = the residual lack of closure error.

$R_{cullis} = S||F_{ph} \pm F_p| - |F_{hcalc}||/S|F_{ph} \pm F_p|$, where F_{ph} is the derivative structure factor amplitude.

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For the Pt and Au datasets, the wavelength was chosen to be 200 eV above the absorption edge of the metal, in order to maximize the anomalous signal for each heavy atom. Heavy atom data were collected using reverse beam protocols to optimize the anomalous diffraction signal. Diffraction data were collected with a Mar300 Image plate

5   (SSRL) or a MarCCD detector (DND-CAT), and integrated and scaled with DENZO/SCALEPACK; see, Otwinowski et al., 1997, In *Methods in Enzymology: Macromolecular Crystallography*, part A, Academic Press, pp 307-326. The CCP4 suite of programs (Collaborative Computational Project, 1994, *Acta Cryst. D50*, 760-763) was used for further processing and identification of heavy atom sites.

10   Heavy atom positions were identified from peaks in the anomalous and isomorphous difference patterson maps. Heavy atom positions were refined and phases calculated with the program MLPHARE, followed by solvent flattening and density modification with the program DM (Collaborative Computational Project, 1994, *ibid.*). The subsequent model was using the CNS program (Brunger et al., 1998, *Acta*

15   *Crystallogr D Biol Crystallogr 54*, 905-921) with the combined maximum likelihood and experimental phase target (MLHL). Specifically, the structure of the FcεRIα protein PhFcεRIα$_{1-176}$ was determined by multiple isomorphous replacement using gold and platinum heavy atom derivatives with the anomalous signal from both derivatives. The data collection and heavy atom phasing statistics are shown in Table 3. The MIRAS

20   phases were used as input to the density modification program DM and the electron density map was of sufficient quality that the entire model except for two flexible loops and five residues at the termini could be built; see Fig. 1A and 1B. The model was further improved by cycles of automated refinement using the program CNS followed by manual rebuilding. The current R-factor and Rfree are 24.2% and 27.1% respectively for

25   all the data to 2.4 angstroms. No electron density was observed for three residues at the N-terminus (1-3) and 2 residues at the C-terminus (175-176), and poor density was observed for two loops (residues 32-35 and 70-73) that are disordered in the crystal. Final statistics for the model are shown in Table 3.

Example 5

30   This Example describes the structure of a FcεRIα protein predicted by a three-dimensional model of the present invention.

A. Overall structure

The model of extracellular domain of the human FcεRIα protein, also referred to herein as the hFcεRIα model or hFcεRIα structure, indicates that PhFcεRIα$_{1-176}$ is composed of two immunoglobulin (Ig) domains, D1 and D2, each about 85 residues in length, that are bent at an acute angle relative to each other and form an extended convex surface; see Fig. 2. The domain arrangement generates a flat surface at the top of the receptor that has been implicated in binding to the Fc domain of an ιgE antibody. The domains are small compared to canonical variable and constant Ig domains and the shorter sequence is accommodated by truncation of the CC'E crossover region; see Fig. 2. Both domains D1 and D2 of the hFcεRIα model are composed of beta-strands AA'BCC'EFG, differing from the previously described I-set domains (Harpaz et al., 1994, *J. Mol. Biol. 238*, 528-539) by the absence of strand D. The nearly antiparallel domain packing places the A'B, CC' and EF loops of D1 and the BC, C'E and FG loops of D2 near the top of the receptor; see Fig. 2. One feature of the topology is a crossover of the A strand from the ABE sheet to the CC'FG sheet, forming a short segment of parallel beta sheet in an otherwise antiparallel structure; see Fig. 2 and Fig. 3. In D1, the AA' crossover make contacts in the D1D2 interface (see below), while in the D2 domain, residues in the A strand interact with D1; see Fig. 3.

Significant structural differences are also observed between D1 and D2 of the hFcεRIα model. The D1 and D2 sequences contain about 28% identical residues and superimpose with an RMS deviation of 1.2 angstroms for the Cα atoms. The F-G strands and loop differ between the two domains. In D2, these strands are longer and the FG loop projects above the D2 domain surface. The C' strands also differ between the two domains. In D2, a series of aromatic residues (tyrosines at positions 120 and 131) form a hydrophobic core that pushes the C' strand and loop away from the C strand, altering the local conformation of this region. The FG loop and C-C' strands of D2 form part of the binding site for IgE (see below).

The tertiary packing arrangement of the hFcεRIα D1 and D2 domains is distinct from other tandem Ig domain structures; see Fig. 4. Comparison of the hFcεRIα model with other bent two-Ig domain structures reveals a high degree of variability in the bend angles and packing surfaces between domains. A subset of D1 and D2 representative

structures of are shown in Fig. 4, including those from human FcεRIα (designated as IgE-FcR), the natural killer cell inhibitory receptor, (KIR, Fan et al., 1997, *Nature 389*, 96-100), the human growth hormone receptor (HGHBP, de Vos et al., 1992, *Science 255*, 306-312), the interleukin-1 receptor, (IL1R, Vigers et al., 1997, *Nature 386*, 190-
5   194) and the insect defense protein hemolin (Su et al., 1998, *Science 281*, 991-995). The structures are oriented similarly with respect to the carboxyl-termini of the two Ig domains being compared. The figures on top show side views and the figures below show top views. The FcεRIα and hemolin structures have the most acute angles relating two sequential Ig domains. The top view of these domains shows that the orientation of
10   the hemolin and FcεRIα domains are more closely related, but between this selected subset of proteins there is significant variability in the relative orientations of tandem Ig domain structures. The bend angle between domains and domain packing interfaces are clearly unique, and this variation is likely to be important in ligand binding interactions. For example, the FG loop of D2 in hFcεRIα is oriented quite differently with respect to
15   D1 residues as compared to the same region of the KIR or HGHBP, thus changing the spatial relationships of D1D2 loops that may be involved in ligand interactions. To the inventors' knowledge, the hFcεRIα structure defines a new group of two sequential Ig domain structures that differs from other known tertiary arrangements.

B.   The D1D2 interface

20   The bent shape of the FcεRIα structure produces a large interface between the D1D2 domains that buries 1280 $Å^2$ of accessible surface area of 28 D1D2 residues. There are 11 residues from the D1 domain (12-18, 20, 84-86) and 17 residues from the D2 domain that are buried at the interface (87-93, 95, 104, 106, 108, 110-111, 161, 163-165). Of these 28 residues, 8 are completely conserved in all human FcgR and FcεRIα
25   sequences (corresponding to residues 13, 87, 88, 90, 91, 106, 108, 110 of SEQ ID NO:2); see Fig. 5. These conserved residues form a significant fraction to one side of the buried interface, suggesting that related FcRs would have a similar acute packing of the D1D2 domains as observed in the FcεRIα model.

       However, 20 residues that form the D1D2 interface in the FcεRIα model differ in
30   other FcRs and these differences could alter the relative orientations of the two domains. For example, the conserved tryptophan at position 110 packs against a phenylalanine at

position 17 of FceRIα. In related FcRs, this phenylalanine is changed to a leucine, which may lead to slight alterations in the packing of the two domains. Another central residue in the FceRIα D1D2 interaction is residue R15, which forms a hydrogen bond with the carbonyl of L90 and is packed against L89, F84, and L165. In related human

5   FcRs, arginine 15 is changed to serine or asparagine, which corresponds to a significant volume and charge change at the center of the D1D2 interaction. Since the interactions of the FcR with antibody are near the D1D2 interface, alterations in residues at the interface might influence receptor specificity. Other residues that are variable amongst the FcR sequences in the region of the D1D2 could also perturb the D1D2 interactions.

10   The bent hFceRIα structure generates a cleft between the two domains that is near the trans-membrane anchor at the C-terminus of D2; see Fig. 2. This cleft is located far from the IgE binding site identified by mutagenesis studies (see below). Although there is no known function attributed to this region, while not being bound by theory, it is believed that this region could be a site of interaction with the extracellular regions of

15   the beta or gamma subunits of the receptor. It has been suggested that interactions between the FcgRI and FcgRIIIA alpha and gamma subunits increase the binding affinity of the receptor for IgG (Miller et al., 1996, *J. Exp. Med. 183*, 2227-2233). Although the extracellular regions of the human FceR gamma chain are short (about 5 to 7 amino acids), these regions could potentially interact with the D1D2 cleft and thereby affect the

20   affinity of the receptor for antibody. In addition, recent binding studies with recombinant, soluble FceRIα and IgE have demonstrated a 10-fold lower affinity than had previously been determined in cell-binding assays (Cook et al., 1997, *ibid.*).

C. Carbohydrate attachment sites

The human FceRIα protein PhFceRIα$_{1-176}$ is the most highly glycosylated protein

25   structure solved by X-ray crystallography to date, having seven N-linked glycosylation sites in 176 amino-acid residues. The intact FceRIα on mast cells is approximately 40% carbohydrate by weight (Kanellopoulos, et al., 1980, *E. J. Biol. Chem. 255*, 9060-9066); LaCroix, et al., 1993, *ibid.*), with a heterogeneous molecular weight on SDS-PAGE gels of about 50 kilodaltons (kD). Human FceRIα expressed in insect cells has a molecular

30   weight of about 34 kD as observed using SDS-PAGE, but, based on typical insect cell glycosylation structures ($-GlcNAc_2-Man_3-GlcNAc$), could be expected to have a

molecular weight of about 27.5 kD, suggesting the protein is about 30% carbohydrate by weight. While the presence of carbohydrate at the seven N-glycosylation sites is not required for binding to IgE (Letourneur et al., 1995, *ibid.*; Robertson, 1993, *ibid.*; Scarselli et al., 1993, *ibid.*), mutation of these sites or treatment of FceRI-expressing

5   cells with tunicamycin leads to the aggregation of the receptor during biosynthesis.

In the hFcεRIα structure, carbohydrate density is observed at three of the seven predicted glycosylation sites. For two of these sites, asparagines 42 and 166, three sugar moieties were built. The carbohydrate at position 42 extends up towards the top of the FcεRIα structure, covering residues F60, S63 and V83. The carbohydrate attached to

10 position 166 projects away from the protein surface, potentially as a result of crystal contacts and the modification of the third and sixth positions of the first GlcNac residue. The third carbohydrate attachment site is the arginine at position 21.

Many of the related FcR proteins are also highly glycosylated proteins and the glycosylation sites vary between receptors. Rat and mouse FcεRIα proteins each have six

15 potential N-linked glycosylation sites, of which two sites and one site, respectively are shared in common with the human FcεRIα protein. Comparison of seventeen human and animal FcR sequences identifies twenty-five different potential N-linked carbohydrate attachment sites in related FcRs. The twenty-five sites are distributed evenly between D1 and D2, with fourteen sites in D1 and eleven sites in D2. Five of

20 these sites are relatively well conserved sites in all FcRs (found in > 9/17 sequences analyzed) and they correspond to residues 35, 42, 61, 135, and 142 of SEQ ID NO:2. These sites cover a significant fraction of the FcεRIα surface on both major faces of D1 and D2, placing limitations on the surface available for interactions with antibody.

It is not known why FcRs are so heavily glycosylated. Many potential roles for

25 carbohydrate sites on proteins have been suggested, including specific roles in determining the tertiary (Wyss et al., 1995, *Science 269*, 1273-1278) or quaternary structures of proteins (Huber et al., 1976, *Nature 264*, 415-420; Vaughn et al., 1998, *Structure 6*, 63-73). In the case of the human FcRs, the number of potential N-linked glycosylation sites correlates to some degree with the affinity of the FcR for

30 immunoglobulin. Table 4 shows the number of glycosylation sites in the domains corresponding to the extracellular domain of the human FcεRIα protein along with the

total number of glycosylation sites in parentheses. Affinity data are taken from
Ravetch et al., 1998, *ibid.*; Ravetch et al., 1991, *Annu. Rev. Immunol. 9*, 457-492.

Table 4. Comparison of the number of predicted glycosylation sites and the affinity of different FcRs for antibody.

FcR	# CHO sites (total)	Affinity
Human		
FcεRI	7	high (10^{-9}-10^{-10}M)
FcγRIA (CD64)	5 (7)	high (3 domains, 10^{-8}-10^{-9}M)
FcγRIB (CD64)	5 (7)	high (3 domains, 10^{-8}-10^{-9}M)
FcγRIIA (CD32)	2 (3)	low (10^{-6}M)
FcγRIIB (CD32)	3	low (10^{-6}M)
FcγRIIC (CD32)	3 (4)	low (10^{-6}M)
FcγRIIIA (CD16)	5 (6 in variant)	low (10^{-6}M)
Mouse		
FcεRI	6	high (10^{-9}-10^{-10}M)
FcγRI	4(5)	high (3 domains, 10^{-7}-10^{-8}M)
FcγRIIb	4(5)	low (10^{-6}M)
FcγRIIIa	4	low (10^{-6}M)
Rat		
FcεRI	7	high (10^{-9}-10^{-10}M)
FcγRII	6 (7 total)	low
FcγRIII	5	low
Other		
FcγRII (guinea pig)	5(6)	low
FcγRIII (pig)	3	low
FcγRII (bovine)	6	low

In the high affinity FcRs, there are typically 5 to 7 potential N-linked glycosylation sites, whereas in the low affinity FcRs there are as few as two sites. One significant difference in the function of the high and low affinity FcRs is the probability that they will bind antibody in the absence of antigen. The high affinity receptors such as FcεRI can bind

5   IgE prior to interacting with antigens. While not being bound by theory, it is believed that since FcR activation requires crosslinking of receptors, glycosylation might prevent the aggregation of large antibodies at the cell surface bound by FcRs. Crystallization of proteins at lipid/water interfaces can occur readily, and the potentially high local concentrations of membrane-bound antibodies might lead to FcR activation in the

10 absence of antigen. The low affinity IgG receptors interact with antibody-antigen aggregates that can simultaneously bind and activate multiple FcRs. While not being bound by theory, it is believed that glycosylation may not be quite as important for these receptors, since interaction with the antibody could occur after the binding of antigen.

        However, it is likely that there are additional explanations for the glycosylation

15 that is observed in the FcRs. The non-human FcRs do not show an obvious correlation of the number of carbohydrate sites and FcR affinity. While not being bound by theory, it is believed that glycosylation might be important in FcR signaling, by orienting receptor:antibody complexes into functional signaling complexes (i.e. by preventing antigen-crosslinked complexes from forming non-functional aggregates). It is known

20 that activation through FcεRI is sensitive to some geometrical constraints imposed by antigen crosslinkers, although the nature of these physical constraints is poorly understood. The recent crystal structure determination of an erythropoietin-receptor complex suggests that the orientation of ligand-mediated dimerization of cell-surface receptors may be important in efficient signal transduction (Syed et al., 1998, *Nature*

25 *395*, 511-516).

    D. Receptor binding site for IgE (IgE binding domain)

        A number of mutagenesis studies have been carried out in an effort to elucidate the regions of the FcεRI that are critical for the interaction with IgE molecules (Cook et al., 1997, *ibid.*; Hulett et al., 1993, *ibid.*; Hulett et al., 1994, *ibid.*; Hulett et al.,

30 1995; Mallamaci et al., 1993, *ibid.*). These experiments have demonstrated an important

role for amino acids in the D2 domain of the receptor, although some regions of D1 are also likely to be involved in IgE binding. Studies suggesting that D1 plays a role in IgE binding include the deletion of D1 (Robertson, 1993, *ibid.*; Scarselli et al., 1993, *ibid.*) or substitution with a homologous IgG receptor (Hulett et al., 1994, *ibid.*). These experiments do not determine conclusively whether D1 interacts directly with the IgE or whether D1 indirectly alters the structure of D2 and subsequent interactions with IgE. Analysis of the hFcεRIα model of the present invention is needed to predict important IgE binding regions in the protein. For example, the substitution or elimination of residues at the D1D2 interface can influence D2 interactions with antibody Fc regions.

In addition, there are a number of regions of D1 which have been excluded as determinants of the specificity of the receptor for IgE, since these FcεRIα segments can be substituted by the corresponding residues in the FcgRIIIA protein (Mallamaci et al., 1993, *ibid.*). These residues include segments 25-38, 43-54, 67-79, and 77-86. Substitution of residues 10-21 or 55-67 disrupt the binding of IgE and 5 different monoclonal antibodies, suggesting that residue differences in these segments may affect the folding of hybrid molecules. The 3-D models of the present invention, however, are needed to conduct an amino acid by amino acid analysis of which residues actually directly interact with IgE antibodies.

The FcεRIα residues which have been implicated in past studies include residues in the D2 BC loop (amino acid 115), in the C strand (amino acids 117, 118, 120-123), in the C'E loop (amino acids 129, 131), the F strand (amino acids 149, 153) and the FG loop (amino acids 155 and 159) (Cook et al., 1997, *ibid.*; Hulett et al., 1994, *ibid.*; Hulett et al., 1995, *ibid.*). In addition, residues 87 (at the D1D2 interface) and 128 (in the C'E loop) are likely to be part of the IgE interaction site, since mutation of these residues have been shown to influence receptor binding to the IgE point mutant R334A (Cook et al., 1997, *ibid.*). Furthermore, a synthetic peptide corresponding to residues 119-129 has been demonstrated to block IgE binding to the FcεRIα, with an apparent K_D of about 3 mM (McDonnell et al., 1997, *ibid.*; McDonnell et al., 1996, *ibid.*).

Analysis of the hFcεRIα model, however, is needed to indicate that of the fifteen residues (i.e., amino acids 87, 115 117, 118, 120-123, 128, 129, 131, 149, 153, 155 and 159), six are buried in the protein core (i.e., amino acids 115, 118, 120, 131, 149, 155)

and predicts that substitution at these positions may lead to indirect structural changes that affect IgE binding. Three of the residues are either partially buried or glycine (i.e., amino acids 122, 129, 153), and substitution may affect the conformation of the local residues. The remaining residues (i.e., amino acids 87, 117, 121, 123, 128, 159) are all

5   exposed amino acids at the FcεRIα surface. All of the implicated residues form a contiguous surface extending from the back side of the D2 domain to the top region near the D1D2 interface. Four of the residues are conserved in all human FcRs (i.e., amino acids 87, 118, 149, and 153) and may define a set of common interactions between all FcR receptors and their target Ig molecules.

10   The hFcεRIα model also indicates that the region of the D2 domain defined by mutagenesis also borders on a number of surface accessible aromatic residues, including four prominent tryptophans at the top of the FcεRIα molecule, namely residues 87, 110, 113, and 156. These four tryptophans form a flat, hydrophobic ridge that neighbors the D2 FG loop. This unusual arrangement of four surface tryptophans probably forms a

15   contact surface for a complementary interaction with an IgE antibody. Tryptophan 87 has already been implicated by mutagenesis studies and tryptophan 156 is prominently displayed at the top of the FG loop. Tryptophan 156 is a glycine in all FcgRs and grafting of residues 154-161 of the FcεRIα FG-loop to FcgRII confers IgE binding. It is to be noted, however, that such a graft does not eliminate IgG binding. The hFcεRIα

20   model predicts that other amino acids, e.g., the tryptophan at residue 87, may be important for antibody class recognition specificity. Other exposed aromatic residues are found concentrated near the IgE binding domain; Fig 6 shows a surface representation of all of the exposed aromatic groups in the hFcεRIα structure, clearly outlining the tryptophan ridge and residues in D2 near the CC'E region.

25   E. Implications for the binding of other FcRs

           Since carbohydrate would be expected to disrupt any close-packed protein:protein interface, it is interesting to compare the known carbohydrate sites with the proposed IgE-binding site on the receptor surface as defined by models of the present invention. The positions of the carbohydrate attachment sites for seventeen related FcRs

30   indicated that the N-linked carbohydrate sites delineate a boundary around the proposed IgE binding site. This is consistent with the suggestion that related FcRs share a

common binding surface for antibody molecules. Studies of the FcgRII specificity for IgG, for example, have implicated the following residues: amino acids 113-116, 129, 131, 133, 134, 155, 156, and 159-161 (Hulett et al., 1994, *ibid.*; Hulett et al., 1995, *ibid.*). In addition, domain-swap experiments have demonstrated that two of the related

5   FcgRs can form functional hybrid molecules with FcεRIα (Hulett et al., 1995, *ibid.*; Mallamaci et al., 1993, *ibid.*), suggesting that these receptors share a common binding surface with their respective antibody ligands.   Once again, however, it should be noted that only with the model can one predict exactly which FcR residues directly interact with an Fc domain of an antibody.

10   The hFcεRIα model indicates that the top of the FcR structure is devoid of carbohydrate-attachment sites in the region of D2 that has been implicated in direct interactions with Ig molecules. The neighboring surface of the D1 domain including loops A'B and EF, are also devoid of carbohydrate and could form part of an extended antibody binding site across the D1D2 interface. If these D1 loops are important in

15   determining the specificity and affinity of the FcR:antibody interaction, one might observe sequence variability between high affinity and low IgG receptors and the IgE receptor. This variability in the human IgG and IgE receptors is shown in Fig. 5. For residues 3-173 of the hFcεRIα protein, there are 73 amino acid differences that are unique to the IgE receptor as compared to any of the IgG receptors and these are

20   indicated below the sequence alignments. Of these 73 amino acids unique to the human FcεRIα protein, 27 positions are highly variable in the different FcR sequences (> 4/7 different amino acids. There are five regions that stand out with clusters of variable residues : residues 27-30, 47-49, 54-5ɔ, 94-98 and 155-159. Residues 155-159 (the FG loop) are highly variable and do at least partially determine the specificity of FcR

25   interactions. It is again to be noted that without the model one cannot determine which regions of sequence variability are important in determining FcR protein functional domains.

          Previous experiments have shown that residues 27-30 and 47-49 are not critical for FcR specificity (Mallamaci et al., 1993, *ibid.*), and the presence of glycosylation sites

30   within these segments in related FcRs support the suggestion that these regions are not part of the FcR:antibody interaction. The hFcεRIα model indicates that residues 94-98

are found in the A' strand near the D1D2 cleft and therefore are not likely to interact with antibody directly, but these residues might influence interactions indirectly by altering the D1D2 packing interface.

The remaining group of highly variable residues (54-59) are in the D1 E strand
5   (see Fig. 7), near the FcεRIα binding site as predicted by the hFcεRIα model. Residues 54-59 could form a D1 surface of interaction with the Fc domains of antibodies, extending the binding site across both FcεRIα domains. This prediction is supported by a study reporting that the exchange of FcεRIα residues 55-67 with residues from the FcgRIIIA receptor disrupts the folding of the protein (Mallamaci et al., 1993, *ibid.*), as
10 some of the residue changes form part of the D1 hydrophobic core. The hFcεRIα model also predicts that the neighboring D1 A'B loop (residues 18-21) could also form part of an extended surface of interaction with the antibody. Thus, models of the present invention are needed to interpret data from mutagenesis and swapping experiments.

F. Stoichiometry of binding between FcR and antibody

15   The activation of FcR-bearing cells requires crosslinking of the receptors, which leads to the activation of intracellular kinase cascades analogous to those in B and T cells. For both high and low high affinity receptors FceRI and FcgRIII, a stoichiometry of 1:1 is observed between the receptor and the Fc domains of the respective antibodies to which they bind (Ghirlando et al., 1995, *Biochemistry 34*, 13320-13327;
20 Kanellopoulos et al., 1980, *ibid.*; Keown et al., 1997, *Eur. Biophys. J. 25*, 471-476), consistent with a requirement for antigen to cause receptor aggregation and activation. The binding site on the Fc domain of an IgE antibody for its receptor has been extensively studied by mutagenesis, implicating amino acids in the third constant domain (Ce3) of the IgE (Basu et al., 1993, *J. Biol. Chem. 268*, 13118-13127; Henry et
25 al., 1997, *Biochemistry 36*, 15568-15578; Nissim et al., 1991, *Embo J. 10*, 101-107; Presta et al., 1994, *J. Biol. Chem. 269*, 26368-26373). The structure of the Fc domain of IgE antibodies (also referred to as IgE-Fc domains) has not been experimentally determined, but is homologous to the Fc domain of IgG antibodies (also referred to as IgG-Fc domains), for which a number of crystal structures are available (Harris et al.,
30 1998, *J. Mol. Biol. 275*, 861-872; Huber et al., 1976, *Nature 264*, 415-420). The residues of the IgE-Fc domain implicated in binding to FceRs based on mutagenesis

analysis are shown mapped onto the structure of the IgG-Fc domain in Fig. 8. The site on an IgG-Fc domain to which FcgRI and FcgRII receptors bind has been mapped to a similar, although smaller, surface that primarily includes residues in the hinge region before the Cg2 domain (Canfield et al., 1991, *J. Exp.Med. 173*, 1483-1491; Duncan et

5 al., 1988, *Nature 332*, 563-564; Jefferis et al., 1990, *Mol. Immunol. 27*, 1237-1240; Lund et al., 1991, *J. Immunol. 147*, 2657-2662).

An antibody Fc domain is a homodimeric structure that is significantly larger than its respective FcR; see Fig. 8. The observed 1:1 stoichiometry between receptor and antibody indicates that the two-fold symmetry of the Fc domain does not lead to the

10 binding of two FcRs, even with isolated molecules in solution. Without being bound by theory, it is believed that the large and convex nature of the FcR binding surface could span two antibody domains (Cg2 in IgG and Ce3 in IgE) and induce a conformational change in the Fc domain that would prevent the binding of a second FcR to the same antibody. The FcR structure could also form an asymmetric complex with the antibody

15 that sterically blocks the binding of a second FcR, perhaps using the protruding FG loop to block symmetric interactions with the Fc hinge region.

<u>Example 6</u>

This Example describes the production of additional three-dimensional models of the present invention as well as descriptions of FcɛRIα proteins predicted therefrom.

20   A.   Production and description of a crystal of PhFcɛRIα$_{1-172}$ that belongs to tetragonal space group P4$_3$, with a=b=145.08Å, c=62.74Å, a=b=g=90° , referred to herein as crystal form T1

Protein PhFcɛRIα$_{1-172}$, having SEQ ID NO:4, was produced using techniques known to those skilled in the art by a lec1 Chinese hamster ovary (CHO) cell line

25 transformed with a nucleic acid molecule encoding the protein, i.e., a nucleic acid molecule comprising SEQ ID NO:3. Crystals were grown in a manner similar to that described in Example 2 via vapor diffusion using a well solution of 20% to 32% PEG 10000, 0.1 M ammonium citrate pH 5.6, and 0.1 M sodium chloride, and a protein starting concentration of 5 to 10 mg/ml. Other size PEGs from 4000 to 20000 were also

30 used, as well as sodium citrate pH 5.6 as a buffer. Other salts such as sodium acetate and ammonium sulfate were also used to grow crystals. The crystal used in the structure

determination, analyzed in a manner similar to that described in Example 4, had five

copies of the receptor in the crystallographic asymmetric unit and diffracted to a

maximum resolution of 3.1Å. This crystal form, form T1, was refined to a

crystallographic R_{free}/R_{work} of 32.78%/29.19% using all the observed data |F| > 0 to 3.1Å

5   and a non-crystallographic symmetry (NCS) restraint constant of 300 kcal/mol Å² for all

atoms. There were no waters included in the model. The atomic coordinates of

PhFcεRIα$_{1-172}$, form T1, are listed in Table 5. The solvent accessibilities of the amino

acids of PhFcεRIα$_{1-172}$, form T1, are indicated in Table 9. Table 13 provides

crystallographic data and model refinement statistics of PhFcεRIα$_{1-172}$, form T1. A root

10   mean square (rms) deviation analysis of the alpha carbon positions of PhFcεRIα$_{1-172}$,

form T1, as compared to PhFcεRIα$_{1-176}$, form M1, is shown in Table 14. The first line is

an overall rms on the segments that align in space. The second two lines are the rms

deviations for the loops when the molecules are superimposed according to the first

line. Only one copy of model in T1 is compared because the models do not differ by

15   much because of tight NCS restraints.

B.   Production and description of a crystal of PhFcεRIα$_{1-172}$ that belongs to

tetragonal space group P4$_3$, with a=b=150.50Å, c=74.18Å, α=β=γ=90° , referred to

herein as crystal form T2.

Protein PhFcεRIα$_{1-172}$, having SEQ ID NO:4, was produced using techniques

20   known to those skilled in the art by a lec1 Chinese hamster ovary (CHO) cell line

transformed with a nucleic acid molecule encoding the protein, i.e., a nucleic acid

molecule comprising SEQ ID NO:3. Crystals were grown and analyzed as described in

Example 6A. The crystal used in the structure determination had five copies of the

receptor in the crystallographic asymmetric unit and diffracted to a maximum resolution

25   of 3.8Å. This crystal form, form T2, was refined to a crystallographic R_{free}/R_{work} of

30.64%/27.99% using all the observed data |F| > 0 to 3.8Å and a NCS restraint constant

of 300 kcal/mol Å² for all atoms. There were no waters included in the model. The

atomic coordinates of PhFcεRIα$_{1-172}$, form T2, are listed in Table 6. The solvent

accessibilities of the amino acids of PhFcεRIα$_{1-172}$, form T2, are indicated in Table 10.

30   Table 13 provides crystallographic data and model refinement statistics of PhFcεRIα$_{1-172}$,

form T2. A rms deviation analysis of the alpha carbon positions of PhFcεRIα$_{1-172}$, form

T2, as compared to PhFcεRIα$_{1-176}$, form M1, is shown in Table 14.

       C.   Production and description of a crystal of PhFcεRIα$_{1-176}$ that belongs to

monoclinic space group C2, with a=136.90Å, b=73.79Å, c=79.40Å, α=γ=90°, and

5   β=117.74°, referred to herein as crystal form M2.

       Protein PhFcεRIα$_{1-176}$, having SEQ ID NO:2, was produced in *T. ni* Hi-5 cells as

described in Example 1. Crystals were grown in a manner similar to that described in

Example 2 via vapor diffusion using a well solution of 12% to 20% PEG 4000, 0.1 M

HEPES (or Tris) pH 7.5, and 0 to 10% isopropanol, and a protein starting concentration

10   of 5 to 30 mg/ml. The crystal used in the structure determination, analyzed in a manner

similar to that described in Example 4, had two copies of the receptor in the

crystallographic asymmetric unit and diffracted to a maximum resolution of 3.2Å. This

crystal form, form M2, was refined to a crystallographic R_{free}/R_{work} of 28.30%/25.69%

using all the observed data |F| > 0 to 3.2Å. A NCS restraint constant of 300 kcal/mol Å^2

15   has been imposed for all atoms except certain ones in loops and crystal contacts

(residues 1-3, 27-38, 41-43, 69-75, 87, 98, 111-117, 125-135, 144, 152-158 of SEQ ID

NO:2) and the N-linked carbohydrate atoms. There were no waters included in the

model. The atomic coordinates of PhFcεRIα$_{1-176}$, form M2, are listed in Table 7. The

solvent accessibilities of the amino acids of PhFcεRIα$_{1-176}$, form M2, are indicated in

20   Table 11. Table 13 provides crystallographic data and model refinement statistics of

PhFcεRIα$_{1-176}$, form M2. A rms deviation analysis of the alpha carbon positions of

PhFcεRIα$_{1-176}$, form M2, as compared to PhFcεRIα$_{1-176}$, form M1, is shown in Table 14.

       D.   Production and description of a crystal of PhFcεRIα$_{1-172}$ that belongs to

hexagonal space group P6$_1$22, with a=b=58.62Å, c=229.19Å, α=β=γ=90° , referred to

25   herein as crystal form H1.

       Protein PhFcεRIα$_{1-172}$, having SEQ ID NO:4 except that the isoleucine at position

170 was replaced with cysteine, was produced in a manner similar to that described in

Example 1, except that *Spodoptera frugiperda* Sf9 cells were used instead of *T. ni* Hi-5

cells. Crystals were grown in a manner similar to that described in Example 2 via vapor

30   diffusion using a well solution of 20% to 30% PEG 4000, 0.1 M sodium citrate pH 5.6,

-99-

0.1 M sodium chloride, and 5-40mM Methyl-6-O-(N-heptylcarbamoyl)-a-D-
glucopyranoside (HECAMEG), a protein starting concentration of 10 mg/mL. The
crystal used in the structure determination, analyzed in a manner similar to that
described in Example 4, had one copy of the receptor in the crystallographic asymmetric
5 unit and diffracted to a maximum resolution of 3.2Å. This crystal form, form H1, was
refined to a crystallographic R_{free}/R_{work} of 31.27%/28.78% using all the observed data |F|
> 0 to 3.2Å. The atomic coordinates of PhFcεRIα$_{1-172}$, form H1, are listed in Table 8.
The solvent accessibilities of the amino acids of PhFcεRIα$_{1-172}$, form H1, are indicated in
Table 12. Table 13 provides crystallographic data and model refinement statistics of
10 PhFcεRIα$_{1-172}$, form H1. A rms deviation analysis of the alpha carbon positions of
PhFcεRIα$_{1-172}$, form H1, as compared to PhFcεRIα$_{1-176}$, form M1, is shown in Table 14.

E.   The principal differences in the structures from the various crystal forms
occurred in the BC loop in domain 1 (the "30 loop"), the C' strand in domain 2 (the "130
region") and the carbohydrate sites. There were also smaller differences in the termini of
15 the structures and the FG loop in domain 1 (the "72 loop").

The 30 loop showed the greatest variability across the different space groups.
The density for this loop was often the poorest density in the map, suggesting that the
loop may vary in conformation even within a single crystal. In T1 and T2, the density for
this loop was higher than the rest (when the molecule was viewed in the normal
20 orientation, with the FG loop of domain 2 at the top and the cleft between the domains at
the bottom.) In the tetragonal cells, the 30 loop passed close to residue 51. In the two
copies of the receptor in the larger monoclinic cell M2, the 30 loop was pulled down by
crystallographic contacts. In these two copies, the density for the 30 loop clearly showed
the loop was pulled away from the rest of the molecule to reveal an empty space inside
25 the loop. The location of the 30 loops in H1 and M1 was intermediate to those of the
tetragonal cells and M2.

The 130 strand varied across the crystal forms as well. In T1, T2, and the B copy
in M2, this strand hydrogen bonded with the C strand in domain 2 to form a canonical
C' strand. In the H1 form, the strand crossed over to the other side of the sheet to form a
30 D strand. In the forms M1 and the A copy of M2, this strand was intermediate to a
canonical C' and D strand.

The density at the termini tended to be poorly ordered, but the M2 crystal showed density for the N-terminus. All of the other models began at amino acid 4. The M1 and M2 models were built to residue 174 out of 176 total residues, the H1 model was built to the C-terminal residue 172, and the two tetragonal forms have models that were built to

5   residue 171 out of 172 total residues.

Table 5. Atomic coordinates of PhFceRIα_{1-172}, Form T1

ATOM NUMBER	ATOM TYPE	RESIDUE		#	X	Y	Z	OCC	B
1	CB	LYS	C	4	14.321	45.864	45.068	1.00	151.11
2	CG	LYS	C	4	15.396	44.???	44.650	1.00	151.11
3	CD	LYS	C	4	16.203	44.418	45.852	1.00	151.11
4	CE	LYS	C	4	17.285	43.425	45.453	1.00	151.11
5	NZ	LYS	C	4	18.066	42.968	46.639	1.00	151.11
6	C	LYS	C	4	12.828	45.080	43.246	1.00	214.46
7	O	LYS	C	4	12.702	44.022	43.863	1.00	214.46
8	N	LYS	C	4	12.367	47.226	44.431	1.00	214.46
9	CA	LYS	C	4	13.426	46.310	43.920	1.00	214.46
10	N	PRO	C	5	12.448	45.209	41.965	1.00	98.70
11	CD	PRO	C	5	12.271	46.470	41.224	1.00	125.98
12	CA	PRO	C	5	11.863	44.086	41.229	1.00	98.70
13	CB	PRO	C	5	10.998	44.785	40.181	1.00	125.98
14	CG	PRO	C	5	11.793	45.9??	39.866	1.00	125.38
15	C	PRO	C	5	12.912	43.157	40.611	1.00	98.70
16	O	PRO	C	5	14.063	43.545	40.398	1.00	98.70
17	N	LYS	C	6	12.509	41.923	40.330	1.00	208.77
18	CA	LYS	C	6	13.417	40.948	39.747	1.00	208.77
19	CB	LYS	C	6	14.011	40.068	40.851	1.00	249.20
20	CG	LYS	C	6	15.074	39.104	40.363	1.00	249.20
21	CD	LYS	C	6	15.769	38.385	41.512	1.00	249.20
22	CE	LYS	C	6	16.860	37.456	40.986	1.00	249.20
23	NZ	LYS	C	6	17.633	36.780	42.068	1.00	249.20
24	C	LYS	C	6	12.709	40.087	38.703	1.00	208.77
25	O	LYS	C	6	11.779	39.341	39.022	1.00	208.77
26	N	VAL	C	7	13.159	40.207	37.454	1.00	73.65
27	CA	VAL	C	7	12.599	39.454	36.315	1.00	73.65
28	CB	VAL	C	7	13.163	39.923	34.968	1.00	90.39
29	CG1	VAL	C	7	12.395	39.255	33.860	1.00	90.39
30	CG2	VAL	C	7	13.095	41.425	34.847	1.00	90.39
31	C	VAL	C	7	12.876	37.955	36.338	1.00	73.65
32	O	VAL	C	7	14.017	37.539	36.224	1.00	73.65
33	N	SER	C	8	11.833	37.148	36.461	1.00	91.19
34	CA	SER	C	8	12.002	35.707	36.469	1.00	91.19
35	CB	SER	C	8	11.113	35.074	37.541	1.00	89.05
36	OG	SER	C	8	9.751	35.407	37.345	1.00	89.05
37	C	SER	C	8	11.625	35.174	35.091	1.00	91.19
38	O	SER	C	8	10.978	35.870	34.308	1.00	91.19
39	N	LEU	C	9	12.047	33.946	34.794	1.00	76.39
40	CA	LEU	C	9	11.750	33.300	33.511	1.00	76.39
41	CB	LEU	C	9	13.016	33.111	32.687	1.00	48.15
42	CG	LEU	C	9	13.863	34.301	32.245	1.00	48.15
43	CD1	LEU	C	9	14.684	33.924	31.048	1.00	48.15
44	CD2	LEU	C	9	12.964	35.448	31.863	1.00	48.15
45	C	LEU	C	9	11.124	31.922	33.685	1.00	76.39
46	O	LEU	C	9	11.321	31.262	34.690	1.00	76.39
47	N	ASN	C	10	10.380	31.476	32.687	1.00	56.03
48	CA	ASN	C	10	9.756	30.161	32.739	1.00	56.03
49	CB	ASN	C	10	8.459	30.216	33.531	1.00	97.06
50	CG	ASN	C	10	7.912	28.844	33.807	1.00	97.06
51	OD1	ASN	C	10	8.527	28.062	34.532	1.00	97.06
52	ND2	ASN	C	10	6.764	28.528	33.218	1.00	97.06
53	C	ASN	C	10	9.460	29.670	31.333	1.00	56.03
54	O	ASN	C	10	8.594	30.226	30.649	1.00	56.03
55	N	PRO	C	11	10.173	28.619	30.873	1.00	62.47
56	CD	PRO	C	11	10.022	28.168	29.482	1.00	141.22
57	CA	PRO	C	11	11.225	27.865	31.546	1.00	62.47
58	CB	PRO	C	11	11.726	26.836	30.444	1.00	141.22
59	CG	PRO	C	11	10.542	26.774	29.564	1.00	141.22
60	C	PRO	C	11	12.362	28.734	32.097	1.00	62.47
61	O	PRO	C	11	12.512	29.887	31.703	1.00	62.47
62	N	PRO	C	12	13.197	28.186	33.000	1.00	68.33
63	CD	PRO	C	12	13.127	26.826	33.565	1.00	71.60
64	CA	PRO	C	12	14.315	28.913	33.606	1.00	68.33

	65	CB	PRO	C	12	·14.839	27.958	34.664	1.00	71.60
	66	CG	PRO	C	12	13.707	27.044	34.925	1.00	71.60
	67	C	PRO	C	12	15.383	29.190	32.567	1.00	68.33
	68	O	PRO	C	12	16.176	30.127	32.696	1.00	68.33
5	69	N	TRP	C	13	15.395	28.352	31.538	1.00	58.74
	70	CA	TRP	C	13	16.378	28.444	30.466	1.00	58.74
	71	CB	TRP	C	13	16.076	27.401	29.401	1.00	68.19
	72	CG	TRP	C	13	15.812	26.077	29.969	1.00	68.19
	73	CD2	TRP	C	13	16.476	25.473	31.064	1.00	68.19
10	74	CE2	TRP	C	13	15.848	24.241	31.307	1.00	68.19
	75	CE3	TRP	C	13	17.547	25.852	31.873	1.00	68.19
	76	CD1	TRP	C	13	14.844	25.220	29.588	1.00	68.19
	77	NE1	TRP	C	13	14.848	24.114	30.391	1.00	68.19
	78	CZ2	TRP	C	13	16.252	23.380	32.324	1.00	68.19
15	79	CZ3	TRP	C	13	17.950	24.993	32.892	1.00	68.19
	80	CH2	TRP	C	13	17.300	23.771	33.107	1.00	68.19
	81	C	TRP	C	13	16.409	29.810	29.826	1.00	58.74
	82	O	TRP	C	13	15.409	30.264	29.288	1.00	58.74
	83	N	ASN	C	14	17.570	30.454	29.879	1.00	57.67
20	84	CA	ASN	C	14	17.729	31.775	29.295	1.00	57.67
	85	CB	ASN	C	14	18.371	32.746	30.304	1.00	148.07
	86	CG	ASN	C	14	19.809	32.414	30.614	1.00	148.07
	87	OD1	ASN	C	14	20.127	31.304	31.041	1.00	148.07
	88	ND2	ASN	C	14	20.692	33.383	30.408	1.00	148.07
25	89	C	ASN	C	14	18.508	31.761	27.990	1.00	57.67
	90	O	ASN	C	14	18.992	32.785	27.550	1.00	57.67
	91	N	ARG	C	15	18.645	30.590	27.378	1.00	58.44
	92	CA	ARG	C	15	19.311	30.455	26.078	1.00	58.44
	93	CB	ARG	C	15	20.634	29.728	26.174	1.00	68.23
30	94	CG	ARG	C	15	21.469	30.131	27.329	1.00	68.23
	95	CD	ARG	C	15	22.779	29.404	27.261	1.00	68.23
	96	NE	ARG	C	15	23.607	29.885	26.172	1.00	68.23
	97	CZ	ARG	C	15	24.492	29.119	25.560	1.00	68.23
	98	NH1	ARG	C	15	24.614	27.865	25.950	1.00	68.23
35	99	NH2	ARG	C	15	25.267	29.599	24.589	1.00	68.23
	100	C	ARG	C	15	18.345	29.540	25.394	1.00	58.44
	101	O	ARG	C	15	18.206	28.379	25.805	1.00	58.44
	102	N	ILE	C	16	17.648	30.048	24.386	1.00	56.07
	103	CA	ILE	C	16	16.691	29.214	23.693	1.00	56.07
40	104	CB	ILE	C	16	15.279	29.668	23.844	1.00	49.05
	105	CG2	ILE	C	16	14.939	29.490	25.385	1.00	49.05
	106	CG1	ILE	C	16	15.128	31.116	23.520	1.00	49.05
	107	CD1	ILE	C	16	13.760	31.675	23.801	1.00	49.05
	108	C	ILE	C	16	16.889	29.154	22.201	1.00	56.07
45	109	O	ILE	C	16	17.607	29.956	21.610	1.00	56.07
	110	N	PHE	C	17	16.221	28.178	21.608	1.00	80.97
	111	CA	PHE	C	17	16.247	27.906	20.188	1.00	80.97
	112	CB	PHE	C	17	15.846	26.458	19.984	1.00	52.57
	113	CG	PHE	C	17	16.996	25.503	19.872	1.00	52.57
50	114	CD1	PHE	C	17	16.878	24.248	20.554	1.00	52.57
	115	CD2	PHE	C	17	18.173	25.830	19.278	1.00	52.57
	116	CE1	PHE	C	17	17.897	23.329	20.455	1.00	52.57
	117	CE2	PHE	C	17	19.207	24.912	19.167	1.00	52.57
	118	CZ	PHE	C	17	19.063	23.648	19.759	1.00	52.57
55	119	C	PHE	C	17	15.251	28.793	19.468	1.00	80.97
	120	O	PHE	C	17	14.320	29.320	20.074	1.00	80.97
	121	N	LYS	C	18	15.429	28.937	18.161	1.00	59.00
	122	CA	LYS	C	18	14.529	29.761	17.349	1.00	59.00
	123	CB	LYS	C	18	15.065	29.846	15.921	1.00	195.91
60	124	CG	LYS	C	18	14.313	30.790	15.003	1.00	195.91
	125	CD	LYS	C	18	15.142	31.059	13.761	1.00	195.91
	126	CE	LYS	C	18	14.441	32.000	12.803	1.00	195.91
	127	NZ	LYS	C	18	13.160	31.413	12.321	1.00	195.91
	128	C	LYS	C	18	13.123	29.162	17.349	1.00	59.00
65	129	O	LYS	C	18	12.937	27.974	17.129	1.00	59.00
	130	N	GLY	C	19	12.122	29.973	17.630	1.00	76.33
	131	CA	GLY	C	19	10.774	29.457	17.582	1.00	76.33
	132	C	GLY	C	19	10.178	28.991	18.886	1.00	76.33
	133	O	GLY	C	19	8.971	28.747	18.970	1.00	76.33
70	134	N	GLU	C	20	10.998	28.857	19.916	1.00	72.26

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	135	CA	GLU	C	20	·10.460	28.427	21.211	1.00	72.26
	136	CB	GLU	C	20	11.590	27.847	22.059	1.00	102.87
	137	CG	GLU	C	20	12.410	26.815	21.296	1.00	102.87
5	138	CD	GLU	C	20	13.457	26.129	22.152	1.00	102.87
	139	OE1	GLU	C	20	14.291	26.830	22.758	1.00	102.87
	140	OE2	GLU	C	20	13.452	24.884	22.210	1.00	102.87
	141	C	GLU	C	20	9.739	29.579	21.956	1.00	72.26
	142	O	GLU	C	20	9.803	30.730	21.525	1.00	72.26
10	143	N	ASN	C	21	9.030	29.264	23.040	1.00	57.87
	144	CA	ASN	C	21	8.336	30.295	23.787	1.00	57.87
	145	CB	ASN	C	21	6.839	30.041	23.853	1.00	107.77
	146	CG	ASN	C	21	6.273	29.544	22.563	1.00	107.77
	147	OD1	ASN	C	21	6.639	30.019	21.477	1.00	107.77
15	148	ND2	ASN	C	21	5.353	28.591	22.690	1.00	107.77
	149	C	ASN	C	21	8.841	30.401	25.220	1.00	57.87
	150	O	ASN	C	21	9.136	29.391	25.859	1.00	57.87
	151	N	VAL	C	22	8.921	31.625	25.735	1.00	64.18
	152	CA	VAL	C	22	9.364	31.858	27.099	1.00	64.18
	153	CB	VAL	C	22	10.797	32.278	27.139	1.00	42.75
20	154	CG1	VAL	C	22	10.981	33.583	26.376	1.00	42.75
	155	CG2	VAL	C	22	11.231	32.452	28.585	1.00	42.75
	156	C	VAL	C	22	8.542	32.997	27.677	1.00	64.18
	157	O	VAL	C	22	8.115	33.897	26.936	1.00	64.18
	158	N	THR	C	23	8.347	32.977	28.998	1.00	75.81
25	159	CA	THR	C	23	7.534	33.987	29.693	1.00	75.81
	160	CB	THR	C	23	6.369	33.301	30.399	1.00	170.16
	161	OG1	THR	C	23	5.651	32.492	29.459	1.00	170.16
	162	CG2	THR	C	23	5.442	34.327	31.005	1.00	170.16
	163	C	THR	C	23	8.328	34.776	30.730	1.00	75.81
30	164	O	THR	C	23	8.978	34.183	31.572	1.00	75.81
	165	N	LEU	C	24	8.292	36.101	30.684	1.00	82.13
	166	CA	LEU	C	24	9.071	36.861	31.656	1.00	82.13
	167	CB	LEU	C	24	9.899	37.962	30.995	1.00	55.82
	168	CG	LEU	C	24	10.586	37.719	29.653	1.00	55.82
35	169	CD1	LEU	C	24	11.621	38.790	29.358	1.00	55.82
	170	CD2	LEU	C	24	11.241	36.405	29.664	1.00	55.82
	171	C	LEU	C	24	8.182	37.506	32.677	1.00	82.13
	172	O	LEU	C	24	7.526	38.505	32.391	1.00	82.13
	173	N	THR	C	25	8.184	36.967	33.888	1.00	46.04
40	174	CA	THR	C	25	7.333	37.517	34.921	1.00	46.04
	175	CB	THR	C	25	6.859	36.406	35.852	1.00	88.77
	176	OG1	THR	C	25	6.235	35.384	35.064	1.00	88.77
	177	CG2	THR	C	25	5.846	36.939	36.851	1.00	88.77
	178	C	THR	C	25	8.047	38.614	35.693	1.00	46.04
45	179	O	THR	C	25	9.225	38.493	36.009	1.00	46.04
	180	N	CYS	C	26	7.360	39.719	35.962	1.00	99.22
	181	CA	CYS	C	26	7.988	40.779	36.730	1.00	99.22
	182	C	CYS	C	26	7.833	40.454	38.201	1.00	99.22
	183	O	CYS	C	26	6.787	39.984	38.644	1.00	99.22
50	184	CB	CYS	C	26	7.353	42.132	36.440	1.00	145.11
	185	SG	CYS	C	26	8.267	43.513	37.198	1.00	145.11
	186	N	ASN	C	27	8.897	40.697	38.944	1.00	197.95
	187	CA	ASN	C	27	8.936	40.461	40.370	1.00	197.95
	188	CB	ASN	C	27	9.427	41.723	41.048	1.00	249.36
55	189	CG	ASN	C	27	9.941	41.459	42.424	1.00	249.36
	190	OD1	ASN	C	27	10.558	40.419	42.666	1.00	249.36
	191	ND2	ASN	C	27	9.710	42.399	43.346	1.00	249.36
	192	C	ASN	C	27	7.618	40.026	41.003	1.00	197.95
	193	O	ASN	C	27	6.829	40.859	41.440	1.00	197.95
60	194	N	GLY	C	28	7.392	38.719	41.065	1.00	214.74
	195	CA	GLY	C	28	6.162	38.203	41.644	1.00	214.74
	196	C	GLY	C	28	6.121	36.711	41.398	1.00	214.74
	197	O	GLY	C	28	6.177	36.276	40.255	1.00	214.74
	198	N	ASN	C	29	6.006	35.922	42.456	1.00	249.28
65	199	CA	ASN	C	29	6.011	34.476	42.322	1.00	249.28
	200	CB	ASN	C	29	6.332	33.825	43.676	1.00	216.11
	201	CG	ASN	C	29	6.655	32.353	43.552	1.00	216.11
	202	OD1	ASN	C	29	6.877	31.849	42.450	1.00	216.11
	203	ND2	ASN	C	29	6.701	31.657	44.681	1.00	216.11
70	204	C	ASN	C	29	4.731	33.880	41.751	1.00	249.28

	205	O	ASN	C	29	·4.781	33.119	40.788	1.00	249.28
	206	N	ASN	C	30	3.584	34.225	42.328	1.00	235.48
	207	CA	ASN	C	30	2.325	33.663	41.851	1.00	235.48
	208	CB	ASN	C	30	1.763	32.685	42.889	1.00	219.86
5	209	CG	ASN	C	30	2.660	31.487	43.106	1.00	219.86
	210	OD1	ASN	C	30	3.006	31.152	44.240	1.00	219.86
	211	ND2	ASN	C	30	3.040	30.831	42.019	1.00	219.86
	212	C	ASN	C	30	1.251	34.682	41.498	1.00	235.48
	213	O	ASN	C	30	0.931	34.878	40.325	1.00	235.48
10	214	N	PHE	C	31	0.690	35.329	42.515	1.00	241.86
	215	CA	PHE	C	31	-0.373	36.291	42.280	1.00	241.86
	216	CB	PHE	C	31	-1.597	35.920	43.123	1.00	249.47
	217	CG	PHE	C	31	-2.076	34.504	42.908	1.00	249.47
	218	CD1	PHE	C	31	-1.432	33.431	43.523	1.00	249.47
15	219	CD2	PHE	C	31	-3.154	34.240	42.066	1.00	249.47
	220	CE1	PHE	C	31	-1.858	32.115	43.307	1.00	249.47
	221	CE2	PHE	C	31	-3.588	32.927	41.843	1.00	249.47
	222	CZ	PHE	C	31	-2.936	31.863	42.463	1.00	249.47
	223	C	PHE	C	31	0.022	37.743	42.516	1.00	241.86
20	224	O	PHE	C	31	0.520	38.109	43.587	1.00	241.86
	225	N	PHE	C	32	-0.212	38.559	41.489	1.00	249.62
	226	CA	PHE	C	32	0.108	39.985	41.512	1.00	249.62
	227	CB	PHE	C	32	1.132	40.302	40.423	1.00	249.66
	228	CG	PHE	C	32	1.755	41.655	40.560	1.00	249.66
25	229	CD1	PHE	C	32	2.582	41.907	41.614	1.00	249.66
	230	CD2	PHE	C	32	1.510	42.675	39.643	1.00	249.66
	231	CE1	PHE	C	32	3.147	43.108	41.753	1.00	249.66
	232	CE2	PHE	C	32	2.093	43.918	39.791	1.00	249.66
	233	CZ	PHE	C	32	2.900	44.146	40.828	1.00	249.66
30	234	C	PHE	C	32	-1.151	40.815	41.269	1.00	249.62
	235	O	PHE	C	32	-2.197	40.259	40.930	1.00	249.62
	236	N	GLU	C	33	-1.054	42.139	41.416	1.00	249.77
	237	CA	GLU	C	33	-2.224	42.994	41.200	1.00	249.77
35	238	CB	GLU	C	33	-2.704	43.604	42.503	1.00	249.65
	239	CG	GLU	C	33	-4.023	44.344	42.358	1.00	249.65
	240	CD	GLU	C	33	-5.159	43.406	42.025	1.00	249.65
	241	OE1	GLU	C	33	-5.159	42.298	42.562	1.00	249.65
	242	OE2	GLU	C	33	-6.051	43.779	41.239	1.00	249.65
	243	C	GLU	C	33	-2.110	44.128	40.194	1.00	249.77
40	244	O	GLU	C	33	-2.952	44.257	39.301	1.00	249.77
	245	N	VAL	C	34	-1.107	44.982	40.365	1.00	243.09
	246	CA	VAL	C	34	-0.949	46.113	39.471	1.00	243.09
	247	CB	VAL	C	34	0.351	46.880	39.775	1.00	249.25
	248	CG1	VAL	C	34	0.508	48.060	38.826	1.00	249.25
45	249	CG2	VAL	C	34	0.302	47.386	41.184	1.00	249.25
	250	C	VAL	C	34	-0.990	45.721	38.002	1.00	243.09
	251	O	VAL	C	34	-0.603	44.616	37.615	1.00	243.09
	252	N	SER	C	35	-1.494	46.644	37.196	1.00	146.24
	253	CA	SER	C	35	-1.605	46.453	35.764	1.00	146.24
50	254	CB	SER	C	35	-3.021	46.778	35.290	1.00	174.88
	255	OG	SER	C	35	-3.296	48.166	35.411	1.00	174.83
	256	C	SER	C	35	-0.617	47.400	35.103	1.00	146.24
	257	O	SER	C	35	-0.518	47.438	33.878	1.00	146.2·
	258	N	SER	C	36	0.095	48.179	35.919	1.00	112.51
55	259	CA	SER	C	36	1.091	49.114	35.408	1.00	112.51
	260	CB	SER	C	36	0.986	50.475	36.105	1.00	242.80
	261	OG	SER	C	36	1.420	50.408	37.452	1.00	242.80
	262	C	SER	C	36	2.486	48.535	35.635	1.00	112.51
	263	O	SER	C	36	3.088	48.707	36.700	1.00	112.51
60	264	N	THR	C	37	2.985	47.834	34.620	1.00	147.41
	265	CA	THR	C	37	4.301	47.220	34.655	1.00	147.41
	266	CB	THR	C	37	4.185	45.679	34.635	1.00	242.04
	267	OG1	THR	C	37	3.393	45.242	35.748	1.00	242.04
	268	CG2	THR	C	37	5.553	45.039	34.720	1.00	242.04
65	269	C	THR	C	37	5.004	47.708	33.399	1.00	147.41
	270	O	THR	C	37	4.382	47.834	32.345	1.00	147.41
	271	N	LYS	C	38	6.289	48.009	33.512	1.00	114.65
	272	CA	LYS	C	38	7.046	48.490	32.361	1.00	114.65
	273	CB	LYS	C	38	7.794	49.755	32.733	1.00	121.59
70	274	CG	LYS	C	38	6.890	50.832	33.262	1.00	121.59

	275	CD	LYS	C	38	· 7.679	52.074	33.632	1.00	121.59
	276	CE	LYS	C	38	6.757	53.183	34.088	1.00	121.59
	277	NZ	LYS	C	38	7.518	54.413	34.415	1.00	121.59
	278	C	LYS	C	38	8.045	47.459	31.856	1.00	114.65
5	279	O	LYS	C	38	8.640	46.745	32.652	1.00	114.65
	280	N	TRP	C	39	· 8.222	47.373	30.538	1.00	83.37
	281	CA	TRP	C	39	9.182	46.434	29.954	1.00	83.37
	282	CB	TRP	C	39	8.477	45.308	29.202	1.00	59.20
	283	CG	TRP	C	39	7.651	44.439	30.060	1.00	59.20
10	284	CD2	TRP	C	39	8.116	43.493	31.026	1.00	59.20
	285	CE2	TRP	C	39	6.973	42.881	31.590	1.00	59.20
	286	CE3	TRP	C	39	9.391	43.100	31.474	1.00	59.20
	287	CD1	TRP	C	39	6.298	44.369	30.071	1.00	59.20
	288	NE1	TRP	C	39	5.881	43.435	30.990	1.00	59.20
15	289	CZ2	TRP	C	39	7.061	41.892	32.576	1.00	59.20
	290	CZ3	TRP	C	39	9.476	42.119	32.456	1.00	59.20
	291	CH2	TRP	C	39	8.312	41.524	32.998	1.00	59.20
	292	C	TRP	C	39	10.086	47.179	28.990	1.00	83.37
	293	O	TRP	C	39	9.612	47.932	28.144	1.00	83.37
20	294	N	PHE	C	40	11.387	46.963	29.116	1.00	81.86
	295	CA	PHE	C	40	12.330	47.639	28.248	1.00	81.86
	296	CB	PHE	C	40	13.204	48.591	29.062	1.00	132.74
	297	CG	PHE	C	40	12.433	49.601	29.852	1.00	132.74
	298	CD1	PHE	C	40	11.846	49.258	31.063	1.00	132.74
25	299	CD2	PHE	C	40	12.305	50.903	29.393	1.00	132.74
	300	CE1	PHE	C	40	11.141	50.201	31.812	1.00	132.74
	301	CE2	PHE	C	40	11.603	51.853	30.130	1.00	132.74
	302	CZ	PHE	C	40	11.020	51.501	31.344	1.00	132.74
	303	C	PHE	C	40	13.225	46.677	27.474	1.00	81.86
30	304	O	PHE	C	40	14.321	46.333	27.917	1.00	81.86
	305	N	HIS	C	41	12.761	46.239	26.314	1.00	70.61
	306	CA	HIS	C	41	13.552	45.334	25.490	1.00	70.61
	307	CB	HIS	C	41	12.633	44.671	24.470	1.00	75.99
	308	CG	HIS	C	41	13.339	43.759	23.528	1.00	75.99
35	309	CD2	HIS	C	41	13.192	43.567	22.198	1.00	75.99
	310	ND1	HIS	C	41	14.327	42.893	23.933	1.00	75.99
	311	CE1	HIS	C	41	14.765	42.207	22.892	1.00	75.99
	312	NE2	HIS	C	41	14.093	42.598	21.826	1.00	75.99
	313	C	HIS	C	41	14.671	46.118	24.794	1.00	70.61
40	314	O	HIS	C	41	14.408	46.922	23.918	1.00	70.61
	315	N	ASN	C	42	15.916	45.879	25.177	1.00	90.99
	316	CA	ASN	C	42	17.063	46.600	24.615	1.00	90.99
	317	CB	ASN	C	42	17.150	46.463	23.085	1.00	90.93
	318	CG	ASN	C	42	17.611	45.087	22.641	1.00	90.93
45	319	OD1	ASN	C	42	17.149	44.097	23.186	1.00	90.93
	320	ND2	ASN	C	42	18.495	45.007	21.649	1.00	90.93
	321	C	ASN	C	42	16.966	48.077	24.971	1.00	90.99
	322	O	ASN	C	42	17.474	48.926	24.246	1.00	90.99
	323	N	GLY	C	43	16.315	48.394	26.086	1.00	101.51
50	324	CA	GLY	C	43	16.177	49.792	26.478	1.00	101.51
	325	C	GLY	C	43	14.909	50.456	25.997	1.00	101.51
	326	O	GLY	C	43	14.265	51.235	26.721	1.00	101.51
	327	N	SER	C	44	14.492	50.140	24.769	1.00	159.89
	328	CA	SER	C	44	13.276	50.686	24.182	1.00	159.89
55	329	CB	SER	C	44	13.183	50.282	22.705	1.00	153.29
	330	OG	SER	C	44	14.375	50.612	22.007	1.00	153.29
	331	C	SER	C	44	12.046	50.168	24.931	1.00	159.89
	332	O	SER	C	44	11.886	48.962	25.114	1.00	159.89
	333	N	LEU	C	45	11.179	51.076	25.368	1.00	127.30
60	334	CA	LEU	C	45	9.969	50.682	26.091	1.00	127.30
	335	CB	LEU	C	45	9.143	51.925	26.443	1.00	113.27
	336	CG	LEU	C	45	7.855	51.691	27.238	1.00	113.27
	337	CD1	LEU	C	45	8.167	50.902	28.502	1.00	113.27
	338	CD2	LEU	C	45	7.210	53.024	27.583	1.00	113.27
65	339	C	LEU	C	45	9.126	49.705	25.261	1.00	127.30
	340	O	LEU	C	45	9.084	49.805	24.039	1.00	127.30
	341	N	SER	C	46	8.458	48.758	25.915	1.00	104.59
	342	CA	SER	C	46	7.636	47.784	25.206	1.00	104.59
	343	CB	SER	C	46	7.802	46.400	25.829	1.00	120.90
70	344	OG	SER	C	46	7.052	45.423	25.111	1.00	120.90

	345	C	SER	C	46	6.194	48.226	25.309	1.00	104.59
	346	O	SER	C	46	5.867	49.072	26.127	1.00	104.59
	347	N	GLU	C	47	5.320	47.643	24.495	1.00	161.06
	348	CA	GLU	C	47	3.919	48.057	24.551	1.00	161.06
5	349	CB	GLU	C	47	3.295	48.100	23.152	1.00	249.30
	350	CG	GLU	C	47	4.218	48.523	22.010	1.00	249.30
	351	CD	GLU	C	47	3.700	48.108	20.617	1.00	249.30
	352	OE1	GLU	C	47	4.006	46.969	20.155	1.00	249.30
	353	OE2	GLU	C	47	2.988	48.918	19.972	1.00	249.30
10	354	C	GLU	C	47	3.070	47.171	25.505	1.00	161.06
	355	O	GLU	C	47	1.875	47.409	25.648	1.00	161.06
	356	N	GLU	C	48	3.655	46.147	26.142	1.00	104.22
	357	CA	GLU	C	48	2.859	45.337	27.077	1.00	104.22
	358	CB	GLU	C	48	3.427	43.913	27.244	1.00	144.62
15	359	CG	GLU	C	48	2.742	43.070	28.349	1.00	144.62
	360	CD	GLU	C	48	1.288	42.704	28.064	1.00	144.62
	361	OE1	GLU	C	48	1.034	41.897	27.140	1.00	144.62
	362	OE2	GLU	C	48	0.396	43.221	28.775	1.00	144.62
20	363	C	GLU	C	48	2.829	46.060	28.424	1.00	104.22
	364	O	GLU	C	48	3.708	46.968	28.724	1.00	104.22
	365	N	THR	C	49	1.813	45.771	29.229	1.00	87.76
	366	CA	THR	C	49	1.677	46.399	30.529	1.00	87.76
	367	CB	THR	C	49	0.505	47.406	30.547	1.00	167.47
25	368	OG1	THR	C	49	-0.713	46.751	30.168	1.00	167.47
	369	CG2	THR	C	49	0.788	48.516	29.576	1.00	167.47
	370	C	THR	C	49	1.461	45.342	31.601	1.00	87.76
	371	O	THR	C	49	1.832	45.537	32.751	1.00	87.76
	372	N	ASN	C	50	0.872	44.210	31.227	1.00	92.41
30	373	CA	ASN	C	50	0.637	43.123	32.180	1.00	92.41
	374	CB	ASN	C	50	0.006	41.921	31.455	1.00	211.05
	375	CG	ASN	C	50	-0.583	40.901	32.411	1.00	211.05
	376	OD1	ASN	C	50	-0.245	40.896	33.593	1.00	211.05
	377	ND2	ASN	C	50	-1.449	40.025	31.907	1.00	211.05
35	378	C	ASN	C	50	2.006	42.743	32.772	1.00	92.41
	379	O	ASN	C	50	3.035	42.908	32.125	1.00	92.41
	380	N	SER	C	51	2.026	42.252	34.005	1.00	91.81
	381	CA	SER	C	51	3.280	41.858	34.640	1.00	91.81
	382	CB	SER	C	51	3.042	41.518	36.117	1.00	188.83
40	383	OG	SER	C	51	2.293	40.322	36.271	1.00	188.83
	384	C	SER	C	51	3.948	40.661	33.944	1.00	91.81
	385	O	SER	C	51	5.130	40.414	34.137	1.00	91.81
	386	N	SER	C	52	3.199	39.919	33.136	1.00	82.66
	387	CA	SER	C	52	3.750	38.764	32.450	1.00	82.66
45	388	CB	SER	C	52	2.862	37.530	32.662	1.00	107.08
	389	OG	SER	C	52	2.845	37.147	34.025	1.00	107.08
	390	C	SER	C	52	3.860	39.064	30.976	1.00	82.66
	391	O	SER	C	52	2.866	39.155	30.271	1.00	82.66
	392	N	LEU	C	53	5.089	39.228	30.524	1.00	52.71
50	393	CA	LEU	C	53	5.386	39.501	29.126	1.00	52.71
	394	CB	LEU	C	53	6.563	40.483	29.036	1.00	59.51
	395	CG	LEU	C	53	7.380	40.539	27.742	1.00	59.51
	396	CD1	LEU	C	53	6.474	40.524	26.514	1.00	59.51
	397	CD2	LEU	C	53	8.217	41.797	27.765	1.00	59.51
55	398	C	LEU	C	53	5.741	38.215	28.378	1.00	52.71
	399	O	LEU	C	53	6.880	37.750	28.462	1.00	52.71
	400	N	ASN	C	54	4.794	37.650	27.631	1.00	78.83
	401	CA	ASN	C	54	5.073	36.425	26.889	1.00	78.83
	402	CB	ASN	C	54	3.777	35.731	26.511	1.00	114.28
60	403	CG	ASN	C	54	3.093	35.117	27.699	1.00	114.28
	404	OD1	ASN	C	54	3.685	34.315	28.415	1.00	114.28
	405	ND2	ASN	C	54	1.842	35.488	27.922	1.00	114.28
	406	C	ASN	C	54	5.898	36.641	25.629	1.00	78.83
	407	O	ASN	C	54	5.983	37.745	25.099	1.00	78.83
	408	N	ILE	C	55	6.527	35.566	25.174	1.00	69.41
65	409	CA	ILE	C	55	7.321	35.571	23.962	1.00	69.41
	410	CB	ILE	C	55	8.814	35.555	24.270	1.00	55.40
	411	CG2	ILE	C	55	9.596	35.167	23.036	1.00	55.40
	412	CG1	ILE	C	55	9.238	36.952	24.724	1.00	55.40
	413	CD1	ILE	C	55	10.730	37.122	25.012	1.00	55.40
70	414	C	ILE	C	55	6.935	34.320	23.210	1.00	69.41

	415	O	ILE	C	55	·7.048	33.232	23.744	1.00	69.41
	416	N	VAL	C	56	6.442	34.473	21.989	1.00	107.00
	417	CA	VAL	C	56	6.046	33.317	21.199	1.00	107.00
5	418	CB	VAL	C	56	4.721	33.566	20.504	1.00	128.23
	419	CG1	VAL	C	56	4.126	32.254	20.058	1.00	128.23
	420	CG2	VAL	C	56	3.772	34.277	21.453	1.00	128.23
	421	C	VAL	C	56	7.132	33.041	20.171	1.00	107.00
	422	O	VAL	C	56	8.236	33.546	20.317	1.00	107.00
	423	N	ASN	C	57	6.837	32.251	˙19.142	1.00	99.37
10	424	CA	ASN	C	57	7.833	31.906	18.123	1.00	99.37
	425	CB	ASN	C	57	7.201	31.916	16.733	1.00	170.52
	426	CG	ASN	C	57	6.217	30.781	16.541	1.00	170.52
	427	OD1	ASN	C	57	6.543	29.617	16.766	1.00	170.52
	428	ND2	ASN	C	57	5.000	31.115	16.127	1.00	170.52
15	429	C	ASN	C	57	9.053	32.828	18.157	1.00	99.37
	430	O	ASN	C	57	9.105	33.850	17.480	1.00	99.37
	431	N	ALA	C	58	10.033	32.443	18.966	1.00	78.85
	432	CA	ALA	C	58	11.241	33.220	19.162	1.00	78.85
	433	CB	ALA	C	58	12.180	32.478	20.085	1.00	109.58
20	434	C	ALA	C	58	11.951	33.558	17.878	1.00	78.85
	435	O	ALA	C	58	12.358	32.681	17.139	1.00	78.85
	436	N	LYS	C	59	12.094	34.845	17.610	1.00	66.66
	437	CA	LYS	C	59	12.812	35.317	16.428	1.00	66.66
	438	CB	LYS	C	59	11.988	36.405	15.726	1.00	201.62
25	439	CG	LYS	C	59	10.597	35.939	15.295	1.00	201.62
	440	CD	LYS	C	59	9.751	37.070	14.724	1.00	201.62
	441	CE	LYS	C	59	8.374	36.569	14.307	1.00	201.62
	442	NZ	LYS	C	59	7.518	37.663	13.775	1.00	201.62
	443	C	LYS	C	59	14.146	35.890	16.953	1.00	66.66
30	444	O	LYS	C	59	14.194	36.455	18.055	1.00	66.66
	445	N	PHE	C	60	15.224	35.743	16.188	1.00	69.57
	446	CA	PHE	C	60	16.515	36.265	16.616	1.00	69.57
	447	CB	PHE	C	60	17.455	36.314	15.438	1.00	112.86
	448	CG	PHE	C	60	17.775	34.974	14.896	1.00	112.86
35	449	CD1	PHE	C	60	18.097	34.805	13.562	1.00	112.86
	450	CD2	PHE	C	60	17.757	33.867	15.718	1.00	112.86
	451	CE1	PHE	C	60	18.396	33.553	13.046	1.00	112.86
	452	CE2	PHE	C	60	18.050	32.608	15.217	1.00	112.86
	453	CZ	PHE	C	60	18.372	32.452	13.877	1.00	112.86
40	454	C	PHE	C	60	16.436	37.644	17.258	1.00	69.57
	455	O	PHE	C	60	17.213	37.958	18.172	1.00	69.57
	456	N	GLU	C	61	15.498	38.466	16.785	1.00	114.60
	457	CA	GLU	C	61	15.308	39.823	17.303	1.00	114.60
	458	CB	GLU	C	61	14.268	40.583	16.482	1.00	179.88
45	459	CG	GLU	C	61	14.629	40.775	15.025	1.00	179.88
	460	CD	GLU	C	61	14.804	39.464	14.296	1.00	179.88
	461	OE1	GLU	C	61	13.874	38.631	14.334	1.00	179.88
	462	OE2	GLU	C	61	15.871	39.269	13.682	1.00	179.88
	463	C	GLU	C	61	14.865	39.831	18.757	1.00	114.60
50	464	O	GLU	C	61	15.064	40.828	19.451	1.00	114.60
	465	N	ASP	C	62	14.251	38.737	19.214	1.00	61.26
	466	CA	ASP	C	62	13.807	38.654	20.605	1.00	61.26
	467	CB	ASP	C	62	12.884	37.457	20.801	1.00	109.78
	468	CG	ASP	C	62	11.707	37.472	19.842	1.00	109.78
55	469	OD1	ASP	C	62	11.182	38.574	19.564	1.00	109.78
	470	OD2	ASP	C	62	11.296	36.385	19.374	1.00	109.78
	471	C	ASP	C	62	15.018	38.559	21.542	1.00	61.26
	472	O	ASP	C	62	14.915	38.859	22.726	1.00	61.26
	473	N	SER	C	63	16.166	38.159	20.999	1.00	49.60
60	474	CA	SER	C	63	17.390	38.050	21.776	1.00	49.60
	475	CB	SER	C	63	18.539	37.599	20.873	1.00	59.31
	476	OG	SER	C	63	18.360	36.265	20.405	1.00	59.31
	477	C	SER	C	63	17.669	39.432	22.294	1.00	49.60
	478	O	SER	C	63	17.647	40.359	21.520	1.00	49.60
65	479	N	GLY	C	64	17.918	39.595	23.583	1.00	66.63
	480	CA	GLY	C	64	18.192	40.936	24.070	1.00	66.63
	481	C	GLY	C	64	18.223	41.119	25.579	1.00	66.63
	482	O	GLY	C	64	18.210	40.154	26.339	1.00	66.63
	483	N	GLU	C	65	18.288	42.371	26.018	1.00	55.08
70	484	CA	GLU	C	65	18.306	42.725	27.440	1.00	55.08

	485	CB	GLU	C	65	·19.339	43.828	27.632	1.00	156.42
	486	CG	GLU	C	65	19.349	44.480	28.979	1.00	156.42
	487	CD	GLU	C	65	20.163	45.756	28.978	1.00	156.42
	488	OE1	GLU	C	65	19.785	46.700	28.254	1.00	156.42
5	489	OE2	GLU	C	65	21.183	45.817	29.696	1.00	156.42
	490	C	GLU	C	65	16.899	43.218	27.844	1.00	55.08
	491	O	GLU	C	65	16.346	44.123	27.213	1.00	55.08
	492	N	TYR	C	66	16.307	42.625	28.871	1.00	61.99
	493	CA	TYR	C	66	14.981	43.056	29.291	1.00	61.99
10	494	CB	TYR	C	66	14.013	41.901	29.181	1.00	58.17
	495	CG	TYR	C	66	13.740	41.415	27.806	1.00	58.17
	496	CD1	TYR	C	66	14.658	40.634	27.133	1.00	58.17
	497	CE1	TYR	C	66	14.365	40.112	25.886	1.00	58.17
	498	CD2	TYR	C	66	12.520	41.681	27.198	1.00	58.17
15	499	CE2	TYR	C	66	12.213	41.170	25.953	1.00	58.17
	500	CZ	TYR	C	66	13.134	40.379	25.300	1.00	58.17
	501	OH	TYR	C	66	12.786	39.826	24.081	1.00	58.17
	502	C	TYR	C	66	14.950	43.525	30.746	1.00	61.99
	503	O	TYR	C	66	15.850	43.192	31.522	1.00	61.99
20	504	N	LYS	C	67	13.899	44.254	31.132	1.00	84.17
	505	CA	LYS	C	67	13.751	44.703	32.516	1.00	84.17
	506	CB	LYS	C	67	14.789	45.766	32.837	1.00	116.03
	507	CG	LYS	C	67	14.858	46.850	31.807	1.00	116.03
	508	CD	LYS	C	67	15.986	47.803	32.118	1.00	116.03
25	509	CE	LYS	C	67	16.177	48.787	30.983	1.00	116.03
	510	NZ	LYS	C	67	17.324	49.693	31.252	1.00	116.03
	511	C	LYS	C	67	12.369	45.249	32.762	1.00	84.17
	512	O	LYS	C	67	11.696	45.655	31.819	1.00	84.17
	513	N	CYS	C	68	11.933	45.229	34.020	1.00	81.35
30	514	CA	CYS	C	68	10.624	45.780	34.350	1.00	81.35
	515	C	CYS	C	68	10.749	46.788	35.467	1.00	81.35
	516	O	CYS	C	68	11.761	46.811	36.145	1.00	81.35
	517	CB	CYS	C	68	9.619	44.672	34.717	1.00	117.98
	518	SG	CYS	C	68	9.997	43.610	36.128	1.00	117.98
35	519	N	GLN	C	69	9.734	47.628	35.627	1.00	106.08
	520	CA	GLN	C	69	9.722	48.638	36.664	1.00	106.08
	521	CB	GLN	C	69	10.471	49.900	36.188	1.00	124.18
	522	CG	GLN	C	69	10.166	51.173	36.978	1.00	124.18
	523	CD	GLN	C	69	10.841	52.407	36.397	1.00	124.18
40	524	OE1	GLN	C	69	10.720	52.687	35.205	1.00	124.18
	525	NE2	GLN	C	69	11.542	53.160	37.244	1.00	124.18
	526	C	GLN	C	69	8.265	48.974	36.930	1.00	106.08
	527	O	GLN	C	69	7.416	48.787	36.054	1.00	106.08
	528	N	HIS	C	70	7.967	49.457	38.131	1.00	181.43
45	529	CA	HIS	C	70	6.609	49.830	38.469	1.00	181.43
	530	CB	HIS	C	70	6.177	49.107	39.764	1.00	144.62
	531	CG	HIS	C	70	6.062	47.635	39.606	1.00	144.62
	532	CD2	HIS	C	70	6.901	46.634	39.977	1.00	144.62
	533	ND1	HIS	C	70	4.972	47.041	39.030	1.00	144.62
50	534	CE1	HIS	C	70	5.121	45.722	39.060	1.00	144.62
	535	NE2	HIS	C	70	6.283	45.464	39.631	1.00	144.62
	536	C	HIS	C	70	6.421	51.335	38.609	1.00	181.43
	537	O	HIS	C	70	7.299	52.112	38.268	1.00	181.43
	538	N	GLN	C	71	5.254	51.714	39.108	1.00	249.25
55	539	CA	GLN	C	71	4.925	53.108	39.290	1.00	249.25
	540	CB	GLN	C	71	3.550	53.209	39.950	1.00	249.45
	541	CG	GLN	C	71	2.717	54.409	39.544	1.00	249.45
	542	CD	GLN	C	71	2.659	54.624	38.057	1.00	249.45
	543	OE1	GLN	C	71	1.970	53.886	37.367	1.00	249.45
60	544	NE2	GLN	C	71	3.360	55.626	37.553	1.00	249.45
	545	C	GLN	C	71	5.988	53.876	40.093	1.00	249.25
	546	O	GLN	C	71	6.510	54.891	39.634	1.00	249.25
	547	N	GLN	C	72	6.321	53.366	41.276	1.00	190.92
	548	CA	GLN	C	72	7.312	54.001	42.145	1.00	190.92
65	549	CB	GLN	C	72	6.639	54.552	43.406	1.00	249.44
	550	CG	GLN	C	72	7.556	55.342	44.333	1.00	249.44
	551	CD	GLN	C	72	6.833	55.900	45.543	1.00	249.44
	552	OE1	GLN	C	72	5.871	56.656	45.411	1.00	249.44
	553	NE2	GLN	C	72	7.296	55.530	46.734	1.00	249.44
70	554	C	GLN	C	72	8.427	53.034	42.546	1.00	190.92

	555	O	GLN	C	72	· 8.660	52.788	43.734	1.00	190.92
	556	N	VAL	C	73	9.118	52.481	41.556	1.00	211.52
	557	CA	VAL	C	73	10.183	51.531	41.836	1.00	211.52
5	558	CB	VAL	C	73	9.649	50.092	41.803	1.00	215.95
	559	CG1	VAL	C	73	10.667	49.148	42.403	1.00	215.95
	560	CG2	VAL	C	73	8.338	50.011	42.539	1.00	215.95
	561	C	VAL	C	73	11.297	51.639	40.816	1.00	211.52
	562	O	VAL	C	73	11.053	51.942	39.649	1.00	211.52
10	563	N	ASN	C	74	12.525	51.391	41.256	1.00	137.61
	564	CA	ASN	C	74	13.656	51.454	40.349	1.00	137.61
	565	CB	ASN	C	74	14.950	51.650	41.136	1.00	154.43
	566	CG	ASN	C	74	14.895	52.860	42.037	1.00	154.43
	567	OD1	ASN	C	74	14.408	53.920	41.631	1.00	154.43
15	568	ND2	ASN	C	74	15.401	52.711	43.259	1.00	154.43
	569	C	ASN	C	74	13.708	50.169	39.523	1.00	137.61
	570	O	ASN	C	74	13.641	49.062	40.063	1.00	137.61
	571	N	GLU	C	75	13.807	50.341	38.205	1.00	102.99
	572	CA	GLU	C	75	13.862	49.236	37.248	1.00	102.99
20	573	CB	GLU	C	75	14.305	49.764	35.881	1.00	231.35
	574	CG	GLU	C	75	15.294	50.916	35.952	1.00	231.35
	575	CD	GLU	C	75	15.534	51.559	34.601	1.00	231.35
	576	OE1	GLU	C	75	14.547	51.970	33.952	1.00	231.35
	577	OE2	GLU	C	75	16.710	51.657	34.190	1.00	231.35
25	578	C	GLU	C	75	14.749	48.080	37.693	1.00	102.99
	579	O	GLU	C	75	15.794	48.281	38.296	1.00	102.99
	580	N	SER	C	76	14.305	46.868	37.383	1.00	85.19
	581	CA	SER	C	76	14.987	45.629	37.747	1.00	85.19
	582	CB	SER	C	76	14.101	44.448	37.402	1.00	104.06
30	583	OG	SER	C	76	13.920	44.371	35.992	1.00	104.06
	584	C	SER	C	76	16.308	45.424	37.044	1.00	85.19
	585	O	SER	C	76	16.560	46.020	35.998	1.00	85.19
	586	N	GLU	C	77	17.140	44.553	37.612	1.00	76.77
	587	CA	GLU	C	77	18.444	44.238	37.023	1.00	76.77
35	588	CB	GLU	C	77	19.263	43.355	37.962	1.00	228.57
	589	CG	GLU	C	77	19.643	44.039	39.268	1.00	228.57
	590	CD	GLU	C	77	20.577	45.228	39.070	1.00	228.57
	591	OE1	GLU	C	77	20.709	45.703	37.921	1.00	228.57
	592	OE2	GLU	C	77	21.172	45.695	40.068	1.00	228.57
40	593	C	GLU	C	77	18.178	43.498	35.728	1.00	76.77
	594	O	GLU	C	77	17.573	42.420	35.746	1.00	76.77
	595	N	PRO	C	78	18.600	44.080	34.585	1.00	81.92
	596	CD	PRO	C	78	19.176	45.434	34.463	1.00	75.82
	597	CA	PRO	C	78	18.417	43.503	33.255	1.00	81.92
45	598	CB	PRO	C	78	19.357	44.328	32.394	1.00	75.82
	599	CG	PRO	C	78	19.130	·45.681	32.940	1.00	75.82
	600	C	PRO	C	78	18.717	42.029	33.190	1.00	81.92
	601	O	PRO	C	78	19.475	41.508	34.000	1.00	81.92
	602	N	VAL	C	79	18.094	41.357	32.233	1.00	71.44
50	603	CA	VAL	C	79	18.300	39.938	32.036	1.00	71.44
	604	CB	VAL	C	79	17.121	39.139	32.538	1.00	74.89
	605	CG1	VAL	C	79	17.199	37.717	32.029	1.00	74.89
	606	CG2	VAL	C	79	17.131	39.154	34.047	1.00	74.89
	607	C	VAL	C	79	18.454	39.707	30.552	1.00	71.44
55	608	O	VAL	C	79	17.646	40.184	29.748	1.00	71.44
	609	N	TYR	C	80	19.502	38.989	30.179	1.00	69.00
	610	CA	TYR	C	80	19.710	38.728	28.773	1.00	69.00
	611	CB	TYR	C	80	21.184	38.;-7	28.406	1.00	132.22
	612	CG	TYR	C	80	21.361	38.905	26.921	1.00	132.22
60	613	CD1	TYR	C	80	20.962	40.075	26.284	1.00	132.22
	614	CE1	TYR	C	80	21.102	40.236	24.923	1.00	132.22
	615	CD2	TYR	C	80	21.902	37.891	26.143	1.00	132.22
	616	CE2	TYR	C	80	22.039	38.046	24.754	1.00	132.22
	617	CZ	TYR	C	80	21.636	39.228	24.163	1.00	132.22
65	618	OH	TYR	C	80	21.777	39.415	22.807	1.00	132.22
	619	C	TYR	C	80	19.150	37.401	28.300	1.00	69.00
	620	O	TYR	C	80	19.295	36.380	28.939	1.00	69.00
	621	N	LEU	C	81	18.534	37.423	27.141	1.00	61.97
	622	CA	LEU	C	81	17.988	36.232	26.557	1.00	61.97
70	623	CB	LEU	C	81	16.501	36.449	26.351	1.00	56.21
	624	CG	LEU	C	81	15.878	35.304	25.589	1.00	56.21

	625	CD1	LEU C	81	16.017	34.060	26.431	1.00	56.21
	626	CD2	LEU C	81	14.424	35.608	25.294	1.00	56.21
	627	C	LEU C	81	18.700	36.019	25.213	1.00	61.97
	628	O	LEU C	81	18.814	36.949	24.423	1.00	61.97
5	629	N	GLU C	82	19.191	34.816	24.948	1.00	70.61
	630	CA	GLU C	82	19.855	34.581	23.674	1.00	70.61
	631	CB	GLU C	82	21.326	34.242	23.882	1.00	114.25
	632	CG	GLU C	82	22.179	34.569	22.675	1.00	114.25
	633	CD	GLU C	82	23.657	34.256	22.884	1.00	114.25
10	634	OE1	GLU C	82	24.149	34.456	24.020	1.00	114.25
	635	OE2	GLU C	82	24.331	33.827	21.913	1.00	114.25
	636	C	GLU C	82	19.172	33.457	22.896	1.00	70.61
	637	O	GLU C	82	18.913	32.381	23.440	1.00	70.61
	638	N	VAL C	83	18.886	33.706	21.622	1.00	70.46
15	639	CA	VAL C	83	18.225	32.717	20.795	1.00	70.46
	640	CB	VAL C	83	17.114	33.346	20.004	1.00	68.26
	641	CG1	VAL C	83	16.531	32.318	19.057	1.00	68.26
	642	CG2	VAL C	83	16.045	33.848	20.941	1.00	68.26
	643	C	VAL C	83	19.156	32.014	19.825	1.00	70.46
20	644	O	VAL C	83	19.955	32.663	19.157	1.00	70.46
	645	N	PHE C	84	19.031	30.694	19.718	1.00	54.26
	646	CA	PHE C	84	19.913	29.944	18.845	1.00	54.26
	647	CB	PHE C	84	20.793	28.988	19.650	1.00	65.02
	648	CG	PHE C	84	21.645	29.643	20.638	1.00	65.02
25	649	CD1	PHE C	84	21.104	30.128	21.788	1.00	65.02
	650	CD2	PHE C	84	22.996	29.767	20.426	1.00	65.02
	651	CE1	PHE C	84	21.897	30.746	22.733	1.00	65.02
	652	CE2	PHE C	84	23.811	30.384	21.359	1.00	65.02
	653	CZ	PHE C	84	23.262	30.872	22.519	1.00	65.02
30	654	C	PHE C	84	19.247	29.092	17.790	1.00	54.26
	655	O	PHE C	84	18.045	28.781	17.861	1.00	54.26
	656	N	SER C	85	20.101	28.686	16.849	1.00	85.79
	657	CA	SER C	85	19.768	27.807	15.750	1.00	85.79
	658	CB	SER C	85	19.683	28.583	14.435	1.00	134.11
35	659	OG	SER C	85	19.375	27.719	13.355	1.00	134.11
	660	C	SER C	85	20.951	26.860	15.700	1.00	85.79
	661	O	SER C	85	22.063	27.274	15.360	1.00	85.79
	662	N	ASP C	86	20.731	25.607	16.083	1.00	52.64
	663	CA	ASP C	86	21.798	24.604	16.049	1.00	52.64
40	664	CB	ASP C	86	22.912	24.984	17.015	1.00	115.87
	665	CG	ASP C	86	24.265	24.581	16.504	1.00	115.87
	666	OD1	ASP C	86	24.448	23.384	16.194	1.00	115.87
	667	OD2	ASP C	86	25.144	25.459	16.411	1.00	115.87
	668	C	ASP C	86	21.199	23.235	16.420	1.00	52.64
45	669	O	ASP C	86	20.051	23.168	16.879	1.00	52.64
	670	N	TRP C	87	21.944	22.146	16.202	1.00	58.25
	671	CA	TRP C	87	21.424	20.809	16.522	1.00	58.25
	672	CB	TRP C	87	22.372	19.723	16.049	1.00	247.83
	673	CG	TRP C	87	22.083	19.354	14.675	1.00	247.83
50	674	CD2	TRP C	87	22.700	19.899	13.518	1.00	247.83
	675	CE2	TRP C	87	22.052	19.344	12.404	1.00	247.83
	676	CE3	TRP C	87	23.742	20.812	13.311	1.00	247.83
	677	CD1	TRP C	87	21.106	18.504	14.235	1.00	247.83
	678	NE1	TRP C	87	21.082	18.496	12.867	1.00	247.83
55	679	CZ2	TRP C	87	22.418	19.660	11.113	1.00	247.83
	680	CZ3	TRP C	87	24.098	21.132	12.023	1.00	247.83
	681	CH2	TRP C	87	23.444	20.552	10.944	1.00	247.83
	682	C	TRP C	87	21.220	20.656	18.009	1.00	58.25
	683	O	TRP C	87	20.141	20.260	18.463	1.00	58.25
60	684	N	LEU C	88	22.264	20.985	18.760	1.00	79.45
	685	CA	LEU C	88	22.230	20.887	20.197	1.00	79.45
	686	CB	LEU C	88	23.225	19.845	20.659	1.00	57.97
	687	CG	LEU C	88	22.896	18.431	20.245	1.00	57.97
	688	CD1	LEU C	88	23.876	17.490	20.880	1.00	57.97
65	689	CD2	LEU C	88	21.495	18.114	20.693	1.00	57.97
	690	C	LEU C	88	22.558	22.194	20.870	1.00	79.45
	691	O	LEU C	88	23.432	22.940	20.419	1.00	79.45
	692	N	LEU C	89	21.872	22.451	21.976	1.00	57.52
70	693	CA	LEU C	89	22.097	23.669	22.732	1.00	57.52
	694	CB	LEU C	89	20.919	24.616	22.578	1.00	59.32

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	695	CG	LEU	C	89	· 21.105	25.884	23.373	1.00	59.32
	696	CD1	LEU	C	89	22.513	26.439	23.134	1.00	59.32
	697	CD2	LEU	C	89	20.081	26.861	22.941	1.00	59.32
	698	C	LEU	C	89	22.246	23.316	24.184	1.00	57.52
5	699	O	LEU	C	89	21.432	22.577	24.697	1.00	57.52
	700	N	LEU	C	90	23.287	23.815	24.846	1.00	64.90
	701	CA	LEU	C	90	23.472	23.521	26.267	1.00	64.90
	702	CB	LEU	C	90	24.948	23.512	26.638	1.00	46.55
	703	CG	LEU	C	90	25.227	23.312	28.119	1.00	46.55
10	704	CD1	LEU	C	90	24.701	21.955	28.491	1.00	46.55
	705	CD2	LEU	C	90	26.712	23.409	28.423	1.00	46.55
	706	C	LEU	C	90	22.781	24.591	27.083	1.00	64.90
	707	O	LEU	C	90	23.167	25.754	27.032	1.00	64.90
	708	N	GLN	C	91	21.769	24.208	27.852	1.00	56.08
15	709	CA	GLN	C	91	21.052	25.187	28.650	1.00	56.08
	710	CB	GLN	C	91	19.573	24.944	28.517	1.00	49.57
	711	CG	GLN	C	91	19.115	25.036	27.094	1.00	49.57
	712	CD	GLN	C	91	17.606	25.013	26.979	1.00	49.57
	713	OE1	GLN	C	91	16.947	23.977	27.245	1.00	49.57
20	714	NE2	GLN	C	91	17.030	26.167	26.601	1.00	49.57
	715	C	GLN	C	91	21.440	25.146	30.103	1.00	56.08
	716	O	GLN	C	91	21.697	24.066	30.638	1.00	56.08
	717	N	ALA	C	92	21.494	26.309	30.752	1.00	47.15
	718	CA	ALA	C	92	21.852	26.335	32.166	1.00	47.15
25	719	CB	ALA	C	92	23.160	26.962	32.345	1.00	42.48
	720	C	ALA	C	92	20.828	27.102	32.955	1.00	47.15
	721	O	ALA	C	92	20.300	28.102	32.474	1.00	47.15
	722	N	SER	C	93	20.510	26.620	34.151	1.00	67.10
	723	CA	SER	C	93	19.541	27.289	35.013	1.00	67.10
30	724	CB	SER	C	93	19.475	26.625	36.392	1.00	100.79
	725	OG	SER	C	93	20.758	26.434	36.965	1.00	100.79
	726	C	SER	C	93	20.040	28.705	35.137	1.00	67.10
	727	O	SER	C	93	19.395	29.632	34.692	1.00	67.10
	728	N	ALA	C	94	21.220	28.868	35.704	1.00	57.34
35	729	CA	ALA	C	94	21.818	30.179	35.875	1.00	57.34
	730	CB	ALA	C	94	21.716	30.609	37.326	1.00	92.07
	731	C	ALA	C	94	23.279	30.072	35.462	1.00	57.34
	732	O	ALA	C	94	23.912	29.048	35.694	1.00	57.34
	733	N	GLU	C	95	23.825	31.123	34.860	1.00	69.09
40	734	CA	GLU	C	95	25.212	31.088	34.419	1.00	69.09
	735	CB	GLU	C	95	25.403	31.994	33.214	1.00	142.79
	736	CG	GLU	C	95	24.526	31.618	32.048	1.00	142.79
	737	CD	GLU	C	95	24.954	32.288	30.759	1.00	142.79
	738	OE1	GLU	C	95	24.268	32.084	29.733	1.00	142.79
45	739	OE2	GLU	C	95	25.976	33.013	30.767	1.00	142.79
	740	C	GLU	C	95	26.232	31.459	35.494	1.00	69.09
	741	O	GLU	C	95	27.435	31.238	35.316	1.00	69.09
	742	N	VAL	C	96	25.765	32.041	36.598	1.00	86.41
	743	CA	VAL	C	96	26.640	32.419	37.713	1.00	86.41
50	744	CB	VAL	C	96	26.922	33.903	37.702	1.00	74.25
	745	CG1	VAL	C	96	28.119	34.207	38.587	1.00	74.25
	746	CG2	VAL	C	96	27.176	34.357	36.277	1.00	74.25
	747	C	VAL	C	96	25.910	32.052	38.990	1.00	86.41
	748	O	VAL	C	96	24.733	32.348	39.135	1.00	86.41
55	749	N	VAL	C	97	26.610	31.434	39.931	1.00	73.13
	750	CA	VAL	C	97	25.953	30.955	41.142	1.00	73.13
	751	CB	VAL	C	97	25.697	29.456	41.001	1.00	48.19
	752	CG1	VAL	C	97	24.767	28.999	42.037	1.00	48.19
	753	CG2	VAL	C	97	25.176	29.146	39.634	1.00	48.19
60	754	C	VAL	C	97	26.715	31.125	42.448	1.00	73.13
	755	O	VAL	C	97	27.924	30.893	42.513	1.00	73.13
	756	N	MET	C	98	25.999	31.490	43.503	1.00	70.97
	757	CA	MET	C	98	26.612	31.622	44.828	1.00	70.97
	758	CB	MET	C	98	25.638	32.331	45.763	1.00	151.84
65	759	CG	MET	C	98	25.295	33.728	45.318	1.00	151.84
	760	SD	MET	C	98	26.581	34.857	45.790	1.00	151.84
	761	CE	MET	C	98	26.247	34.962	47.553	1.00	151.84
	762	C	MET	C	98	28.930	30.228	45.390	1.00	70.97
	763	O	MET	C	98	26.094	29.335	45.348	1.00	70.97
70	764	N	GLU	C	99	28.130	30.037	45.923	1.00	61.59

	765	CA	GLU	C	99	28.508	28.740	46.475	1.00	61.59
	766	CB	GLU	C	99	29.762	28.874	47.339	1.00	200.85
	767	CG	GLU	C	99	30.525	27.574	47.520	1.00	200.85
	768	CD	GLU	C	99	31.561	27.657	48.623	1.00	200.85
5	769	OE1	GLU	C	99	32.197	28.724	48.761	1.00	200.85
	770	OE2	GLU	C	99	31.746	26.651	49.342	1.00	200.85
	771	C	GLU	C	99	27.354	28.221	47.325	1.00	61.59
	772	O	GLU	C	99	26.851	28.934	48.184	1.00	61.59
	773	N	GLY	C	100	26.901	27.000	47.076	1.00	69.94
10	774	CA	GLY	C	100	25.819	26.456	47.876	1.00	69.94
	775	C	GLY	C	100	24.468	26.355	47.191	1.00	69.94
	776	O	GLY	C	100	23.600	25.591	47.657	1.00	69.94
	777	N	GLN	C	101	24.266	27.111	46.105	1.00	57.42
	778	CA	GLN	C	101	22.990	27.083	45.370	1.00	57.42
15	779	CB	GLN	C	101	22.778	28.399	44.634	1.00	124.38
	730	CG	GLN	C	101	22.627	29.570	45.551	1.00	124.38
	781	CD	GLN	C	101	21.628	29.295	46.641	1.00	124.38
	782	OE1	GLN	C	101	21.911	28.587	47.605	1.00	124.38
	783	NE2	GLN	C	101	20.438	29.839	46.485	1.00	124.38
20	784	C	GLN	C	101	22.854	25.918	44.369	1.00	57.42
	785	O	GLN	C	101	23.834	25.2	44.031	1.00	57.42
	786	N	PRO	C	102	21.627	25.663	43.893	1.00	52.71
	787	CD	PRO	C	102	20.356	26.358	44.165	1.00	80.58
	788	CA	PRO	C	102	21.438	24.573	42.942	1.00	52.71
25	789	CB	PRO	C	102	19.957	24.318	43.044	1.00	80.58
	790	CG	PRO	C	102	19.422	25.709	43.171	1.00	80.58
	791	C	PRO	C	102	21.870	25.005	41.531	1.00	52.71
	792	O	PRO	C	102	21.853	26.203	41.189	1.00	52.71
	793	N	LEU	C	103	22.242	24.033	40.705	1.00	64.68
30	794	CA	LEU	C	103	22.661	24.323	39.344	1.00	64.68
	795	CB	LEU	C	103	24.172	24.347	39.273	1.00	81.00
	796	CG	LEU	C	103	24.605	24.608	37.838	1.00	81.00
	797	CD1	LEU	C	103	24.136	25.987	37.435	1.00	81.00
	798	CD2	LEU	C	103	26.113	24.488	37.718	1.00	81.00
35	799	C	LEU	C	103	22.147	23.244	38.403	1.00	64.68
	800	O	LEU	C	103	22.418	22.063	38.642	1.00	64.68
	801	N	PHE	C	104	21.409	23.616	37.355	1.00	64.85
	802	CA	PHE	C	104	20.923	22.599	36.423	1.00	64.85
	803	CB	PHE	C	104	19.392	22.530	36.418	1.00	111.94
40	804	CG	PHE	C	104	18.787	22.248	37.758	1.00	111.94
	805	CD1	PHE	C	104	18.694	23.250	38.710	1.00	111.94
	806	CD2	PHE	C	104	18.300	20.980	38.068	1.00	111.94
	807	CE1	PHE	C	104	18.128	23.000	39.962	1.00	111.94
	808	CE2	PHE	C	104	17.731	20.717	39.320	1.00	111.94
45	809	CZ	PHE	C	104	17.644	21.732	40.268	1.00	111.94
	810	C	PHE	C	104	21.410	22.829	34.993	1.00	64.85
	811	O	PHE	C	104	21.254	23.915	34.462	1.00	64.85
	812	N	LEU	C	105	22.009	21.817	34.371	1.00	49.42
	813	CA	LEU	C	105	22.469	21.933	32.983	1.00	49.42
50	814	CB	LEU	C	105	23.928	21.502	32.848	1.00	35.01
	815	CG	LEU	C	105	24.870	22.289	33.757	1.00	35.01
	816	CD1	LEU	C	105	26.346	21.971	33.451	1.00	35.01
	817	CD2	LEU	C	105	24.579	23.735	33.535	1.00	35.01
	818	C	LEU	C	105	21.603	21.000	32.181	1.00	49.42
55	819	O	LEU	C	105	21.225	19.854	32.679	1.00	49.42
	820	N	ARG	C	106	21.290	21.353	30.946	1.00	67.77
	821	CA	ARG	C	106	20.438	20.487	30.155	1.00	67.77
	822	CB	ARG	C	106	19.027	21.043	30.194	1.00	104.09
	823	CG	ARG	C	106	18.058	20.302	29.334	1.00	104.09
60	824	CD	ARG	C	106	16.745	21.071	29.217	1.00	104.09
	825	NE	ARG	C	106	15.814	20.401	28.316	1.00	104.09
	826	CZ	ARG	C	106	14.812	21.002	27.694	1.00	104.09
	827	NH1	ARG	C	106	14.616	22.292	27.879	1.00	104.09
	828	NH2	ARG	C	106	14.023	20.314	26.879	1.00	104.09
65	829	C	ARG	C	106	20.911	20.391	28.710	1.00	67.77
	830	O	ARG	C	106	21.063	21.431	28.053	1.00	67.77
	831	N	CYS	C	107	21.160	19.179	28.205	1.00	64.22
	832	CA	CYS	C	107	21.599	19.074	26.819	1.00	64.22
	833	C	CYS	C	107	20.320	19.044	26.063	1.00	64.22
70	834	O	CYS	C	107	19.579	18.067	26.143	1.00	64.22

	5	CB	CYS	C	107	-22.396	17.808	26.547	1.00	74.81
	J6	SG	CYS	C	107	23.369	17.892	24.999	1.00	74.81
	37	N	HIS	C	108	20.054	20.132	25.351	1.00	62.02
	J38	CA	HIS	C	108	18.815	20.288	24.593	1.00	62.02
	J39	CB	HIS	C	108	18.257	21.669	24.859	1.00	73.41
	J40	CG	HIS	C	108	16.893	21.884	24.302	1.00	73.41
	J41	CD2	HIS	C	108	16.409	22.839	23.479	1.00	73.41
	842	ND1	HIS	C	108	15.821	21.093	24.648	1.00	73.41
	843	CE1	HIS	C	108	14.731	21.558	24.067	1.00	73.41
	844	NE2	HIS	C	108	15.061	22.618	23.353	1.00	73.41
	845	C	HIS	C	108	18.925	20.085	23.089	1.00	62.02
	846	O	HIS	C	108	19.750	20.724	22.412	1.00	62.02
	847	N	GLY	C	109	18.066	19.207	22.578	1.00	82.12
15	848	CA	GLY	C	109	18.075	18.907	21.161	1.00	82.12
	849	C	GLY	C	109	17.196	19.859	20.396	1.00	82.12
	850	O	GLY	C	109	16.281	20.439	20.963	1.00	82.12
	851	N	TRP	C	110	17.473	20.020	19.107	1.00	66.53
	852	CA	TRP	C	110	16.691	20.916	18.282	1.00	66.53
	853	CB	TRP	C	110	17.327	21.057	16.911	1.00	113.55
20	854	CG	TRP	C	110	16.487	21.825	15.969	1.00	113.55
	855	CD2	TRP	C	110	16.565	23.226	15.701	1.00	113.55
	856	CE2	TRP	C	110	15.552	23.532	14.769	1.00	113.55
	857	CE3	TRP	C	110	17.401	24.260	16.157	1.00	113.55
	858	CD1	TRP	C	110	15.460	21.348	15.216	1.00	113.55
25	859	NE1	TRP	C	110	14.892	22.364	14.490	1.00	113.55
	860	CZ2	TRP	C	110	15.345	24.831	14.280	1.00	113.55
	861	CZ3	TRP	C	110	17.193	25.561	15.668	1.00	113.55
	862	CH2	TRP	C	110	16.171	25.829	14.742	1.00	113.55
30	863	C	TRP	C	110	15.284	20.383	18.160	1.00	66.53
	864	O	TRP	C	110	15.060	19.188	18.276	1.00	66.53
	865	N	ARG	C	111	14.334	21.285	17.951	1.00	82.69
	866	CA	ARG	C	111	12.928	20.924	17.807	1.00	82.69
	867	CB	ARG	C	111	12.677	20.368	16.432	1.00	249.07
35	868	CG	ARG	C	111	12.367	21.439	15.493	1.00	249.07
	869	CD	ARG	C	111	11.908	20.831	14.270	1.00	249.07
	870	NE	ARG	C	111	10.767	21.587	13.769	1.00	249.07
	871	CZ	ARG	C	111	9.568	21.660	14.334	1.00	249.07
	872	NH1	ARG	C	111	9.309	20.994	15.438	1.00	249.07
	873	NH2	ARG	C	111	8.601	22.346	13.736	1.00	249.07
40	874	C	ARG	C	111	12.433	19.928	18.828	1.00	82.69
	875	O	ARG	C	111	11.471	19.213	18.595	1.00	82.69
	876	N	ASN	C	112	13.119	19.872	19.953	1.00	79.91
	877	CA	ASN	C	112	12.756	18.976	21.027	1.00	79.91
	878	CB	ASN	C	112	11.354	19.288	21.540	1.00	134.30
45	879	CG	ASN	C	112	11.152	18.815	22.957	1.00	134.30
	880	OD1	ASN	C	112	11.850	17.902	23.427	1.00	134.30
	881	ND2	ASN	C	112	10.194	19.424	23.653	1.00	134.30
	882	C	ASN	C	112	12.833	17.513	20.651	1.00	79.91
	883	O	ASN	C	112	12.172	16.683	21.270	1.00	79.91
50	884	N	TRP	C	113	13.637	17.180	19.650	1.00	91.68
	885	CA	TRP	C	113	13.771	15.780	19.287	1.00	91.68
	886	CB	TRP	C	113	14.648	15.601	18.062	1.00	105.58
	887	CG	TRP	C	113	13.958	15.923	16.805	1.00	105.58
	888	CD2	TRP	C	113	14.528	16.557	15.662	1.00	105.58
55	889	CE2	TRP	C	113	13.524	16.609	14.670	1.00	105.58
	890	CE3	TRP	C	113	15.803	17.083	15.373	1.00	105.58
	891	CD1	TRP	C	113	12.660	15.829	16.478	1.00	105.58
	892	NE1	TRP	C	113	12.393	16.038	15.194	1.00	105.58
	893	CZ2	TRP	C	113	13.750	17.164	13.413	1.00	105.58
60	894	CZ3	TRP	C	113	16.030	17.637	14.119	1.00	105.58
	895	CH2	TRP	C	113	15.005	17.676	13.155	1.00	105.58
	896	C	TRP	C	113	14.393	15.003	20.425	1.00	91.68
	897	O	TRP	C	113	14.528	15.502	21.543	1.00	91.68
	898	N	ASP	C	114	14.780	13.770	20.133	1.00	96.80
65	899	CA	ASP	C	114	15.398	12.926	21.133	1.00	96.80
	900	CB	ASP	C	114	14.675	11.576	21.213	1.00	249.33
	901	CG	ASP	C	114	13.402	11.645	22.044	1.00	249.33
	902	OD1	ASP	C	114	13.493	12.001	23.239	1.00	249.33
	903	OD2	ASP	C	114	12.314	11.344	21.507	1.00	249.33
70	904	C	ASP	C	114	16.866	12.727	20.813	1.00	96.80

905	O	ASP	C	114	17.257	12.561	19.652	1.00	96.80
906	N	VAL	C	115	17.678	12.771	21.860	1.00	71.72
907	CA	VAL	C	115	19.112	12.593	21.728	1.00	71.72
908	CB	VAL	C	115	19.875	13.783	22.274	1.00	77.93
909	CG1	VAL	C	115	21.344	13.665	21.884	1.00	77.93
910	CG2	VAL	C	115	19.257	15.061	21.751	1.00	77.93
911	C	VAL	C	115	19.535	11.382	22.516	1.00	71.72
912	O	VAL	C	115	18.999	11.111	23.589	1.00	71.72
913	N	TYR	C	116	20.502	10.653	21.979	1.00	67.55
914	CA	TYR	C	116	20.999	9.454	22.644	1.00	67.55
915	CB	TYR	C	116	20.610	8.219	21.826	1.00	100.42
916	CG	TYR	C	116	19.121	8.010	21.689	1.00	100.42
917	CD1	TYR	C	116	18.431	8.465	20.572	1.00	100.42
918	CE1	TYR	C	116	17.049	8.284	20.454	1.00	100.42
919	CD2	TYR	C	116	18.403	7.371	22.690	1.00	100.42
920	CE2	TYR	C	116	17.028	7.185	22.590	1.00	100.42
921	CZ	TYR	C	116	16.352	7.644	21.468	1.00	100.42
922	OH	TYR	C	116	14.991	7.468	21.357	1.00	100.42
923	C	TYR	C	116	22.514	9.501	22.853	1.00	67.55
924	O	TYR	C	116	23.187	10.404	22.351	1.00	67.55
925	N	LYS	C	117	23.040	8.518	23.578	1.00	124.33
926	CA	LYS	C	117	24.466	8.443	23.848	1.00	124.33
927	CB	LYS	C	117	25.233	7.946	22.617	1.00	168.92
928	CG	LYS	C	117	25.319	6.439	22.465	1.00	168.92
929	CD	LYS	C	117	26.431	6.073	21.494	1.00	168.92
930	CE	LYS	C	117	27.782	6.589	21.988	1.00	168.92
931	NZ	LYS	C	117	28.904	6.284	21.056	1.00	168.92
932	C	LYS	C	117	24.974	9.822	24.229	1.00	124.33
933	O	LYS	C	117	25.904	10.347	23.608	1.00	124.33
934	N	VAL	C	118	24.361	10.406	25.253	1.00	96.88
935	CA	VAL	C	118	24.752	11.731	25.714	1.00	96.88
936	CB	VAL	C	118	23.572	12.432	26.338	1.00	47.91
937	CG1	VAL	C	118	24.036	13.463	27.307	1.00	47.91
938	CG2	VAL	C	118	22.786	13.114	25.264	1.00	47.91
939	C	VAL	C	118	25.914	11.799	26.692	1.00	96.88
940	O	VAL	C	118	25.980	11.030	27.648	1.00	96.88
941	N	ILE	C	119	26.815	12.746	26.455	1.00	44.35
942	CA	ILE	C	119	27.968	12.917	27.316	1.00	44.35
943	CB	ILE	C	119	29.214	12.377	26.650	1.00	99.63
944	CG2	ILE	C	119	30.395	12.468	27.585	1.00	99.63
945	CG1	ILE	C	119	28.973	10.939	26.239	1.00	99.63
946	CD1	ILE	C	119	30.044	10.421	25.309	1.00	99.63
947	C	ILE	C	119	28.227	14.396	27.618	1.00	44.35
948	O	ILE	C	119	28.466	15.166	26.683	1.00	44.35
949	N	TYR	C	120	28.193	14.816	28.889	1.00	48.39
950	CA	TYR	C	120	28.478	16.224	29.185	1.00	48.39
951	CB	TYR	C	120	27.803	16.687	30.458	1.00	42.29
952	CG	TYR	C	120	26.322	16.785	30.363	1.00	42.29
953	CD1	TYR	C	120	25.537	15.697	30.581	1.00	42.29
954	CE1	TYR	C	120	24.185	15.775	30.485	1.00	42.29
955	CD2	TYR	C	120	25.710	17.982	30.035	1.00	42.29
956	CE2	TYR	C	120	24.340	18.088	29.924	1.00	42.29
957	CZ	TYR	C	120	23.584	16.968	30.155	1.00	42.29
958	OH	TYR	C	120	22.206	17.007	30.061	1.00	42.29
959	C	TYR	C	120	29.962	16.358	29.412	1.00	48.39
960	O	TYR	C	120	30.602	15.447	29.935	1.00	48.39
961	N	TYR	C	121	30.518	17.498	29.053	1.00	53.29
962	CA	TYR	C	121	31.942	17.700	29.246	1.00	53.29
963	CB	TYR	C	121	32.664	17.828	27.887	1.00	75.15
964	CG	TYR	C	121	32.747	16.569	27.044	1.00	75.15
965	CD1	TYR	C	121	31.598	15.971	26.525	1.00	75.15
966	CE1	TYR	C	121	31.669	14.849	25.717	1.00	75.15
967	CD2	TYR	C	121	33.976	16.002	26.731	1.00	75.15
968	CE2	TYR	C	121	34.055	14.881	25.921	1.00	75.15
969	CZ	TYR	C	121	32.895	14.315	25.421	1.00	75.15
970	OH	TYR	C	121	32.960	13.214	24.613	1.00	75.15
971	C	TYR	C	121	32.219	18.966	30.056	1.00	53.29
972	O	TYR	C	121	31.547	19.984	29.872	1.00	53.29
973	N	LYS	C	122	33.199	18.908	30.954	1.00	72.38
974	CA	LYS	C	122	33.580	20.077	31.725	1.00	72.38

	975	CB	LYS	C	122	-33.217	19.930	33.197	1.00	98.98
	976	CG	LYS	C	122	33.582	21.162	34.003	1.00	98.98
	977	CD	LYS	C	122	33.532	20.901	35.481	1.00	98.98
	978	CE	LYS	C	122	34.071	22.074	36.260	1.00	98.98
5	979	NZ	LYS	C	122	34.151	21.706	37.694	1.00	98.98
	980	C	LYS	C	122	35.080	20.238	31.595	1.00	72.38
	981	O	LYS	C	122	35.836	19.379	32.017	1.00	72.38
	982	N	ASP	C	123	35.507	21.342	31.001	1.00	92.01
	983	CA	ASP	C	123	36.918	21.628	30.809	1.00	92.01
10	984	CB	ASP	C	123	37.606	21.819	32.161	1.00	107.76
	985	CG	ASP	C	123	37.288	23.167	32.785	1.00	107.76
	986	OD1	ASP	C	123	37.362	24.186	32.052	1.00	107.76
	987	OD2	ASP	C	123	36.979	23.215	34.000	1.00	107.76
	988	C	ASP	C	123	37.613	20.553	29.996	1.00	92.01
15	989	O	ASP	C	123	38.719	20.144	30.322	1.00	92.01
	990	N	GLY	C	124	36.956	20.110	28.929	1.00	87.40
	991	CA	GLY	C	124	37.516	19.094	28.054	1.00	87.40
	992	C	GLY	C	124	37.465	17.665	28.570	1.00	87.40
	993	O	GLY	C	124	37.795	16.741	27.826	1.00	87.40
20	994	N	GLU	C	125	37.047	17.474	29.821	1.00	63.88
	995	CA	GLU	C	125	36.991	16.139	30.427	1.00	63.88
	996	CB	GLU	C	125	37.331	16.197	31.931	1.00	184.13
	997	CG	GLU	C	125	38.775	16.547	32.294	1.00	184.13
	998	CD	GLU	C	125	39.723	15.367	32.176	1.00	184.13
25	999	OE1	GLU	C	125	39.524	14.369	32.903	1.00	184.13
	1000	OE2	GLU	C	125	40.665	15.445	31.359	1.00	184.13
	1001	C	GLU	C	125	35.626	15.490	30.284	1.00	63.88
	1002	O	GLU	C	125	34.611	16.164	30.370	1.00	63.88
	1003	N	ALA	C	126	35.587	14.182	30.067	1.00	91.37
30	1004	CA	ALA	C	126	34.302	13.501	29.985	1.00	91.37
	1005	CB	ALA	C	126	34.516	12.040	29.654	1.00	171.72
	1006	C	ALA	C	126	33.727	13.657	31.399	1.00	91.37
	1007	O	ALA	C	126	34.492	13.626	32.369	1.00	91.37
	1008	N	LEU	C	127	32.410	13.835	31.533	1.00	55.93
35	1009	CA	LEU	C	127	31.815	14.011	32.861	1.00	55.93
	1010	CB	LEU	C	127	31.291	15.421	33.033	1.00	79.78
	1011	CG	LEU	C	127	31.277	15.727	34.519	1.00	79.78
	1012	CD1	LEU	C	127	32.708	15.528	35.062	1.00	79.78
	1013	CD2	LEU	C	127	30.796	17.133	34.754	1.00	79.78
40	1014	C	LEU	C	127	30.722	13.050	33.267	1.00	55.93
	1015	O	LEU	C	127	30.851	12.396	34.292	1.00	55.93
	1016	N	LYS	C	128	29.633	12.998	32.501	1.00	71.66
	1017	CA	LYS	C	128	28.530	12.063	32.771	1.00	71.66
	1018	CB	LYS	C	128	27.354	12.774	33.419	1.00	111.82
45	1019	CG	LYS	C	128	27.672	13.421	34.740	1.00	111.82
	1020	CD	LYS	C	128	27.814	12.412	35.853	1.00	111.82
	1021	CE	LYS	C	128	27.997	13.133	37.204	1.00	111.82
	1022	NZ	LYS	C	128	28.021	12.205	38.387	1.00	111.82
	1023	C	LYS	C	128	28.096	11.462	31.430	1.00	71.66
50	1024	O	LYS	C	128	28.281	12.090	30.386	1.00	71.66
	1025	N	TYR	C	129	27.537	10.252	31.447	1.00	51.68
	1026	CA	TYR	C	129	27.110	9.616	30.208	1.00	51.68
	1027	CB	TYR	C	129	28.197	8.680	29.692	1.00	75.51
	1028	CG	TYR	C	129	27.655	7.647	28.732	1.00	75.51
55	1029	CD1	TYR	C	129	27.412	7.957	27.399	1.00	75.51
	1030	CE1	TYR	C	129	26.846	7.041	26.529	1.00	75.51
	1031	CD2	TYR	C	129	27.316	6.383	29.173	1.00	75.51
	1032	CE2	TYR	C	129	26.739	5.454	28.309	1.00	75.51
	1033	CZ	TYR	C	129	26.510	5.789	26.992	1.00	75.51
60	1034	OH	TYR	C	129	25.950	4.855	26.144	1.00	75.51
	1035	C	TYR	C	129	25.817	8.822	30.371	1.00	51.68
	1036	O	TYR	C	129	25.656	8.097	31.360	1.00	51.68
	1037	N	TRP	C	130	24.912	8.945	29.390	1.00	122.00
	1038	CA	TRP	C	130	23.641	8.226	29.404	1.00	122.00
65	1039	CB	TRP	C	130	22.531	9.082	29.995	1.00	131.84
	1040	CG	TRP	C	130	22.854	9.740	31.299	1.00	131.84
	1041	CD2	TRP	C	130	22.370	9.360	32.590	1.00	131.84
	1042	CE2	TRP	C	130	22.886	10.292	33.518	1.00	131.84
	1043	CE3	TRP	C	130	21.557	8.317	33.053	1.00	131.84
70	1044	CD1	TRP	C	130	23.613	10.850	31.489	1.00	131.84

	1045	NE1	TRP	C	130	23.636	11.194	32.819	1.00	131.84
	1046	CZ2	TRP	C	130	22.613	10.216	34.887	1.00	131.84
	1047	CZ3	TRP	C	130	21.283	8.239	34.422	1.00	131.84
	1048	CH2	TRP	C	130	21.809	9.190	35.319	1.00	131.84
5	1049	C	TRP	C	130	23.199	7.805	28.010	1.00	122.00
	1050	O	TRP	C	130	23.720	8.292	27.015	1.00	122.00
	1051	N	TYR	C	131	22.229	6.898	27.944	1.00	94.11
	1052	CA	TYR	C	131	21.710	6.443	26.663	1.00	94.11
	1053	CB	TYR	C	131	21.108	5.048	26.756	1.00	199.39
10	1054	CG	TYR	C	131	20.805	4.505	25.386	1.00	199.39
	1055	CD1	TYR	C	131	21.836	4.074	24.552	1.00	199.39
	1056	CE1	TYR	C	131	21.583	3.681	23.247	1.00	199.39
	1057	CD2	TYR	C	131	19.503	4.522	24.879	1.00	199.39
	1058	CE2	TYR	C	131	19.236	4.132	23.570	1.00	199.39
15	1059	CZ	TYR	C	131	20.283	3.716	22.761	1.00	199.39
	1060	OH	TYR	C	131	20.033	3.369	21.456	1.00	199.39
	1061	C	TYR	C	131	20.629	7.440	26.306	1.00	94.11
	1062	O	TYR	C	131	20.894	8.379	25.554	1.00	94.11
	1063	N	GLU	C	132	19.411	7.221	26.817	1.00	108.28
20	1064	CA	GLU	C	132	18.318	8.171	26.599	1.00	108.28
	1065	CB	GLU	C	132	16.986	7.670	27.185	1.00	249.42
	1066	CG	GLU	C	132	16.250	6.597	26.375	1.00	249.42
	1067	CD	GLU	C	132	14.874	7.058	25.901	1.00	249.42
	1068	OE1	GLU	C	132	14.343	8.036	26.469	1.00	249.42
25	1069	OE2	GLU	C	132	14.320	6.434	24.968	1.00	249.42
	1070	C	GLU	C	132	18.899	9.243	27.491	1.00	108.28
	1071	O	GLU	C	132	19.243	8.953	28.636	1.00	108.28
	1072	N	ASN	C	133	19.029	10.468	26.989	1.00	132.29
	1073	CA	ASN	C	133	19.665	11.502	27.790	1.00	132.29
30	1074	CB	ASN	C	133	19.946	12.758	26.960	1.00	123.07
	1075	CG	ASN	C	133	18.786	13.702	26.928	1.00	123.07
	1076	OD1	ASN	C	133	17.659	13.297	26.651	1.00	123.07
	1077	ND2	ASN	C	133	19.047	14.979	27.200	1.00	123.07
	1078	C	ASN	C	133	18.983	11.879	29.090	1.00	132.29
35	1079	O	ASN	C	133	17.884	11.434	29.412	1.00	132.29
	1080	N	HIS	C	134	19.677	12.730	29.824	1.00	77.87
	1081	CA	HIS	C	134	19.271	13.173	31.140	1.00	77.87
	1082	CB	HIS	C	134	20.089	12.388	32.162	1.00	247.23
	1083	CG	HIS	C	134	19.688	12.628	33.579	1.00	247.23
40	1084	CD2	HIS	C	134	20.364	13.171	34.619	1.00	247.23
	1085	ND1	HIS	C	134	18.451	12.270	34.071	1.00	247.23
	1086	CE1	HIS	C	134	18.385	12.581	35.352	1.00	247.23
	1087	NE2	HIS	C	134	19.532	13.127	35.710	1.00	247.23
	1088	C	HIS	C	134	19.573	14.664	31.255	1.00	77.87
45	1089	O	HIS	C	134	19.843	15.338	30.252	1.00	77.87
	1090	N	ASN	C	135	19.539	15.167	32.484	1.00	77.12
	1091	CA	ASN	C	135	19.779	16.576	32.747	1.00	77.12
	1092	CB	ASN	C	135	18.442	17.308	32.868	1.00	227.67
	1093	CG	ASN	C	135	17.690	17.335	31.558	1.00	227.67
50	1094	OD1	ASN	C	135	18.287	17.624	30.520	1.00	227.67
	1095	ND2	ASN	C	135	16.390	17.049	31.585	1.00	227.67
	1096	C	ASN	C	135	20.595	16.748	34.004	1.00	77.12
	1097	O	ASN	C	135	20.049	16.927	35.075	1.00	77.12
	1098	N	ILE	C	136	21.914	16.671	33.862	1.00	56.71
55	1099	CA	ILE	C	136	22.855	16.810	34.974	1.00	56.71
	1100	CB	ILE	C	136	24.267	17.147	34.439	1.00	111.08
	1101	CG2	ILE	C	136	24.215	18.298	33.468	1.00	111.08
	1102	CG1	ILE	C	136	25.189	17.479	35.590	1.00	111.08
	1103	CD1	ILE	C	136	26.605	17.684	35.143	1.00	111.08
60	1104	C	ILE	C	136	22.387	17.870	35.956	1.00	56.71
	1105	O	ILE	C	136	22.276	19.044	35.623	1.00	56.71
	1106	N	SER	C	137	22.090	17.429	37.172	1.00	99.75
	1107	CA	SER	C	137	21.594	18.308	38.225	1.00	99.75
	1108	CB	SER	C	137	20.218	17.820	38.673	1.00	125.93
65	1109	OG	SER	C	137	19.833	18.438	39.884	1.00	125.93
	1110	C	SER	C	137	22.517	18.411	39.437	1.00	99.75
	1111	O	SER	C	137	23.195	17.457	39.807	1.00	99.75
	1112	N	ILE	C	138	22.530	19.580	40.062	1.00	72.38
	1113	CA	ILE	C	138	23.366	19.816	41.235	1.00	72.38
70	1114	CB	ILE	C	138	24.560	20.663	40.881	1.00	52.39

	1115	CG2	ILE	C	138	·25.241	21.106	42.161	1.00	52.39
	1116	CG1	ILE	C	138	25.503	19.881	39.961	1.00	52.39
	1117	CD1	ILE	C	138	26.574	20.747	39.311	1.00	52.39
	1118	C	ILE	C	138	22.609	20.556	42.335	1.00	72.38
5	1119	O	ILE	C	138	22.109	21.667	42.112	1.00	72.38
	1120	N	THR	C	139	22.535	19.955	43.519	1.00	119.29
	1121	CA	THR	C	139	21.823	20.568	44.634	1.00	119.29
	1122	CB	THR	C	139	21.466	19.521	45.682	1.00	137.72
	1123	OG1	THR	C	139	22.642	18.774	46.024	1.00	137.72
10	1124	CG2	THR	C	139	20.404	18.578	45.139	1.00	137.72
	1125	C	THR	C	139	22.679	21.655	45.275	1.00	119.29
	1126	O	THR	C	139	22.449	22.849	45.063	1.00	119.29
	1127	N	ASN	C	140	23.661	21.232	46.066	1.00	83.41
	1128	CA	ASN	C	140	24.585	22.147	46.730	1.00	83.41
15	1129	CB	ASN	C	140	25.065	21.554	48.052	1.00	209.19
	1130	CG	ASN	C	140	26.123	22.402	48.714	1.00	209.19
	1131	OD1	ASN	C	140	27.087	22.824	48.073	1.00	209.19
	1132	ND2	ASN	C	140	25.950	22.645	50.006	1.00	209.19
	1133	C	ASN	C	140	25.758	22.277	45.780	1.00	83.41
20	1134	O	ASN	C	140	26.403	21.277	45.455	1.00	83.41
	1135	N	ALA	C	141	26.037	23.503	45.343	1.00	87.00
	1136	CA	ALA	C	141	27.121	23.741	44.394	1.00	87.00
	1137	CB	ALA	C	141	26.704	24.753	43.381	1.00	58.59
	1138	C	ALA	C	141	28.440	24.162	44.994	1.00	87.00
25	1139	O	ALA	C	141	28.527	25.112	45.753	1.00	87.00
	1140	N	THR	C	142	29.485	23.450	44.617	1.00	69.33
	1141	CA	THR	C	142	30.822	23.733	45.106	1.00	69.33
	1142	CB	THR	C	142	31.688	22.461	45.035	1.00	195.23
	1143	OG1	THR	C	142	31.001	21.383	45.687	1.00	195.23
30	1144	CG2	THR	C	142	33.012	22.679	45.722	1.00	195.23
	1145	C	THR	C	142	31.388	24.815	44.202	1.00	69.33
	1146	O	THR	C	142	30.753	25.185	43.219	1.00	69.33
	1147	N	VAL	C	143	32.561	25.341	44.531	1.00	71.38
	1148	CA	VAL	C	143	33.154	26.387	43.699	1.00	71.38
35	1149	CB	VAL	C	143	34.082	27.349	44.511	1.00	62.36
	1150	CG1	VAL	C	143	35.270	26.572	45.059	1.00	62.36
	1151	CG2	VAL	C	143	34.571	28.506	43.623	1.00	62.36
	1152	C	VAL	C	143	33.989	25.686	42.654	1.00	71.38
	1153	O	VAL	C	143	34.383	26.277	41.655	1.00	71.38
40	1154	N	GLU	C	144	34.272	24.416	42.897	1.00	78.73
	1155	CA	GLU	C	144	35.065	23.659	41.954	1.00	78.73
	1156	CB	GLU	C	144	35.604	22.384	42.599	1.00	249.12
	1157	CG	GLU	C	144	36.574	22.653	43.732	1.00	249.12
	1158	CD	GLU	C	144	36.019	22.238	45.078	1.00	249.12
45	1159	OE1	GLU	C	144	35.711	21.040	45.239	1.00	249.12
	1160	OE2	GLU	C	144	35.889	23.102	45.972	1.00	249.12
	1161	C	GLU	C	144	34.222	23.316	40.739	1.00	78.73
	1162	O	GLU	C	144	34.767	22.933	39.711	1.00	78.73
	1163	N	ASP	C	145	32.898	23.473	40.853	1.00	62.47
50	1164	CA	ASP	C	145	31.977	23.174	39.754	1.00	62.47
	1165	CB	ASP	C	145	30.545	23.066	40.260	1.00	127.97
	1166	CG	ASP	C	145	30.305	21.798	41.028	1.00	127.97
	1167	OD1	ASP	C	145	30.493	20.714	40.441	1.00	127.97
	1168	OD2	ASP	C	145	29.835	21.883	42.217	1.00	127.97
55	1169	C	ASP	C	145	32.053	24.220	38.663	1.00	62.47
	1170	O	ASP	C	145	31.548	24.011	37.568	1.00	62.47
	1171	N	SER	C	146	32.687	25.348	38.957	1.00	71.91
	1172	CA	SER	C	146	32.824	26.397	37.960	1.00	71.91
	1173	CB	SER	C	146	33.438	27.641	38.599	1.00	151.98
60	1174	OG	SER	C	146	32.599	28.127	39.630	1.00	151.98
	1175	C	SER	C	146	33.711	25.866	36.837	1.00	71.91
	1176	O	SER	C	146	34.648	25.109	37.082	1.00	71.91
	1177	N	GLY	C	147	33.394	26.241	35.606	1.00	84.55
	1178	CA	GLY	C	147	34.170	25.785	34.466	1.00	84.55
65	1179	C	GLY	C	147	33.449	26.062	33.158	1.00	84.55
	1180	O	GLY	C	147	32.552	26.898	33.121	1.00	84.55
	1181	N	THR	C	148	33.836	25.373	32.084	1.00	54.14
	1182	CA	THR	C	148	33.192	25.561	30.781	1.00	54.14
	1183	CB	THR	C	148	34.166	26.153	29.760	1.00	64.28
70	1184	OG1	THR	C	148	34.588	25.133	28.858	1.00	64.28

	1185	CG2	THR	C	148	.35.394	26.717	30.474	1.00	64.28
	1186	C	THR	C	148	32.671	24.216	30.285	1.00	54.14
	1187	O	THR	C	148	33.429	23.287	30.032	1.00	54.14
	1188	N	TYR	C	149	31.359	24.119	30.145	1.00	33.05
5	1189	CA	TYR	C	149	30.725	22.879	29.753	1.00	33.05
	1190	CB	TYR	C	149	29.524	22.656	30.627	1.00	43.72
	1191	CG	TYR	C	149	29.787	22.522	32.108	1.00	43.72
	1192	CD1	TYR	C	149	30.185	23.612	32.391	1.00	43.72
	1193	CE1	TYR	C	149	30.359	23.470	34.266	1.00	43.72
10	1194	CD2	TYR	C	149	29.574	21.296	32.738	1.00	43.72
	1195	CE2	TYR	C	149	29.739	21.143	34.095	1.00	43.72
	1196	CZ	TYR	C	149	30.130	22.222	34.876	1.00	43.72
	1197	OH	TYR	C	149	30.255	22.023	36.258	1.00	43.72
	1198	C	TYR	C	149	30.257	22.872	28.312	1.00	33.05
15	1199	O	TYR	C	149	30.212	23.905	27.666	1.00	33.05
	1200	N	TYR	C	150	29.929	21.687	27.818	1.00	75.60
	1201	CA	TYR	C	150	29.402	21.473	26.481	1.00	75.60
	1202	CB	TYR	C	150	30.453	21.790	25.384	1.00	80.46
	1203	CG	TYR	C	150	31.554	20.780	25.087	1.00	80.46
20	1204	CD1	TYR	C	150	31.282	19.581	24.439	1.00	80.46
	1205	C⁻¹	TYR	C	150	32.288	18.664	24.162	1.00	80.46
	1206	CD2	TYR	C	150	32.874	21.039	25.445	1.00	80.46
	1207	CE2	TYR	C	150	33.889	20.130	25.168	1.00	80.46
	1208	CZ	TYR	C	150	33.590	18.938	24.529	1.00	80.46
25	1209	OH	TYR	C	150	34.597	18.011	24.280	1.00	80.46
	1210	C	TYR	C	150	28.963	20.007	26.498	1.00	75.60
	1211	O	TYR	C	150	29.374	19.239	27.375	1.00	75.60
	1212	N	CYS	C	151	28.090	19.604	25.586	1.00	100.28
	1213	CA	CYS	C	151	27.657	18.211	25.572	1.00	100.28
30	1214	C	CYS	C	151	27.674	17.617	24.167	1.00	100.28
	1215	O	CYS	C	151	27.634	18.349	23.191	1.00	100.28
	1216	CB	CYS	C	151	26.255	18.096	26.172	1.00	64.15
	1217	SG	CYS	C	151	24.959	19.135	25.424	1.00	64.15
	1218	N	THR	C	152	27.746	16.291	24.074	1.00	69.97
35	1219	CA	THR	C	152	27.755	15.598	22.795	1.00	69.97
	1220	CB	THR	C	152	29.089	14.837	22.588	1.00	86.22
	1221	OG1	THR	C	152	29.210	13.780	23.550	1.00	86.22
	1222	CG2	THR	C	152	30.247	15.771	22.765	1.00	86.22
	1223	C	THR	C	152	26.594	14.610	22.813	1.00	69.97
40	1224	O	THR	C	152	26.242	14.082	23.879	1.00	69.97
	1225	N	GLY	C	153	25.992	14.368	21.652	1.00	96.14
	1226	CA	GLY	C	153	24.879	13.441	21.597	1.00	96.14
	1227	C	GLY	C	153	24.588	13.010	20.182	1.00	96.14
	1228	O	GLY	C	153	25.037	13.663	19.247	1.00	96.14
45	1229	N	LYS	C	154	23.845	11.918	20.017	1.00	77.66
	1230	CA	LYS	C	154	23.522	11.431	18.690	1.00	77.66
	1231	CB	LYS	C	154	23.722	9.916	18.603	1.00	222.01
	1232	CG	LYS	C	154	23.538	9.323	17.212	1.00	222.01
	1233	CD	LYS	C	154	23.820	7.833	17.253	1.00	222.01
50	1234	CE	LYS	C	154	23.556	7.151	15.924	1.00	222.01
	1235	NZ	LYS	C	154	23.726	5.689	16.075	1.00	222.01
	1236	C	LYS	C	154	22.086	11.796	18.428	1.00	77.66
	1237	O	LYS	C	154	21.221	11.567	19.269	1.00	77.66
	1238	N	VAL	C	155	21.843	12.405	17.271	1.00	110.66
55	1239	CA	VAL	C	155	20.496	12.796	16.862	1.00	110.66
	1240	CB	VAL	C	155	20.397	14.288	16.58⁵	1.00	77.82
	1241	CG1	VAL	C	155	18.985	14.643	16.163	1.00	77.82
	1242	CG2	VAL	C	155	20.778	15.046	17.834	1.00	77.82
	1243	C	VAL	C	155	20.208	12.046	15.579	1.00	110.66
60	1244	O	VAL	C	155	21.000	12.085	14.629	1.00	110.66
	1245	N	TRP	C	156	19.074	11.363	15.553	1.00	192.10
	1246	CA	TRP	C	156	18.727	10.560	14.401	1.00	192.10
	1247	CB	TRP	C	156	18.811	11.362	13.120	1.00	246.44
	1248	CG	TRP	C	156	17.823	12.399	13.086	1.00	246.44
65	1249	CD2	TRP	C	156	16.417	12.222	13.206	1.00	246.44
	1250	CE2	TRP	C	156	15.830	13.503	13.150	1.00	246.44
	1251	CE3	TRP	C	156	15.592	11.100	13.355	1.00	246.44
	1252	CD1	TRP	C	156	18.042	13.729	12.960	1.00	246.44
	1253	NE1	TRP	C	156	16.846	14.407	13.005	1.00	246.44
70	1254	CZ2	TRP	C	156	14.454	13.698	13.239	1.00	246.44

	1255	CZ3	TRP	C	156	·14.217	11.293	13.438	1.00	246.44
	1256	CH2	TRP	C	156	13.662	12.588	13.378	1.00	246.44
	1257	C	TRP	C	156	19.771	9.496	14.335	1.00	192.10
	1258	O	TRP	C	156	19.673	8.478	15.006	1.00	192.10
5	1259	N	GLN	C	157	20.800	9.769	13.545	1.00	118.64
	1260	CA	GLN	C	157	21.861	8.814	13.373	1.00	118.64
	1261	CB	GLN	C	157	21.511	7.831	12.180	1.00	249.64
	1262	CG	GLN	C	157	20.361	6.995	12.528	1.00	249.64
	1263	CD	GLN	C	157	20.670	6.255	13.803	1.00	249.64
10	1264	OE1	GLN	C	157	21.748	5.725	13.918	1.00	249.64
	1265	NE2	GLN	C	157	19.770	6.241	14.761	1.00	249.64
	1266	C	GLN	C	157	23.230	9.430	13.234	1.00	118.64
	1267	O	GLN	C	157	24.183	8.768	12.826	1.00	118.64
	1268	N	LEU	C	158	23.323	10.707	13.574	1.00	91.98
15	1269	CA	LEU	C	158	24.600	11.404	13.510	1.00	91.98
	1270	CB	LEU	C	158	24.580	12.461	12.418	1.00	164.15
	1271	CG	LEU	C	158	24.775	11.991	10.980	1.00	164.15
	1272	CD1	LEU	C	158	25.736	12.973	10.359	1.00	164.15
	1273	CD2	LEU	C	158	25.383	10.614	10.868	1.00	164.15
20	1274	C	LEU	C	158	25.000	12.046	14.841	1.00	91.98
	1275	O	LEU	C	158	24.147	12.397	15.658	1.00	91.98
	1276	N	ASP	C	159	26.307	12.190	15.047	1.00	113.11
	1277	CA	ASP	C	159	26.839	12.762	16.273	1.00	113.11
	1278	CB	ASP	C	159	28.230	12.173	16.564	1.00	249.37
25	1279	CG	ASP	C	159	28.236	10.645	16.599	1.00	249.37
	1280	OD1	ASP	C	159	27.536	10.057	17.451	1.00	249.37
	1281	OD2	ASP	C	159	28.949	10.033	15.771	1.00	249.37
	1282	C	ASP	C	159	26.939	14.280	16.148	1.00	113.11
	1283	O	ASP	C	159	27.223	14.788	15.063	1.00	113.11
30	1284	N	TYR	C	160	26.701	14.995	17.254	1.00	103.02
	1285	CA	TYR	C	160	26.782	16.464	17.278	1.00	103.02
	1286	CB	TYR	C	160	25.424	17.105	17.057	1.00	177.48
	1287	CG	TYR	C	160	24.711	16.622	15.826	1.00	177.48
	1288	CD1	TYR	C	160	23.860	15.521	15.882	1.00	177.48
35	1289	CE1	TYR	C	160	23.204	15.062	14.752	1.00	177.48
	1290	CD2	TYR	C	160	24.891	17.255	14.600	1.00	177.48
	1291	CE2	TYR	C	160	24.241	16.804	13.458	1.00	177.48
	1292	CZ	TYR	C	160	23.400	15.707	13.545	1.00	177.48
	1293	OH	TYR	C	160	22.763	15.245	12.427	1.00	177.48
40	1294	C	TYR	C	160	27.333	16.998	18.581	1.00	103.02
	1295	O	TYR	C	160	27.095	16.449	19.647	1.00	103.02
	1296	N	GLU	C	161	28.052	18.102	18.474	1.00	74.72
	1297	CA	GLU	C	161	28.687	18.775	19.599	1.00	74.72
	1298	CB	GLU	C	161	30.170	18.972	19.273	1.00	249.14
45	1299	CG	GLU	C	161	30.978	19.729	20.300	1.00	249.14
	1300	CD	GLU	C	161	32.456	19.531	20.085	1.00	249.14
	1301	OE1	GLU	C	161	33.259	20.350	20.582	1.00	249.14
	1302	OE2	GLU	C	161	32.808	18.538	19.417	1.00	249.14
	1303	C	GLU	C	161	27.985	20.117	19.779	1.00	74.72
50	1304	O	GLU	C	·161	27.656	20.780	18.806	1.00	74.72
	1305	N	SER	C	162	27.743	20.516	21.021	1.00	59.53
	1306	CA	SER	C	162	27.055	21.776	21.320	1.00	59.53
	1307	CB	SER	C	162	26.210	21.627	22.573	1.00	71.52
	1308	OG	SER	C	162	27.017	21.253	23.673	1.00	71.52
55	1309	C	SER	C	162	28.038	22.914	21.532	1.00	59.53
	1310	O	SER	C	162	29.247	22.679	21.608	1.00	59.53
	1311	N	GLU	C	163	27.521	24.145	21.615	1.00	68.20
	1312	CA	GLU	C	163	28.371	25.330	21.810	1.00	68.20
	1313	CB	GLU	C	163	27.580	26.610	21.565	1.00	172.64
60	1314	CG	GLU	C	163	27.289	26.902	20.098	1.00	172.64
	1315	CD	GLU	C	163	28.513	27.375	19.334	1.00	172.64
	1316	OE1	GLU	C	163	29.120	28.383	19.757	1.00	172.64
	1317	OE2	GLU	C	163	28.864	26.748	18.311	1.00	172.64
	1318	C	GLU	C	163	28.856	25.296	23.246	1.00	68.20
65	1319	O	GLU	C	163	28.104	24.920	24.131	1.00	68.20
	1320	N	PRO	C	164	30.123	25.683	23.498	1.00	54.78
	1321	CD	PRO	C	164	31.163	26.188	22.601	1.00	96.83
	1322	CA	PRO	C	164	30.609	25.645	24.876	1.00	54.78
	1323	CB	PRO	C	164	32.109	25.851	24.709	1.00	96.83
70	1324	CG	PRO	C	164	32.176	26.765	23.584	1.00	96.83

	1325	C	PRO	C	164	·29.850	26.720	25.688	1.00	54.78
	1326	O	PRO	C	164	29.480	27.695	25.137	1.00	54.78
	1327	N	LEU	C	165	29.898	26.537	27.000	1.00	73.43
	1328	CA	LEU	C	165	29.272	27.513	27.861	1.00	73.43
5	1329	CB	LEU	C	165	27.829	27.112	28.127	1.00	54.02
	1330	CG	LEU	C	165	27.163	27.955	29.201	1.00	54.02
	1331	CD1	LEU	C	165	27.395	29.384	28.820	1.00	54.02
	1332	CD2	LEU	C	165	25.690	27.665	29.329	1.00	54.02
	1333	C	LEU	C	165	30.010	27.634	29.164	1.00	73.43
10	1334	O	LEU	C	165	30.200	26.641	29.859	1.00	73.43
	1335	N	ASN	C	166	30.420	28.853	29.493	1.00	53.84
	1336	CA	ASN	C	166	31.148	29.098	30.736	1.00	53.84
	1337	CB	ASN	C	166	31.979	30.368	30.646	1.00	80.99
	1338	CG	ASN	C	166	33.392	30.110	30.181	1.00	80.99
15	1339	OD1	ASN	C	166	33.956	29.054	30.431	1.00	80.99
	1340	ND2	ASN	C	166	33.973	31.096	29.516	1.00	80.99
	1341	C	ASN	C	166	30.233	29.236	31.918	1.00	53.84
	1342	O	ASN	C	166	29.145	29.756	31.789	1.00	53.84
	1343	N	ILE	C	167	30.693	28.806	33.084	1.00	65.33
20	1344	CA	ILE	C	167	29.878	28.881	34.292	1.00	65.33
	1345	CB	ILE	C	167	29.218	27.527	34.603	1.00	38.60
	1346	CG2	ILE	C	167	28.736	27.503	36.027	1.00	38.60
	1347	CG1	ILE	C	167	28.066	27.269	33.618	1.00	38.60
25	1348	CD1	ILE	C	167	27.261	26.070	33.933	1.00	38.60
	1349	C	ILE	C	167	30.717	29.258	35.475	1.00	65.33
	1350	O	ILE	C	167	31.781	28.681	35.694	1.00	65.33
	1351	N	THR	C	168	3°.²¹⁰	30.223	36.246	1.00	58.90
	1352	CA	THR	C	168	31.015	30.619	37.406	1.00	58.90
30	1353	CB	THR	C	168	31.537	32.023	37.260	1.00	100.28
	1354	OG1	THR	C	168	32.315	32.110	36.067	1.00	100.28
	1355	CG2	THR	C	168	32.406	32.354	38.438	1.00	100.28
	1356	C	THR	C	168	30.230	30.502	38.708	1.00	58.90
	1357	O	THR	C	168	29.042	30.852	38.795	1.00	58.90
35	1358	N	VAL	C	169	30.908	29.965	39.708	1.00	74.23
	1359	CA	VAL	C	169	30.337	29.795	41.021	1.00	74.23
	1360	CB	VAL	C	169	30.424	28.330	41.467	1.00	86.72
	1361	CG1	VAL	C	169	30.314	28.229	42.962	1.00	86.72
	1362	CG2	VAL	C	169	29.323	27.547	40.813	1.00	86.72
	1363	C	VAL	C	169	31.196	30.668	41.924	1.00	74.23
40	1364	O	VAL	C	169	32.359	30.328	42.184	1.00	74.23
	1365	N	ILE	C	170	30.645	31.805	42.365	1.00	66.08
	1366	CA	ILE	C	170	31.376	32.711	43.252	1.00	66.08
	1367	CB	ILE	C	170	30.995	34.166	42.997	1.00	82.85
45	1368	CG2	ILE	C	170	31.079	34.476	41.520	1.00	82.85
	1369	CG1	ILE	C	170	29.572	34.412	43.431	1.00	82.85
	1370	CD1	ILE	C	170	29.097	35.848	43.156	1.00	82.85
	1371	C	ILE	C	170	31.092	32.355	44.701	1.00	66.08
	1372	O	ILE	C	170	30.272	31.482	44.960	1.00	66.08
50	1373	N	LYS	C	171	31.771	32.999	45.644	1.00	110.58
	1374	CA	LYS	C	171	31.545	32.688	47.052	1.00	110.58
	1375	CB	LYS	C	171	32.749	31.935	47.625	1.00	192.81
	1376	CG	LYS	C	171	34.062	32.679	47.478	1.00	192.81
	1377	CD	LYS	C	171	35.247	31.723	47.505	1.00	192.81
55	1378	CE	LYS	C	171	35.319	30.934	48.803	1.00	192.81
	1379	NZ	LYS	C	171	36.464	29.978	48.796	1.00	192.81
	1380	C	LYS	C	171	31.263	33.931	47.882	1.00	110.58
	1381	O	LYS	C	171	30.884	33.830	49.050	1.00	110.58
	1382	C1	NAG	C	221	4.609	28.125	21.539	1.00	248.09
60	1383	C2	NAG	C	221	4.738	26.611	21.473	1.00	248.09
	1384	N2	NAG	C	221	6.129	26.254	21.269	1.00	248.09
	1385	C7	NAG	C	221	6.578	25.075	21.680	1.00	248.09
	1386	O7	NAG	C	221	5.867	24.254	22.257	1.00	248.09
	1387	C8	NAG	C	221	8.042	24.762	21.420	1.00	248.09
65	1388	C3	NAG	C	221	3.908	26.047	20.327	1.00	248.09
	1389	O3	NAG	C	221	3.902	24.630	20.401	1.00	248.09
	1390	C4	NAG	C	221	2.465	26.559	20.341	1.00	248.09
	1391	O4	NAG	C	221	1.852	26.163	19.095	1.00	248.09
	1392	C5	NAG	C	221	2.447	28.096	20.488	1.00	248.09
	1393	O5	NAG	C	221	3.226	28.499	21.641	1.00	248.09
70	1394	C6	NAG	C	221	1.052	28.659	20.692	1.00	248.09

	1395	O6	NAG	C	221	0.460	28.142	21.875	1.00	248.09
	1396	C1	NAG	C	222	0.468	26.179	18.986	1.00	248.99
	1397	C2	NAG	C	222	-0.014	24.897	18.283	1.00	248.99
	1398	N2	NAG	C	222	0.382	23.729	19.048	1.00	248.99
5	1399	C7	NAG	C	222	-0.541	22.909	19.543	1.00	248.99
	1400	O7	NAG	C	222	-1.750	23.088	19.392	1.00	248.99
	1401	C8	NAG	C	222	-0.046	21.704	20.330	1.00	248.99
	1402	C3	NAG	C	222	0.566	24.815	16.861	1.00	248.99
	1403	O3	NAG	C	222	-0.012	23.714	16.171	1.00	248.99
10	1404	C4	NAG	C	222	0.292	26.112	16.083	1.00	248.99
	1405	O4	NAG	C	222	0.989	26.082	14.843	1.00	248.99
	1406	C5	NAG	C	222	0.742	27.337	16.897	1.00	248.99
	1407	O5	NAG	C	222	0.107	27.330	18.201	1.00	248.99
	1408	C6	NAG	C	222	0.396	28.661	16.232	1.00	248.99
15	1409	O6	NAG	C	222	1.499	29.556	16.260	1.00	248.99
	1410	C1	NAG	C	242	18.858	43.706	21.097	1.00	98.91
	1411	C2	NAG	C	242	18.159	43.460	19.760	1.00	98.91
	1412	N2	NAG	C	242	16.728	43.568	19.914	1.00	98.91
	1413	C7	NAG	C	242	16.062	44.435	19.166	1.00	98.91
20	1414	O7	NAG	C	242	16.610	45.163	18.336	1.00	98.91
	1415	C8	NAG	C	242	14.561	44.512	19.366	1.00	98.91
	1416	C3	NAG	C	242	18.507	42.075	19.237	1.00	98.91
	1417	O3	NAG	C	242	17.925	41.880	17.955	1.00	98.91
	1418	C4	NAG	C	242	20.020	41.925	19.144	1.00	98.91
25	1419	O4	NAG	C	242	20.340	40.556	18.833	1.00	98.91
	1420	C5	NAG	C	242	20.708	42.318	20.459	1.00	98.91
	1421	O5	NAG	C	242	20.270	43.615	20.916	1.00	98.91
	1422	C6	NAG	C	242	22.196	42.434	20.243	1.00	98.91
	1423	O6	NAG	C	242	22.917	41.643	21.170	1.00	98.91
30	1424	C1	NAG	C	243	20.966	40.334	17.621	1.00	148.54
	1425	C2	NAG	C	243	21.805	39.050	17.674	1.00	148.54
	1426	N2	NAG	C	243	22.863	39.159	18.662	1.00	148.54
	1427	C7	NAG	C	243	23.081	38.154	19.504	1.00	148.54
	1428	O7	NAG	C	243	22.402	37.126	19.506	1.00	148.54
35	1429	C8	NAG	C	243	24.212	38.320	20.503	1.00	148.54
	1430	C3	NAG	C	243	22.422	38.803	16.299	1.00	148.54
	1431	O3	NAG	C	243	23.126	37.573	16.300	1.00	148.54
	1432	C4	NAG	C	243	21.341	38.791	15.201	1.00	148.54
	1433	O4	NAG	C	243	21.974	38.713	13.890	1.00	148.54
40	1434	C5	NAG	C	243	20.529	40.090	15.296	1.00	148.54
	1435	O5	NAG	C	243	19.954	40.216	16.611	1.00	148.54
	1436	C6	NAG	C	243	19.402	40.197	14.299	1.00	148.54
	1437	O6	NAG	C	243	18.380	39.264	14.597	1.00	148.54
	1438	C1	MAN	C	244	21.585	37.818	12.938	1.00	182.20
45	1439	C2	MAN	C	244	21.654	36.312	13.272	1.00	182.20
	1440	O2	MAN	C	244	20.383	35.858	13.660	1.00	182.20
	1441	C3	MAN	C	244	22.042	35.694	11.892	1.00	182.20
	1442	O3	MAN	C	244	22.157	34.284	11.945	1.00	182.20
	1443	C4	MAN	C	244	21.095	36.131	10.730	1.00	182.20
50	1444	O4	MAN	C	244	21.496	35.520	9.503	1.00	182.20
	1445	C5	MAN	C	244	21.199	37.666	10.607	1.00	182.20
	1446	O5	MAN	C	244	20.771	38.312	11.834	1.00	182.20
	1447	C6	MAN	C	244	20.464	38.264	9.406	1.00	182.20
	1448	O6	MAN	C	244	19.092	38.434	9.670	1.00	182.20
55	1449	C1	NAG	C	250	-1.001	38.689	31.557	1.00	249.77
	1450	C2	NAG	C	250	-1.761	37.609	32.354	1.00	249.77
	1451	N2	NAG	C	250	-1.602	37.821	33.782	1.00	249.77
	1452	C7	NAG	C	250	-2.636	38.209	34.526	1.00	249.77
	1453	O7	NAG	C	250	-3.761	38.414	34.060	1.00	249.77
60	1454	C8	NAG	C	250	-2.384	38.404	36.016	1.00	249.77
	1455	C3	NAG	C	250	-1.221	36.224	31.975	1.00	249.77
	1456	O3	NAG	C	250	-1.975	35.209	32.626	1.00	249.77
	1457	C4	NAG	C	250	-1.287	36.028	30.458	1.00	249.77
	1458	O4	NAG	C	250	-0.662	34.799	30.113	1.00	249.77
65	1459	C5	NAG	C	250	-0.582	37.194	29.736	1.00	249.77
	1460	O5	NAG	C	250	-1.150	38.457	30.150	1.00	249.77
	1461	C6	NAG	C	250	-0.717	37.121	28.224	1.00	249.77
	1462	O6	NAG	C	250	-0.351	38.351	27.612	1.00	249.77
	1463	C1	NAG	C	274	16.034	53.837	43.921	1.00	248.46
70	1464	C2	NAG	C	274	17.088	53.346	44.921	1.00	248.46

	1465	N2	NAG C	274	.16.465	52.511	45.928	1.00	248.46
	1466	C7	NAG C	274	17.189	51.604	46.575	1.00	248.46
	1467	O7	NAG C	274	18.387	51.422	46.354	1.00	248.46
	1468	C8	NAG C	274	16.474	50.767	47.625	1.00	248.46
5	1469	C3	NAG C	274	17.768	54.539	45.598	1.00	248.46
	1470	O3	NAG C	274	18.835	54.081	46.416	1.00	248.46
	1471	C4	NAG C	274	18.306	55.518	44.553	1.00	248.46
	1472	O4	NAG C	274	18.793	56.685	45.202	1.00	248.46
	1473	C5	NAG C	274	17.195	55.898	43.563	1.00	248.46
10	1474	O5	NAG C	274	16.641	54.710	42.959	1.00	248.46
	1475	C6	NAG C	274	17.688	56.784	42.432	1.00	248.46
	1476	O6	NAG C	274	16.703	56.920	41.418	1.00	248.46
	1477	C1	NAG C	335	15.450	18.012	31.039	1.00	249.77
	1478	C2	NAG C	335	14.351	18.418	32.049	1.00	249.77
15	1479	N2	NAG C	335	14.844	18.144	31.387	1.00	249.77
	1480	C7	NAG C	335	15.027	19.131	34.258	1.00	249.77
	1481	O7	NAG C	335	14.782	20.312	34.004	1.00	249.77
	1482	C8	NAG C	335	15.555	18.743	35.627	1.00	249.77
	1483	C3	NAG C	335	13.010	17.686	31.860	1.00	249.77
20	1484	O3	NAG C	335	11.981	18.411	32.519	1.00	249.77
	1485	C4	NAG C	335	12.654	17.546	30.386	1.00	249.77
	1486	O4	NAG C	335	11.455	16.796	30.245	1.00	249.77
	1487	C5	NAG C	335	13.801	16.839	29.679	1.00	249.77
	1488	O5	NAG C	335	14.974	17.683	29.710	1.00	249.77
25	1489	C6	NAG C	335	13.481	16.566	28.214	1.00	249.77
	1490	O6	NAG C	335	13.512	15.176	27.922	1.00	249.77
	1491	C1	NAG C	340	26.860	22.059	50.969	1.00	249.77
	1492	C2	NAG C	340	27.612	23.165	51.681	1.00	249.77
	1493	N2	NAG C	340	28.257	24.040	50.724	1.00	243.77
30	1494	C7	NAG C	340	28.068	25.353	50.821	1.00	249.77
	1495	O7	NAG C	340	27.368	25.865	51.703	1.00	249.77
	1496	C8	NAG C	340	28.755	26.232	49.794	1.00	249.77
	1497	C3	NAG C	340	28.630	22.560	52.634	1.00	249.77
	1498	O3	NAG C	340	29.275	23.608	53.354	1.00	249.77
35	1499	C4	NAG C	340	27.915	21.620	53.612	1.00	249.77
	1500	O4	NAG C	340	28.896	20.922	54.365	1.00	249.77
	1501	C5	NAG C	340	26.987	20.611	52.880	1.00	249.77
	1502	O5	NAG C	340	26.141	21.281	51.923	1.00	249.77
	1503	C6	NAG C	340	26.045	19.869	53.817	1.00	249.77
40	1504	O6	NAG C	340	24.805	19.571	53.193	1.00	249.77
	1505	C1	NAG C	366	35.293	30.923	28.965	1.00	158.36
	1506	C2	NAG C	366	35.391	31.732	27.687	1.00	158.36
	1507	N2	NAG C	366	34.394	31.261	26.748	1.00	158.36
	1508	C7	NAG C	366	33.197	31.835	26.713	1.00	158.36
45	1509	O7	NAG C	366	32.885	32.778	27.446	1.00	158.36
	1510	C8	NAG C	366	32.191	31.285	25.707	1.00	158.36
	1511	C3	NAG C	366	36.780	31.584	27.089	1.00	158.36
	1512	O3	NAG C	366	36.910	32.461	25.981	1.00	158.36
	1513	C4	NAG C	366	37.866	31.903	28.119	1.00	158.36
50	1514	O4	NAG C	366	39.144	31.523	27.573	1.00	158.36
	1515	C5	NAG C	366	37.620	31.138	29.429	1.00	158.36
	1516	O5	NAG C	366	36.277	31.367	29.896	1.00	158.36
	1517	C6	NAG C	366	38.550	31.570	30.549	1.00	158.36
	1518	O6	NAG C	366	38.325	30.807	31.727	1.00	158.36
55	1519	C1	NAG C	367	40.136	32.494	27.559	1.00	249.59
	1520	C2	NAG C	367	41.511	31.828	27.487	1.00	249.59
	1521	N2	NAG C	367	41.702	30.834	28.613	1.00	249.59
	1522	C7	NAG C	367	41.695	29.619	28.418	1.00	249.59
	1523	O7	NAG C	367	41.532	29.106	27.308	1.00	249.59
60	1524	C8	NAG C	367	41.899	28.735	29.639	1.00	249.59
	1525	C3	NAG C	367	42.590	32.914	27.465	1.00	249.59
	1526	O3	NAG C	367	43.877	32.321	27.352	1.00	249.59
	1527	C4	NAG C	367	42.343	33.850	26.278	1.00	249.59
	1528	O4	NAG C	367	43.281	34.917	26.303	1.00	249.59
65	1529	C5	NAG C	367	40.913	34.411	26.335	1.00	249.59
	1530	O5	NAG C	367	39.945	33.331	26.405	1.00	249.59
	1531	C6	NAG C	367	40.576	35.245	25.112	1.00	249.59
	1532	O6	NAG C	367	39.610	34.604	24.292	1.00	249.59
	1533	CB	LYS A	4	5.822	17.052	16.197	1.00	225.85
70	1534	CG	LYS A	4	4.918	18.220	15.853	1.00	225.85

1535	CD	LYS	A	4	4.535	18.995	17.100	1.00	225.85
1536	CE	LYS	A	4	3.638	20.173	16.766	1.00	225.85
1537	NZ	LYS	A	4	3.267	20.934	17.987	1.00	225.85
1538	C	LYS	A	4	7.001	17.239	14.016	1.00	249.21
1539	O	LYS	A	4	7.491	18.292	14.419	1.00	249.21
1540	N	LYS	A	4	7.236	15.183	15.408	1.00	249.21
1541	CA	LYS	A	4	6.316	16.275	14.978	1.00	249.21
1542	N	PRO	A	5	7.053	16.880	12.723	1.00	94.49
1543	CD	PRO	A	5	6.773	15.535	12.187	1.00	84.99
1544	CA	PRO	A	5	7.685	17.735	11.709	1.00	94.49
1545	CB	PRO	A	5	8.092	16.736	10.629	1.00	84.99
1546	CG	PRO	A	5	7.010	15.716	10.691	1.00	84.99
1547	C	PRO	A	5	6.772	18.825	11.164	1.00	94.49
1548	O	PRO	A	5	5.557	18.721	11.227	1.00	94.49
1549	N	LYS	A	6	7.358	19.877	10.617	1.00	99.70
1550	CA	LYS	A	6	6.559	20.973	10.084	1.00	99.70
1551	CB	LYS	A	6	6.444	22.094	11.130	1.00	128.86
1552	CG	LYS	A	6	5.540	23.242	10.711	1.00	128.86
1553	CD	LYS	A	6	5.290	24.223	11.853	1.00	128.86
1554	CE	LYS	A	6	4.321	25.329	11.418	1.00	128.86
1555	NZ	LYS	A	6	3.977	26.285	12.517	1.00	128.86
1556	C	LYS	A	6	7.166	21.512	8.793	1.00	99.70
1557	O	LYS	A	6	8.281	22.029	8.801	1.00	99.70
1558	N	VAL	A	7	6.421	21.395	7.693	1.00	71.19
1559	CA	VAL	A	7	6.878	21.852	6.377	1.00	71.19
1560	CB	VAL	A	7	5.955	21.392	5.243	1.00	54.73
1561	CG1	VAL	A	7	6.584	21.739	3.900	1.00	54.73
1562	CG2	VAL	A	7	5.687	19.922	5.350	1.00	54.73
1563	C	VAL	A	7	6.947	23.354	6.221	1.00	71.19
1564	O	VAL	A	7	5.924	24.023	6.282	1.00	71.19
1565	N	SER	A	8	8.141	23.885	5.988	1.00	76.52
1566	CA	SER	A	8	8.301	25.325	5.804	1.00	76.52
1567	CB	SER	A	8	9.537	25.827	6.563	1.00	232.80
1568	OG	SER	A	8	10.701	25.106	6.196	1.00	232.80
1569	C	SER	A	8	8.437	25.597	4.311	1.00	76.52
1570	O	SER	A	8	8.665	24.679	3.534	1.00	76.52
1571	N	LEU	A	9	8.274	26.851	3.914	1.00	77.48
1572	CA	LEU	A	9	8.388	27.237	2.509	1.00	77.48
1573	CB	LEU	A	9	7.037	27.651	1.935	1.00	70.08
1574	CG	LEU	A	9	5.879	26.663	1.868	1.00	70.08
1575	CD1	LEU	A	9	4.901	27.105	0.816	1.00	70.08
1576	CD2	LEU	A	9	6.399	25.305	1.517	1.00	70.08
1577	C	LEU	A	9	9.321	28.417	2.334	1.00	77.48
1578	O	LEU	A	9	9.506	29.212	3.257	1.00	77.48
1579	N	ASN	A	10	9.896	28.544	1.140	1.00	96.41
1580	CA	ASN	A	10	10.795	29.657	0.844	1.00	96.41
1581	CB	ASN	A	10	12.196	29.384	1.384	1.00	121.54
1582	CG	ASN	A	10	13.074	30.616	1.338	1.00	121.54
1583	OD1	ASN	A	10	12.819	31.598	2.041	1.00	121.54
1584	ND2	ASN	A	10	14.108	30.581	0.496	1.00	121.54
1585	C	ASN	A	10	10.868	29.920	-0.654	1.00	96.41
1586	O	ASN	A	10	11.396	29.110	-1.412	1.00	96.41
1587	N	PRO	A	11	10.325	31.064	-1.105	1.00	78.36
1588	CD	PRO	A	11	10.263	31.320	-2.548	1.00	72.21
1589	CA	PRO	A	11	9.642	32.128	-0.350	1.00	78.36
1590	CB	PRO	A	11	9.130	33.049	-1.455	1.00	72.21
1591	CG	PRO	A	11	10.084	32.803	-2.583	1.00	72.21
1592	C	PRO	A	11	8.492	31.647	0.551	1.00	78.36
1593	O	PRO	A	11	7.992	30.537	0.386	1.00	78.36
1594	N	PRO	A	12	8.056	32.469	1.513	1.00	81.66
1595	CD	PRO	A	12	8.570	33.812	1.833	1.00	122.93
1596	CA	PRO	A	12	6.968	32.110	2.430	1.00	81.66
1597	CB	PRO	A	12	6.925	33.274	3.409	1.00	122.93
1598	CG	PRO	A	12	8.277	33.895	3.290	1.00	122.93
1599	C	PRO	A	12	5.837	31.998	1.663	1.00	81.66
1600	O	PRO	A	12	4.695	31.307	2.081	1.00	81.66
1601	N	TRP	A	13	5.579	32.699	0.538	1.00	66.49
1602	CA	TRP	A	13	4.388	32.725	-0.293	1.00	66.49
1603	CB	TRP	A	13	4.660	33.539	-1.562	1.00	100.34
1604	CG	TRP	A	13	5.336	34.831	-1.277	1.00	100.34

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	1605	CD2	TRP	A	13	· 5.100	35.697	-0.167	1.00	100.34
	1606	CE2	TRP	A	13	6.000	36.762	-0.268	1.00	100.34
	1607	CE3	TRP	A	13	4.210	35.673	0.909	1.00	100.34
	1608	CD1	TRP	A	13	6.339	35.393	-1.996	1.00	100.34
5	1609	NE1	TRP	A	13	6.748	36.552	-1.395	1.00	100.34
	1610	CZ2	TRP	A	13	6.046	37.795	0.664	1.00	100.34
	1611	CZ3	TRP	A	13	4.253	36.698	1.829	1.00	100.34
	1612	CH2	TRP	A	13	5.167	37.745	1.705	1.00	100.34
	1613	C	TRP	A	13 ·	3.913	31.342	-0.666	1.00	66.49
10	1614	O	TRP	A	13	4.637	30.573	-1.270	1.00	66.49
	1615	N	ASN	A	14	2.685	31.031	-0.299	1.00	52.07
	1616	CA	ASN	A	14	2.109	29.738	-0.629	1.00	52.07
	1617	CB	ASN	A	14	1.508	29.082	0.626	1.00	104.36
	1618	CG	ASN	A	14	0.274	29.801	1.152	1.00	104.36
15	1619	OD1	ASN	A	14	0.305	31.001	1.465	1.00	104.36
	1620	ND2	ASN	A	14	-0.822	29.058	1.269	1.00	104.36
	1621	C	ASN	A	14	1.056	29.792	-1.759	1.00	52.07
	1622	O	ASN	A	14	0.271	28.850	-1.928	1.00	52.07
	1623	N	ARG	A	15	1.026	30.900	-2.509	1.00	52.98
20	1624	CA	ARG	A	15	0.131	31.078	-3.667	1.00	52.98
	1625	CB	ARG	A	15	-0.942	32.109	-3.415	1.00	66.97
	1626	CG	ARG	A	15	-1.533	32.043	-2.077	1.00	66.97
	1627	CD	ARG	A	15	-2.626	33.064	-2.014	1.00	66.97
	1628	NE	ARG	A	15	-3.768	32.699	-2.837	1.00	66.97
25	1629	CZ	ARG	A	15	-4.589	33.596	-3.363	1.00	66.97
	1630	NH1	ARG	A	15	-4.370	34.890	-3.150	1.00	66.97
	1631	NH2	ARG	A	15	-5.629	33.213	-4.091	1.00	66.97
	1632	C	ARG	A	15	1.080	31.659	-4.687	1.00	52.98
	1633	O	ARG	A	15	1.510	32.817	-4.563	1.00	52.98
30	1634	N	ILE	A	16	1.431	30.867	-5.684	1.00	61.11
	1635	CA	ILE	A	16	2.362	31.362	-6.667	1.00	61.11
	1636	CB	ILE	A	16	3.662	30.595	-6.632	1.00	64.67
	1637	CG2	ILE	A	16	4.375	30.856	-5.312	1.00	64.67
	1638	CG1	ILE	A	16	3.385	29.117	-6.833	1.00	64.67
35	1639	CD1	ILE	A	16	4.626	28.268	-6.768	1.00	64.67
	1840	C	ILE	A	16	1.849	31.311	-8.070	1.00	61.11
	1641	O	ILE	A	16	0.851	30.662	-8.361	1.00	61.11
	1842	N	PHE	A	17	2.560	32.019	-8.933	1.00	81.85
	1643	CA	PHE	A	17	2.266	32.130	-10.348	1.00	81.85
40	1644	CB	PHE	A	17	2.902	33.411	-10.856	1.00	58.17
	1645	CG	PHE	A	17	2.014	34.604	-10.777	1.00	58.17
	1646	CD1	PHE	A	17	2.531	35.841	-10.422	1.00	58.17
	1647	CD2	PHE	A	17	0.681	34.512	-11.181	1.00	58.17
	1648	CE1	PHE	A	17	· 1.751	36.965	-10.467	1.00	58.17
45	1649	CE2	PHE	A	17	-0.125	35.639	-11.238	1.00	58.17
	1650	CZ	PHE	A	17	0.415	36.876	-10.885	1.00	58.17
	1651	C	PHE	A	17	2.851	30.940	-11.110	1.00	81.85
	1652	O	PHE	A	17	3.749	30.259	-10.621	1.00	81.85
	1653	N	LYS	A	18	2.353	30.699	-12.314	1.00	81.40
50	1654	CA	LYS	A	18	2.842	29.602	-13.129	1.00	81.40
	1655	CB	LYS	A	18	1.981	29.497	-14.385	1.00	133.55
	1656	CG	LYS	A	18	2.281	28.313	-15.277	1.00	133.55
	1657	CD	LYS	A	18	1.153	28.136	-16.287	1.00	133.55
	1658	CE	LYS	A	18	1.389	26.957	-17.216	1.00	133.55
55	1659	NZ	LYS	A	18	2.627	27.139	-18.030	1.00	133.55
	1660	C	LYS	A	18	4.305	29.838	-13.515	1.00	81.40
	1661	O	LYS	A	18	4.683	30.921	-13.972	1.00	81.40
	1662	N	GLY	A	19	5.141	28.834	-13.313	1.00	92.32
	1663	CA	GLY	A	19	6.524	28.975	-13.702	1.00	92.32
60	1664	C	GLY	A	19	7.492	29.428	-12.643	1.00	92.32
	1665	O	GLY	A	19	8.697	29.398	-12.866	1.00	92.32
	1666	N	GLU	A	20	6.996	29.853	-11.491	1.00	67.13
	1667	CA	GLU	A	20	7.896	30.300	-10.422	1.00	67.13
	1668	CB	GLU	A	20	7.153	31.239	-9.477	1.00	115.51
65	1669	CG	GLU	A	20	6.439	32.361	-10.221	1.00	115.51
	1670	CD	GLU	A	20	5.794	33.361	-9.300	1.00	115.51
	1671	OE1	GLU	A	20	4.991	32.949	-8.432	1.00	115.51
	1672	OE2	GLU	A	20	6.091	34.561	-9.454	1.00	115.51
	1673	C	GLU	A	20	8.469	29.094	-9.652	1.00	67.13
70	1674	O	GLU	A	20	8.035	27.953	-9.861	1.00	67.13

	1675	N	ASN	A	21	9.456	29.329	-8.788	1.00	81.05
	1676	CA	ASN	A	21	10.059	28.225	-8.040	1.00	81.05
	1677	CB	ASN	A	21	11.562	28.078	-8.328	1.00	110.52
	1678	CG	ASN	A	21	11.923	28.283	-9.788	1.00	110.52
5	1679	OD1	ASN	A	21	11.250	27.808	-10.699	1.00	110.52
	1680	ND2	ASN	A	21	13.025	28.989	-9.895	1.00	110.52
	1681	C	ASN	A	21	9.915	28.409	-6.547	1.00	81.05
	1682	O	ASN	A	21	10.054	29.521	-6.035	1.00	81.05
	1683	N	VAL	A	22	9.681	27.306	-5.848	1.00	79.17
10	1684	CA	VAL	A	22	9.525	27.341	-4.404	1.00	79.17
	1685	CB	VAL	A	22	8.057	27.304	-4.012	1.00	85.34
	1686	CG1	VAL	A	22	7.431	26.001	-4.486	1.00	85.34
	1687	CG2	VAL	A	22	7.925	27.449	-2.510	1.00	85.34
	1688	C	VAL	A	22	10.194	26.117	-3.815	1.00	79.17
15	1689	O	VAL	A	22	10.247	25.070	-4.469	1.00	79.17
	1690	N	THR	A	23	10.676	26.240	-2.579	1.00	92.04
	1691	CA	THR	A	23	11.367	25.145	-1.908	1.00	92.04
	1692	CB	THR	A	23	12.775	25.585	-1.556	1.00	153.40
	1693	OG1	THR	A	23	13.414	26.089	-2.736	1.00	153.40
20	1694	CG2	THR	A	23	13.567	24.428	-0.993	1.00	153.40
	1695	C	THR	A	23	10.667	24.698	-0.634	1.00	92.04
	1696	O	THR	A	23	10.364	25.525	0.212	1.00	92.04
	1697	N	LEU	A	24	10.403	23.404	-0.485	1.00	64.92
	1698	CA	LEU	A	24	9.742	22.945	0.730	1.00	64.92
25	1699	CB	LEU	A	24	8.564	22.015	0.427	1.00	83.07
	1700	CG	LEU	A	24	7.676	22.301	-0.774	1.00	83.07
	1701	CD1	LEU	A	24	6.400	21.482	-0.676	1.00	83.07
	1702	CD2	LEU	A	24	7.348	23.745	-0.837	1.00	83.07
	1703	C	LEU	A	24	10.701	22.206	1.657	1.00	64.92
30	1704	O	LEU	A	24	11.034	21.049	1.433	1.00	64.92
	1705	N	THR	A	25	11.125	22.863	2.725	1.00	60.46
	1706	CA	THR	A	25	12.026	22.227	3.665	1.00	60.46
	1707	CB	THR	A	25	12.890	23.286	4.309	1.00	96.68
	1708	OG1	THR	A	25	13.523	24.040	3.273	1.00	96.68
35	1709	CG2	THR	A	25	13.943	22.654	5.175	1.00	96.68
	1710	C	THR	A	25	11.264	21.446	4.746	1.00	60.46
	1711	O	THR	A	25	10.270	21.923	5.293	1.00	60.46
	1712	N	CYS	A	26	11.717	20.239	5.048	1.00	126.10
	1713	CA	CYS	A	26	11.060	19.464	6.081	1.00	126.10
40	1714	C	CYS	A	26	11.617	19.884	7.421	1.00	126.10
	1715	O	CYS	A	26	12.813	20.108	7.566	1.00	126.10
	1716	CB	CYS	A	26	11.293	17.971	5.888	1.00	188.87
	1717	SG	CYS	A	26	10.283	16.954	7.005	1.00	188.87
	1718	N	ASN	A	27	10.727	19.999	8.393	1.00	248.12
45	1719	CA	ASN	A	27	11.065	20.379	9.747	1.00	248.12
	1720	CB	ASN	A	27	10.474	19.354	10.685	1.00	249.30
	1721	CG	ASN	A	27	10.331	19.883	12.046	1.00	249.30
	1722	OD1	ASN	A	27	9.999	21.050	12.192	1.00	249.30
	1723	ND2	ASN	A	27	10.582	19.060	13.069	1.00	249.30
50	1724	C	ASN	A	27	12.549	20.546	10.040	1.00	248.12
	1725	O	ASN	A	27	13.220	19.591	10.431	1.00	248.12
	1726	N	GLY	A	28	13.058	21.754	9.840	1.00	150.98
	1727	CA	GLY	A	28	14.469	22.013	10.073	1.00	150.98
	1728	C	GLY	A	28	14.771	23.413	9.596	1.00	150.98
55	1729	O	GLY	A	28	14.541	23.731	8.435	1.00	150.98
	1730	N	ASN	A	29	15.288	24.258	10.480	1.00	168.28
	1731	CA	ASN	A	29	15.576	25.638	10.111	1.00	168.28
	1732	CB	ASN	A	29	15.714	26.494	11.374	1.00	185.34
	1733	CG	ASN	A	29	15.723	27.979	11.072	1.00	185.34
60	1734	OD1	ASN	A	29	15.387	28.400	9.966	1.00	185.34
	1735	ND2	ASN	A	29	16.097	28.782	12.059	1.00	185.34
	1736	C	ASN	A	29	16.799	25.839	9.208	1.00	168.28
	1737	O	ASN	A	29	16.704	26.492	8.165	1.00	168.28
	1738	N	ASN	A	30	17.943	25.279	9.594	1.00	244.43
65	1739	CA	ASN	A	30	19.151	25.453	8.797	1.00	244.43
	1740	CB	ASN	A	30	20.131	26.363	9.543	1.00	249.25
	1741	CG	ASN	A	30	19.592	27.765	9.735	1.00	249.25
	1742	OD1	ASN	A	30	19.601	28.297	10.843	1.00	249.25
	1743	ND2	ASN	A	30	19.122	28.372	8.654	1.00	249.25
70	1744	C	ASN	A	30	19.863	24.172	8.412	1.00	244.43

	1745	O	ASN	A	30	19.859	23.770	7.252	1.00	244.43
	1746	N	PHE	A	31	20.478	23.527	9.386	1.00	249.41
	1747	CA	PHE	A	31	21.210	22.326	9.077	1.00	249.41
	1748	CB	PHE	A	31	22.639	22.474	9.586	1.00	249.46
5	1749	CG	PHE	A	31	23.362	23.675	9.073	1.00	249.46
	1750	CD1	PHE	A	31	23.138	24.925	9.634	1.00	249.46
	1751	CD2	PHE	A	31	24.250	23.563	8.008	1.00	249.46
	1752	CE1	PHE	A	31	23.798	26.050	9.152	1.00	249.46
	1753	CE2	PHE	A	31	24.917	24.682	7.514	1.00	249.46
10	1754	CZ	PHE	A	31	24.682	25.931	8.083	1.00	249.46
	1755	C	PHE	A	31	20.559	21.049	9.617	1.00	249.41
	1756	O	PHE	A	31	20.226	20.949	10.807	1.00	249.41
	1757	N	PHE	A	32	20.393	20.077	8.715	1.00	249.47
	1758	CA	PHE	A	32	19.790	18.777	9.021	1.00	249.47
15	1759	CB	PHE	A	32	18.496	18.614	8.228	1.00	246.45
	1760	CG	PHE	A	32	17.642	17.487	8.707	1.00	246.45
	1761	CD1	PHE	A	32	17.048	17.548	9.963	1.00	246.45
	1762	CD2	PHE	A	32	17.442	16.359	7.921	1.00	246.45
20	1763	CE1	PHE	A	32	16.272	16.499	10.437	1.00	246.45
	1764	CE2	PHE	A	32	16.665	15.302	8.387	1.00	246.45
	1765	CZ	PHE	A	32	16.077	15.378	9.652	1.00	246.45
	1766	C	PHE	A	32	20.742	17.630	8.674	1.00	249.47
	1767	O	PHE	A	32	21.773	17.852	8.051	1.00	249.47
25	1768	N	GLU	A	33	20.392	16.403	9.058	1.00	249.57
	1769	CA	GLU	A	33	21.260	15.270	8.763	1.00	249.57
	1770	CB	GLU	A	33	21.850	14.696	10.034	1.00	249.41
	1771	CG	GLU	A	33	22.893	13.655	9.727	1.00	249.41
	1772	CD	GLU	A	33	24.096	14.255	9.017	1.00	249.41
30	1773	OE1	GLU	A	33	24.471	15.388	9.373	1.00	249.41
	1774	OE2	GLU	A	33	24.695	13.581	8.140	1.00	249.41
	1775	C	GLU	A	33	20.671	14.104	7.992	1.00	249.57
	1776	O	GLU	A	33	21.232	13.684	6.982	1.00	249.57
	1777	N	VAL	A	34	19.566	13.554	8.485	1.00	216.78
35	1778	CA	VAL	A	34	18.961	12.405	7.832	1.00	216.78
	1779	CB	VAL	A	34	17.623	12.017	8.499	1.00	196.07
	1780	CG1	VAL	A	34	17.008	10.816	7.801	1.00	196.07
	1781	CG2	VAL	A	34	17.864	11.683	9.958	1.00	196.07
	1782	C	VAL	A	34	18.754	12.609	6.338	1.00	216.78
40	1783	O	VAL	A	34	18.550	13.729	5.860	1.00	216.78
	1784	N	SER	A	35	18.845	11.506	5.608	1.00	172.95
	1785	CA	SER	A	35	18.669	11.506	4.170	1.00	172.95
	1786	CB	SER	A	35	19.837	10.789	3.489	1.00	249.26
	1787	OG	SER	A	35	19.822	9.399	3.775	1.00	249.26
45	1788	C	SER	A	35	17.368	10.770	3.873	1.00	172.95
	1789	O	SER	A	35	16.978	10.632	2.715	1.00	172.95
	1790	N	SER	A	36	16.706	10.290	4.926	1.00	142.42
	1791	CA	SER	A	36	15.437	9.579	4.773	1.00	142.42
	1792	CB	SER	A	36	15.404	8.320	5.643	1.00	183.21
50	1793	OG	SER	A	36	15.320	8.643	7.020	1.00	183.21
	1794	C	SER	A	36	14.288	10.498	5.168	1.00	142.42
	1795	O	SER	A	36	13.906	10.585	6.337	1.00	142.42
	1796	N	THR	A	37	13.749	11.189	4.171	1.00	91.48
	1797	CA	THR	A	37	12.645	12.117	4.370	1.00	91.48
55	1798	CB	THR	A	37	13.088	13.579	4.085	1.00	110.07
	1799	OG1	THR	A	37	14.193	13.829	4.928	1.00	110.07
	1800	CG2	THR	A	37	11.960	14.535	4.352	1.00	110.07
	1801	C	THR	A	37	11.582	11.689	3.366	1.00	91.48
	1802	O	THR	A	37	11.902	11.294	2.244	1.00	91.48
60	1803	N	LYS	A	38	10.321	11.748	3.769	1.00	121.21
	1804	CA	LYS	A	38	9.233	11.345	2.886	1.00	121.21
	1805	CB	LYS	A	38	8.339	10.344	3.600	1.00	152.68
	1806	CG	LYS	A	38	9.088	9.131	4.112	1.00	152.68
	1807	CD	LYS	A	38	8.151	8.168	4.824	1.00	152.68
65	1808	CE	LYS	A	38	8.877	6.909	5.245	1.00	152.68
	1809	NZ	LYS	A	38	7.952	5.951	5.893	1.00	152.68
	1810	C	LYS	A	38	8.389	12.529	2.442	1.00	121.21
	1811	O	LYS	A	38	8.140	13.440	3.226	1.00	121.21
	1812	N	TRP	A	39	7.954	12.517	1.185	1.00	102.82
	1813	CA	TRP	A	39	7.119	13.592	0.656	1.00	102.82
70	1814	CB	TRP	A	39	7.861	14.401	-0.401	1.00	80.70

	1815	CG	TRP	A	39	9.037	15.167	0.113	1.00	80.70
	1816	CD2	TRP	A	39	9.022	16.295	0.994	1.00	80.70
	1817	CE2	TRP	A	39	10.366	16.677	1.201	1.00	80.70
	1818	CE3	TRP	A	39	8.002	17.015	1.634	1.00	80.70
5	1819	CD1	TRP	A	39	10.351	14.922	-0.168	1.00	80.70
	1820	NE1	TRP	A	39	11.154	15.826	0.484	1.00	80.70
	1821	CZ2	TRP	A	39	10.717	17.745	2.011	1.00	80.70
	1822	CZ3	TRP	A	39	8.355	18.082	2.443	1.00	80.70
	1823	CH2	TRP	A	39	9.703	18.438	2.623	1.00	80.70
10	1824	C	TRP	A	39	5.875	13.008	0.026	1.00	102.82
	1825	O	TRP	A	39	5.956	12.079	-0.765	1.00	102.82
	1826	N	PHE	A	40	4.724	13.562	0.368	1.00	102.87
	1827	CA	PHE	A	40	3.489	13.049	-0.175	1.00	102.87
	1828	CB	PHE	A	40	2.633	12.434	0.936	1.00	104.88
15	1829	CG	PHE	A	40	3.319	11.346	1.706	1.00	104.88
	1830	CD1	PHE	A	40	4.222	11.655	2.715	1.00	104.88
	1831	CD2	PHE	A	40	3.050	10.011	1.438	1.00	104.88
	1832	CE1	PHE	A	40	4.847	10.652	3.448	1.00	104.88
	1833	CE2	PHE	A	40	3.672	8.999	2.167	1.00	104.88
20	1834	CZ	PHE	A	40	4.570	9.321	3.174	1.00	104.88
	1835	C	PHE	A	40	2.676	14.104	-0.898	1.00	102.87
	1836	O	PHE	A	40	1.808	14.741	-0.302	1.00	102.87
	1837	N	HIS	A	41	2.952	14.287	-2.184	1.00	73.61
	1838	CA	HIS	A	41	2.205	15.252	-2.984	1.00	73.61
25	1839	CB	HIS	A	41	2.986	15.552	-4.254	1.00	81.93
	1840	CG	HIS	A	41	2.304	16.514	-5.162	1.00	81.93
	1841	CD2	HIS	A	41	2.173	16.521	-6.507	1.00	81.93
	1842	ND1	HIS	A	41	1.661	17.645	-4.706	1.00	81.93
	1843	CE1	HIS	A	41	1.158	18.309	-5.731	1.00	81.93
30	1844	NE2	HIS	A	41	1.455	17.648	-6.837	1.00	81.93
	1845	C	HIS	A	41	0.811	14.687	-3.318	1.00	73.61
	1846	O	HIS	A	41	0.690	13.733	-4.088	1.00	73.61
	1847	N	ASN	A	42	-0.234	15.280	-2.740	1.00	96.75
	1848	CA	ASN	A	42	-1.617	14.822	-2.940	1.00	96.75
35	1849	CB	ASN	A	42	-2.017	14.809	-4.435	1.00	98.09
	1850	CG	ASN	A	42	-2.244	16.205	-5.004	1.00	98.09
	1851	OD1	ASN	A	42	-1.466	17.108	-4.726	1.00	98.09
	1852	ND2	ASN	A	42	-3.284	16.385	-5.814	1.00	98.09
	1853	C	ASN	A	42	-1.771	13.413	-2.374	1.00	96.75
40	1854	O	ASN	A	42	-2.625	12.652	-2.826	1.00	96.75
	1855	N	GLY	A	43	-0.948	13.068	-1.386	1.00	89.87
	1856	CA	GLY	A	43	-1.019	11.739	-0.789	1.00	89.87
	1857	C	GLY	A	43	-0.054	10.730	-1.410	1.00	89.87
	1858	O	GLY	A	43	0.542	9.901	-0.714	1.00	89.87
45	1859	N	SER	A	44	0.097	10.798	-2.728	1.00	129.29
	1860	CA	SER	A	44	0.990	9.904	-3.449	1.00	129.29
	1861	CB	SER	A	44	0.833	10.113	-4.960	1.00	173.89
	1862	OG	SER	A	44	-0.521	10.004	-5.358	1.00	173.89
	1863	C	SER	A	44	2.436	10.182	-3.043	1.00	129.29
50	1864	O	SER	A	44	2.890	11.322	-3.095	1.00	129.29
	1865	N	LEU	A	45	3.159	9.142	-2.639	1.00	128.43
	1866	CA	LEU	A	45	4.559	9.291	-2.239	1.00	128.43
	1867	CB	LEU	A	45	5.149	7.925	-1.874	1.00	210.08
	1868	CG	LEU	A	45	6.602	7.911	-1.397	1.00	210.08
55	1869	CD1	LEU	A	45	6.768	8.881	-0.237	1.00	210.08
	1870	CD2	LEU	A	45	6.995	6.495	-0.980	1.00	210.08
	1871	C	LEU	A	45	5.379	9.921	-3.365	1.00	128.43
	1872	O	LEU	A	45	5.129	9.671	-4.540	1.00	128.43
	1873	N	SER	A	46	6.354	10.749	-3.007	1.00	150.05
60	1874	CA	SER	A	46	7.200	11.403	-4.006	1.00	150.05
	1875	CB	SER	A	46	7.500	12.846	-3.588	1.00	129.32
	1876	OG	SER	A	46	8.251	13.516	-4.586	1.00	129.32
	1877	C	SER	A	46	8.499	10.623	-4.127	1.00	150.05
	1878	O	SER	A	46	8.801	9.796	-3.275	1.00	150.05
65	1879	N	GLU	A	47	9.274	10.881	-5.177	1.00	207.01
	1880	CA	GLU	A	47	10.534	10.168	-5.357	1.00	207.01
	1881	CB	GLU	A	47	10.798	9.896	-6.851	1.00	249.57
	1882	CG	GLU	A	47	9.574	9.479	-7.672	1.00	249.57
	1883	CD	GLU	A	47	9.801	9.602	-9.185	1.00	249.57
70	1884	OE1	GLU	A	47	9.668	10.722	-9.729	1.00	249.57

	1885	OE2	GLU	A	47	10.133	8.577	-9.821	1.00	249.57
	1886	C	GLU	A	47	11.743	10.894	-4.739	1.00	207.01
	1887	O	GLU	A	47	12.856	10.373	-4.796	1.00	207.01
	1888	N	GLU	A	48	11.556	12.084	-4.163	1.00	127.05
5	1889	CA	GLU	A	48	12.703	12.760	-3.542	1.00	127.05
	1890	CB	GLU	A	48	12.524	14.292	-3.489	1.00	182.29
	1891	CG	GLU	A	48	13.615	15.057	-2.682	1.00	182.29
	1892	CD	GLU	A	48	15.017	15.011	-3.296	1.00	182.29
	1893	OE1	GLU	A	48	15.226	15.631	-4.359	1.00	182.29
10	1894	OE2	GLU	A	48	15.914	14.360	-2.713	1.00	182.29
	1895	C	GLU	A	48	12.882	12.208	-2.126	1.00	127.05
	1896	O	GLU	A	48	11.938	11.681	-1.531	1.00	127.05
	1897	N	THR	A	49	14.099	12.305	-1.600	1.00	86.20
	1898	CA	THR	A	49	14.385	11.817	-0.258	1.00	86.20
15	1899	CB	THR	A	49	15.263	10.549	-0.313	1.00	133.36
	1900	OG1	THR	A	49	16.473	10.832	-1.027	1.00	133.36
	1901	CG2	THR	A	49	14.513	9.419	-1.021	1.00	133.36
	1902	C	THR	A	49	15.074	12.903	0.583	1.00	86.20
	1903	O	THR	A	49	14.950	12.938	1.810	1.00	86.20
20	1904	N	ASN	A	50	15.787	13.801	-0.085	1.00	156.26
	1905	CA	ASN	A	50	16.465	14.888	0.610	1.00	156.26
	1906	CB	ASN	A	50	17.158	15.810	-0.406	1.00	185.93
	1907	CG	ASN	A	50	18.159	16.752	0.245	1.00	185.93
	1908	OD1	ASN	A	50	18.105	16.970	1.452	1.00	185.93
25	1909	ND2	ASN	A	50	19.062	17.323	-0.549	1.00	185.93
	1910	C	ASN	A	50	15.393	15.656	1.382	1.00	156.26
	1911	O	ASN	A	50	14.238	15.689	0.976	1.00	156.26
	1912	N	SER	A	51	15.765	16.264	2.499	1.00	124.65
	1913	CA	SER	A	51	14.804	17.019	3.296	1.00	124.65
30	1914	CB	SER	A	51	15.434	17.440	4.628	1.00	124.86
	1915	OG	SER	A	51	16.427	18.441	4.450	1.00	124.86
	1916	C	SER	A	51	14.281	18.263	2.569	1.00	124.65
	1917	O	SER	A	51	13.257	18.823	2.959	1.00	124.65
	1918	N	SER	A	52	14.979	18.704	1.525	1.00	90.69
35	1919	CA	SER	A	52	14.553	19.884	0.780	1.00	90.69
	1920	CB	SER	A	52	15.708	20.872	0.631	1.00	131.83
	1921	OG	SER	A	52	16.109	21.377	1.894	1.00	131.83
	1922	C	SER	A	52	14.038	19.478	-0.584	1.00	90.69
	1923	O	SER	A	52	14.803	19.073	-1.449	1.00	90.69
40	1924	N	LEU	A	53	12.727	19.584	-0.756	1.00	92.73
	1925	CA	LEU	A	53	12.057	19.239	-2.005	1.00	92.73
	1926	CB	LEU	A	53	10.720	18.547	-1.710	1.00	96.57
	1927	CG	LEU	A	53	9.633	18.561	-2.788	1.00	96.57
	1928	CD1	LEU	A	53	10.226	18.224	-4.145	1.00	96.57
45	1929	CD2	LEU	A	53	8.536	17.571	-2.396	1.00	96.57
	1930	C	LEU	A	53	11.814	20.486	-2.847	1.00	92.73
	1931	O	LEU	A	53	10.874	21.231	-2.601	1.00	92.73
	1932	N	ASN	A	54	12.660	20.710	-3.846	1.00	74.24
	1933	CA	ASN	A	54	12.508	21.879	-4.708	1.00	74.24
50	1934	CB	ASN	A	54	13.819	22.180	-5.442	1.00	143.36
	1935	CG	ASN	A	54	14.883	22.734	-4.526	1.00	143.36
	1936	OD1	ASN	A	54	14.670	23.738	-3.853	1.00	143.36
	1937	ND2	ASN	A	54	16.040	22.086	-4.497	1.00	143.36
	1938	C	ASN	A	54	11.390	21.731	-5.727	1.00	74.24
55	1939	O	ASN	A	54	10.937	20.633	-6.038	1.00	74.24
	1940	N	ILE	A	55	10.936	22.868	-6.233	1.00	93.23
	1941	CA	ILE	A	55	9.898	22.911	-7.249	1.00	93.23
	1942	CB	ILE	A	55	8.542	23.323	-6.659	1.00	75.25
	1943	CG2	ILE	A	55	7.629	23.783	-7.751	1.00	75.25
60	1944	CG1	ILE	A	55	7.932	22.135	-5.918	1.00	75.25
	1945	CD1	ILE	A	55	6.605	22.397	-5.286	1.00	75.25
	1946	C	ILE	A	55	10.359	23.951	-8.241	1.00	93.23
	1947	O	ILE	A	55	10.593	25.100	-7.866	1.00	93.23
	1948	N	VAL	A	56	10.528	23.543	-9.491	1.00	114.64
65	1949	CA	VAL	A	56	10.977	24.469	-10.515	1.00	114.64
	1950	CB	VAL	A	56	12.025	23.820	-11.419	1.00	202.78
	1951	CG1	VAL	A	56	12.782	24.892	-12.183	1.00	202.78
	1952	CG2	VAL	A	56	12.983	22.997	-10.579	1.00	202.78
	1953	C	VAL	A	56	9.771	24.909	-11.333	1.00	114.64
70	1954	O	VAL	A	56	8.649	24.730	-10.883	1.00	114.64

	1955	N	ASN	A	57	9.893	25.480	-12.516	1.00	86.89
	1956	CA	ASN	A	57	8.902	25.961	-13.366	1.00	86.89
	1957	CB	ASN	A	57	9.187	25.646	-14.832	1.00	171.09
	1958	CG	ASN	A	57	10.333	26.468	-15.379	1.00	171.09
5	1959	OD1	ASN	A	57	10.332	27.695	-15.277	1.00	171.09
	1960	ND2	ASN	A	57	11.318	25.799	-15.962	1.00	171.09
	1961	C	ASN	A	57	7.549	25.397	-12.962	1.00	86.89
	1962	O	ASN	A	57	7.112	24.377	-13.473	1.00	86.89
	1963	N	ALA	A	58	6.893	26.087	-12.036	1.00	98.74
10	1964	CA	ALA	A	58	5.610	25.665	-11.500	1.00	98.74
	1965	CB	ALA	A	58	5.094	26.705	-10.525	1.00	108.16
	1966	C	ALA	A	58	4.557	25.376	-12.548	1.00	98.74
	1967	O	ALA	A	58	4.185	26.242	-13.327	1.00	98.74
	1968	N	LYS	A	59	4.082	24.140	-12.560	1.00	74.98
15	1969	CA	LYS	A	59	3.039	23.725	-13.482	1.00	74.98
	1970	CB	LYS	A	59	3.424	22.395	-14.146	1.00	178.83
	1971	CG	LYS	A	59	4.740	22.455	-14.920	1.00	178.83
	1972	CD	LYS	A	59	5.158	21.095	-15.463	1.00	178.83
	1973	CE	LYS	A	59	6.483	21.185	-16.215	1.00	178.83
20	1974	NZ	LYS	A	59	6.932	19.856	-16.725	1.00	178.83
	1975	C	LYS	A	59	1.782	23.569	-12.623	1.00	74.98
	1976	O	LYS	A	59	1.878	23.163	-11.463	1.00	74.98
	1977	N	PHE	A	60	0.614	23.912	-13.166	1.00	60.66
	1978	CA	PHE	A	60	-0.640	23.780	-12.418	1.00	60.66
25	1979	CB	PHE	A	60	-1.815	23.834	-13.371	1.00	124.29
	1980	CG	PHE	A	60	-1.949	25.140	-14.046	1.00	124.29
	1981	CD1	PHE	A	60	-2.524	25.234	-15.301	1.00	124.29
	1982	CD2	PHE	A	60	-1.510	26.294	-13.425	1.00	124.29
	1983	CE1	PHE	A	60	-2.653	26.464	-15.942	1.00	124.29
30	1984	CE2	PHE	A	60	-1.630	27.527	-14.054	1.00	124.29
	1985	CZ	PHE	A	60	-2.209	27.613	-15.313	1.00	124.29
	1986	C	PHE	A	60	-0.714	22.496	-11.595	1.00	60.66
	1987	O	PHE	A	60	-1.287	22.487	-10.504	1.00	60.66
	1988	N	GLU	A	61	-0.124	21.418	-12.112	1.00	94.84
35	1989	CA	GLU	A	61	-0.129	20.123	-11.433	1.00	94.84
	1990	CB	GLU	A	61	0.502	19.037	-12.312	1.00	214.43
	1991	CG	GLU	A	61	-0.208	18.784	-13.625	1.00	214.43
	1992	CD	GLU	A	61	-0.246	20.011	-14.508	1.00	214.43
	1993	OE1	GLU	A	61	0.831	20.583	-14.781	1.00	214.43
40	1994	OE2	GLU	A	61	-1.352	20.403	-14.930	1.00	214.43
	1995	C	GLU	A	61	0.626	20.165	-10.114	1.00	94.84
	1996	O	GLU	A	61	0.397	19.318	-9.253	1.00	94.84
	1997	N	ASP	A	62	1.535	21.130	-9.959	1.00	76.23
	1998	CA	ASP	A	62	2.303	21.242	-8.728	1.00	76.23
45	1999	CB	ASP	A	62	3.493	22.175	-8.913	1.00	161.53
	2000	CG	ASP	A	62	4.380	21.755	-10.072	1.00	161.53
	2001	OD1	ASP	A	62	4.571	20.536	-10.273	1.00	161.53
	2002	OD2	ASP	A	62	4.897	22.644	-10.778	1.00	161.53
	2003	C	ASP	A	62	1.407	21.732	-7.614	1.00	76.23
50	2004	O	ASP	A	62	1.721	21.544	-6.451	1.00	76.23
	2005	N	SER	A	63	0.280	22.341	-7.977	1.00	83.22
	2006	CA	SER	A	63	-0.680	22.828	-6.992	1.00	83.22
	2007	CB	SER	A	63	-1.880	23.464	-7.691	1.00	115.03
	2008	OG	SER	A	63	-1.503	24.633	-8.399	1.00	115.03
55	2009	C	SER	A	63	-1.140	21.621	-6.212	1.00	83.22
	2010	O	SER	A	63	-1.508	20.640	-6.814	1.00	83.22
	2011	N	GLY	A	64	-1.124	21.660	-4.887	1.00	65.94
	2012	CA	GLY	A	64	-1.575	20.488	-4.154	1.00	65.94
	2013	C	GLY	A	64	-1.306	20.493	-2.661	1.00	65.94
60	2014	O	GLY	A	64	-0.942	21.530	-2.082	1.00	65.94
	2015	N	GLU	A	65	-1.509	19.337	-2.032	1.00	82.22
	2016	CA	GLU	A	65	-1.285	19.159	-0.605	1.00	82.22
	2017	CB	GLU	A	65	-2.463	18.376	-0.031	1.00	143.82
	2018	CG	GLU	A	65	-2.304	17.897	1.394	1.00	143.82
65	2019	CD	GLU	A	65	-3.356	16.866	1.773	1.00	143.82
	2020	OE1	GLU	A	65	-3.374	15.779	1.157	1.00	143.82
	2021	OE2	GLU	A	65	-4.169	17.139	2.681	1.00	143.82
	2022	C	GLU	A	65	0.035	18.378	-0.420	1.00	82.22
	2023	O	GLU	A	65	0.207	17.313	-1.011	1.00	82.22
70	2024	N	TYR	A	66	0.971	18.903	0.374	1.00	76.24

	2025	CA	TYR	A	66	2.240	18.224	0.614	1.00	76.24
	2026	CB	TYR	A	66	3.377	19.083	0.150	1.00	67.69
	2027	CG	TYR	A	66	3.426	19.339	-1.314	1.00	67.69
	2028	CD1	TYR	A	66	2.574	20.255	-1.915	1.00	67.69
5	2029	CE1	TYR	A	66	2.680	20.572	-3.265	1.00	67.69
	2030	CD2	TYR	A	66	4.385	18.724	-2.095	1.00	67.69
	2031	CE2	TYR	A	66	4.502	19.017	-3.447	1.00	67.69
	2032	CZ	TYR	A	66	3.647	19.948	-4.032	1.00	67.69
	2033	OH	TYR	A	66	3.792	20.230	-5.378	1.00	67.69
10	2034	C	TYR	A	66	2.490	17.934	2.083	1.00	76.24
	2035	O	TYR	A	66	1.891	18.570	2.941	1.00	76.24
	2036	N	LYS	A	67	3.398	17.000	2.375	1.00	93.48
	2037	CA	LYS	A	67	3.756	16.664	3.759	1.00	93.48
	2038	CB	LYS	A	67	2.619	15.924	4.439	1.00	143.97
15	2039	CG	LYS	A	67	2.079	14.788	3.619	1.00	143.97
	2040	CD	LYS	A	67	0.876	14.176	4.291	1.00	143.97
	2041	CE	LYS	A	67	0.213	13.163	3.385	1.00	143.97
	2042	NZ	LYS	A	67	-1.009	12.616	4.023	1.00	143.97
	2043	C	LYS	A	67	5.011	15.818	3.806	1.00	93.48
20	2044	O	LYS	A	67	5.357	15.166	2.824	1.00	93.48
	2045	N	CYS	A	68	5.715	15.852	4.932	1.00	71.26
	2046	CA	CYS	A	68	6.914	15.044	5.067	1.00	71.26
	2047	C	CYS	A	68	6.823	14.232	6.340	1.00	71.26
	2048	O	CYS	A	68	6.020	14.540	7.208	1.00	71.26
25	2049	CB	CYS	A	68	8.183	15.905	5.041	1.00	93.73
	2050	SG	CYS	A	68	8.385	17.184	6.305	1.00	93.73
	2051	N	GLN	A	69	7.619	13.174	6.425	1.00	106.93
	2052	CA	GLN	A	69	7.651	12.302	7.591	1.00	106.93
	2053	CB	GLN	A	69	6.558	11.233	7.476	1.00	95.79
30	2054	CG	GLN	A	69	6.744	10.032	8.390	1.00	95.79
	2055	CD	GLN	A	69	5.702	8.954	8.161	1.00	95.79
	2056	OE1	GLN	A	69	5.476	8.521	7.024	1.00	95.79
	2057	NE2	GLN	A	69	5.060	8.509	9.244	1.00	95.79
	2058	C	GLN	A	69	9.015	11.641	7.629	1.00	106.93
35	2059	O	GLN	A	69	9.657	11.496	6.594	1.00	106.93
	2060	N	HIS	A	70	9.462	11.243	8.813	1.00	174.41
	2061	CA	HIS	A	70	10.753	10.589	8.928	1.00	174.41
	2062	CB	HIS	A	70	11.601	11.296	9.977	1.00	160.27
	2063	CG	HIS	A	70	12.022	12.673	9.552	1.00	160.27
40	2064	CD2	HIS	A	70	11.502	13.885	9.873	1.00	160.27
	2065	ND1	HIS	A	70	13.085	12.909	8.726	1.00	160.27
	2066	CE1	HIS	A	70	13.203	14.210	8.527	1.00	160.27
	2067	NE2	HIS	A	70	12.257	14.824	9.213	1.00	160.27
	2068	C	HIS	A	70	10.632	9.112	9.268	1.00	174.41
45	2069	O	HIS	A	70	9.543	8.536	9.237	1.00	174.41
	2070	N	GLN	A	71	11.764	8.505	9.590	1.00	242.81
	2071	CA	GLN	A	71	11.815	7.091	9.923	1.00	242.81
	2072	CB	GLN	A	71	13.246	6.724	10.335	1.00	199.62
	2073	CG	GLN	A	71	13.632	5.293	9.992	1.00	199.62
50	2074	CD	GLN	A	71	13.345	4.945	8.543	1.00	199.62
	2075	OE1	GLN	A	71	14.015	5.423	7.634	1.00	199.62
	2076	NE2	GLN	A	71	12.331	4.115	8.324	1.00	199.62
	2077	C	GLN	A	71	10.817	6.722	11.027	1.00	242.81
	2078	O	GLN	A	71	9.989	5.829	10.844	1.00	242.81
55	2079	N	GLN	A	72	10.886	7.419	12.160	1.00	160.50
	2080	CA	GLN	A	72	9.991	7.143	13.289	1.00	160.50
	2081	CB	GLN	A	72	10.803	6.584	14.465	1.00	249.38
	2082	CG	GLN	A	72	9.972	6.150	15.671	1.00	249.38
	2083	CD	GLN	A	72	10.819	5.563	16.791	1.00	249.38
60	2084	OE1	GLN	A	72	11.537	4.581	16.594	1.00	249.38
	2085	NE2	GLN	A	72	10.738	6.164	17.975	1.00	249.38
	2086	C	GLN	A	72	9.237	8.392	13.740	1.00	160.50
	2087	O	GLN	A	72	9.319	8.797	14.901	1.00	160.50
	2088	N	VAL	A	73	8.493	9.001	12.825	1.00	139.31
65	2089	CA	VAL	A	73	7.759	10.217	13.154	1.00	139.31
	2090	CB	VAL	A	73	8.575	11.467	12.795	1.00	182.81
	2091	CG1	VAL	A	73	7.960	12.688	13.430	1.00	182.81
	2092	CG2	VAL	A	73	10.000	11.297	13.237	1.00	182.81
	2093	C	VAL	A	73	6.445	10.284	12.391	1.00	139.31
70	2094	O	VAL	A	73	6.352	9.819	11.254	1.00	139.31

	2095	N	ASN	A	74	5.428	10.864	13.019	1.00	98.24
	2096	CA	ASN	A	74	4.136	10.988	12.376	1.00	98.24
	2097	CB	ASN	A	74	3.045	11.209	13.427	1.00	227.24
	2098	CG	ASN	A	74	3.039	10.124	14.489	1.00	227.24
5	2099	OD1	ASN	A	74	3.176	8.940	14.170	1.00	227.24
	2100	ND2	ASN	A	74	2.875	10.520	15.748	1.00	227.24
	2101	C	ASN	A	74	4.194	12.144	11.378	1.00	98.24
	2102	O	ASN	A	74	4.649	13.246	11.700	1.00	98.24
	2103	N	GLU	A	75	3.750	11.863	10.157	1.00	124.76
10	2104	CA	GLU	A	75	3.730	12.842	9.074	1.00	124.76
	2105	CB	GLU	A	75	2.881	12.302	7.921	1.00	249.33
	2106	CG	GLU	A	75	1.709	11.440	8.364	1.00	249.33
	2107	CD	GLU	A	75	1.032	10.734	7.202	1.00	249.33
	2108	OE1	GLU	A	75	1.730	10.023	6.446	1.00	249.33
15	2109	OE2	GLU	A	75	-0.198	10.888	7.048	1.00	249.33
	2110	C	GLU	A	75	3.245	14.232	9.499	1.00	124.76
	2111	O	GLU	A	75	2.346	14.372	10.327	1.00	124.76
	2112	N	SER	A	76	3.859	15.255	8.912	1.00	84.02
	2113	CA	SER	A	76	3.569	16.653	9.208	1.00	84.02
20	2114	CB	SER	A	76	4.578	17.534	8.509	1.00	92.60
	2115	OG	SER	A	76	4.391	17.395	7.108	1.00	92.60
	2116	C	SER	A	76	2.201	17.096	8.754	1.00	84.02
	2117	O	SER	A	76	1.599	16.468	7.888	1.00	84.02
	2118	N	GLU	A	77	1.722	18.198	9.323	1.00	82.56
25	2119	CA	GLU	A	77	0.415	18.751	8.960	1.00	82.56
	2120	CB	GLU	A	77	0.000	19.918	9.883	1.00	211.53
	2121	CG	GLU	A	77	-0.157	19.511	11.331	1.00	211.53
	2122	CD	GLU	A	77	-1.343	18.579	11.512	1.00	211.53
	2123	OE1	GLU	A	77	-1.831	18.020	10.505	1.00	211.53
30	2124	OE2	GLU	A	77	-1.780	18.396	12.668	1.00	211.53
	2125	C	GLU	A	77	0.550	19.239	7.533	1.00	82.56
	2126	O	GLU	A	77	1.397	20.102	7.252	1.00	82.56
	2127	N	PRO	A	78	-0.250	18.679	6.604	1.00	57.51
	2128	CD	PRO	A	78	-1.105	17.493	6.808	1.00	210.77
35	2129	CA	PRO	A	78	-0.226	19.047	5.186	1.00	57.51
	2130	CB	PRO	A	78	-1.469	18.370	4.644	1.00	210.77
	2131	CG	PRO	A	78	-1.440	17.076	5.376	1.00	210.77
	2132	C	PRO	A	78	-0.193	20.544	4.936	1.00	57.51
	2133	O	PRO	A	78	-0.607	21.338	5.785	1.00	57.51
40	2134	N	VAL	A	79	0.343	20.931	3.789	1.00	75.93
	2135	CA	VAL	A	79	0.396	22.331	3.422	1.00	75.93
	2136	CB	VAL	A	79	1.780	22.859	3.574	1.00	49.48
	2137	CG1	VAL	A	79	1.916	24.215	2.850	1.00	49.48
	2138	CG2	VAL	A	79	2.078	23.010	5.039	1.00	49.48
45	2139	C	VAL	A	79	-0.033	22.466	1.972	1.00	75.93
	2140	O	VAL	A	79	0.463	21.748	1.113	1.00	75.93
	2141	N	TYR	A	80	-0.961	23.375	1.696	1.00	60.67
	2142	CA	TYR	A	80	-1.424	23.519	0.336	1.00	60.67
	2143	CB	TYR	A	80	-2.903	23.814	0.280	1.00	249.12
50	2144	CG	TYR	A	80	-3.420	23.538	-1.115	1.00	249.12
	2145	CD1	TYR	A	80	-3.434	22.256	-1.623	1.00	249.12
	2146	CE1	TYR	A	80	-3.870	22.005	-2.920	1.00	249.12
	2147	CD2	TYR	A	80	-3.902	24.575	-1.927	1.00	249.12
	2148	CE2	TYR	A	80	-4.414	24.332	-3.216	1.00	249.12
55	2149	CZ	TYR	A	80	-4.378	23.015	-3.703	1.00	249.12
	2150	OH	TYR	A	80	-4.926	22.722	-4.929	1.00	249.12
	2151	C	TYR	A	80	-0.736	24.582	-0.438	1.00	60.67
	2152	O	TYR	A	80	-0.537	25.688	0.043	1.00	60.67
	2153	N	LEU	A	81	-0.414	24.264	-1.669	1.00	53.62
60	2154	CA	LEU	A	81	0.237	25.227	-2.520	1.00	53.62
	2155	CB	LEU	A	81	1.547	24.619	-3.003	1.00	66.18
	2156	CG	LEU	A	81	2.237	25.486	-4.035	1.00	66.18
	2157	CD1	LEU	A	81	2.603	26.806	-3.373	1.00	66.18
	2158	CD2	LEU	A	81	3.461	24.803	-4.566	1.00	66.18
65	2159	C	LEU	A	81	-0.703	25.487	-3.698	1.00	53.62
	2160	O	LEU	A	81	-1.229	24.534	-4.283	1.00	53.62
	2161	N	GLU	A	82	-0.956	26.742	-4.048	1.00	63.15
	2162	CA	GLU	A	82	-1.821	26.990	-5.201	1.00	63.15
	2163	CB	GLU	A	82	-3.099	27.700	-4.772	1.00	149.46
70	2164	CG	GLU	A	82	-4.259	27.463	-5.722	1.00	149.46

	2165	CD	GLU	A	82	-5.537	28.157	-5.276	1.00	149.46
	2166	OE1	GLU	A	82	-5.798	28.194	-4.050	1.00	149.46
	2167	OE2	GLU	A	82	-6.286	28.653	-6.151	1.00	149.46
	2168	C	GLU	A	82	-1.100	27.823	-6.283	1.00	63.15
5	2169	O	GLU	A	82	-0.503	28.878	-5.996	1.00	63.15
	2170	N	VAL	A	83	-1.157	27.352	-7.526	1.00	58.52
	2171	CA	VAL	A	83	-0.517	28.050	-8.632	1.00	58.52
	2172	CB	VAL	A	83	0.194	27.083	-9.516	1.00	61.79
	2173	CG1	VAL	A	83	0.749	27.819	-10.728	1.00	61.79
10	2174	CG2	VAL	A	83	1.294	26.427	-8.738	1.00	61.79
	2175	C	VAL	A	83	-1.473	28.859	-9.501	1.00	58.52
	2176	O	VAL	A	83	-2.540	28.364	-9.877	1.00	58.52
	2177	N	PHE	A	84	-1.082	30.088	-9.839	1.00	70.51
	2178	CA	PHE	A	84	-1.947	30.947	-10.632	1.00	70.51
15	2179	CB	PHE	A	84	-2.395	32.164	-9.834	1.00	69.94
	2180	CG	PHE	A	84	-3.130	31.836	-8.588	1.00	69.94
	2181	CD1	PHE	A	84	-2.455	31.374	-7.488	1.00	69.94
	2182	CD2	PHE	A	84	-4.503	32.031	-8.498	1.00	69.94
	2183	CE1	PHE	A	84	-3.134	31.108	-6.323	1.00	69.94
20	2184	CE2	PHE	A	84	-5.199	31.764	-7.324	1.00	69.94
	2185	CZ	PHE	A	84	-4.521	31.312	-6.242	1.00	69.94
	2186	C	PHE	A	84	-1.390	31.480	-11.923	1.00	70.51
	2187	O	PHE	A	84	-0.186	31.452	-12.179	1.00	70.51
	2188	N	SER	A	85	-2.327	31.985	-12.717	1.00	86.88
25	2189	CA	SER	A	85	-2.067	32.625	-13.989	1.00	86.88
	2190	CB	SER	A	85	-2.453	31.714	-15.142	1.00	135.23
	2191	OG	SER	A	85	-2.214	32.358	-16.378	1.00	135.23
	2192	C	SER	A	85	-2.999	33.835	-13.959	1.00	86.88
	2193	O	SER	A	85	-4.226	33.670	-14.007	1.00	86.88
30	2194	N	ASP	A	86	-2.425	35.033	-13.836	1.00	47.41
	2195	CA	ASP	A	86	-3.209	36.256	-13.803	1.00	47.41
	2196	CB	ASP	A	86	-4.131	36.259	-12.589	1.00	131.95
	2197	CG	ASP	A	86	-5.454	36.927	-12.876	1.00	131.95
	2198	OD1	ASP	A	86	-5.433	38.087	-13.345	1.00	131.95
35	2199	OD2	ASP	A	86	-6.509	36.296	-12.629	1.00	131.95
	2200	C	ASP	A	86	-2.245	37.453	-13.756	1.00	47.41
	2201	O	ASP	A	86	-1.043	37.284	-13.502	1.00	47.41
	2202	N	TRP	A	87	-2.760	38.661	-14.004	1.00	62.18
	2203	CA	TRP	A	87	-1.903	39.848	-14.009	1.00	62.18
40	2204	CB	TRP	A	87	-2.668	41.090	-14.457	1.00	225.09
	2205	CG	TRP	A	87	-2.632	41.233	-15.914	1.00	225.09
	2206	CD2	TRP	A	87	-3.596	40.723	-16.830	1.00	225.09
	2207	CE2	TRP	A	87	-3.100	40.950	-18.122	1.00	225.09
	2208	CE3	TRP	A	87	-4.834	40.077	-16.683	1.00	225.09
45	2209	CD1	TRP	A	87	-1.618	41.757	-16.666	1.00	225.09
	2210	NE1	TRP	A	87	-1.891	41.586	-17.994	1.00	225.09
	2211	CZ2	TRP	A	87	-3.794	40.549	-19.261	1.00	225.09
	2212	CZ3	TRP	A	87	-5.528	39.687	-17.820	1.00	225.09
	2213	CH2	TRP	A	87	-5.008	39.923	-19.086	1.00	225.09
50	2214	C	TRP	A	87	-1.350	40.068	-12.645	1.00	62.18
	2215	O	TRP	A	87	-0.139	40.149	-12.468	1.00	62.18
	2216	N	LEU	A	88	-2.249	40.140	-11.673	1.00	74.08
	2217	CA	LEU	A	88	-1.863	40.372	-10.295	1.00	74.08
	2218	CB	LEU	A	88	-2.457	41.681	-9.805	1.00	87.26
55	2219	CG	LEU	A	88	-1.907	42.914	-10.492	1.00	87.26
	2220	CD1	LEU	A	88	-2.496	44.139	-9.837	1.00	87.26
	2221	CD2	LEU	A	88	-0.394	42.908	-10.383	1.00	87.26
	2222	C	LEU	A	88	-2.305	39.274	-9.369	1.00	74.08
	2223	O	LEU	A	88	-3.399	38.723	-9.501	1.00	74.08
60	2224	N	LEU	A	89	-1.456	38.978	-8.399	1.00	49.26
	2225	CA	LEU	A	89	-1.769	37.943	-7.432	1.00	49.26
	2226	CB	LEU	A	89	-0.902	36.718	-7.675	1.00	70.28
	2227	CG	LEU	A	89	-1.170	35.653	-6.637	1.00	70.28
	2228	CD1	LEU	A	89	-2.692	35.436	-6.511	1.00	70.28
65	2229	CD2	LEU	A	89	-0.455	34.401	-7.046	1.00	70.28
	2230	C	LEU	A	89	-1.499	38.470	-6.036	1.00	49.26
	2231	O	LEU	A	89	-0.429	39.008	-5.784	1.00	49.26
	2232	N	LEU	A	90	-2.459	38.342	-5.127	1.00	72.68
	2233	CA	LEU	A	90	-2.240	38.815	-3.760	1.00	72.68
70	2234	CB	LEU	A	90	-3.562	39.231	-3.111	1.00	33.75

2235	CG	LEU	A	90	-3.444	39.630	-1.648	1.00	33.75
2236	CD1	LEU	A	90	-2.488	40.814	-1.620	1.00	33.75
2237	CD2	LEU	A	90	-4.790	40.011	-1.047	1.00	33.75
2238	C	LEU	A	90	-1.623	37.701	-2.931	1.00	72.68
2239	O	LEU	A	90	-2.254	36.674	-2.710	1.00	72.68
2240	N	GLN	A	91	-0.398	37.896	-2.462	1.00	48.17
2241	CA	GLN	A	91	0.255	36.864	-1.656	1.00	48.17
2242	CB	GLN	A	91	1.692	36.682	-2.110	1.00	50.84
2243	CG	GLN	A	91	1.773	36.315	-3.559	1.00	50.84
2244	CD	GLN	A	91	3.159	35.954	-3.971	1.00	50.84
2245	OE1	GLN	A	91	4.041	36.801	-4.013	1.00	50.84
2246	NE2	GLN	A	91	3.371	34.688	-4.271	1.00	50.84
2247	C	GLN	A	91	0.218	37.151	-0 165	1.00	48.17
2248	O	GLN	A	91	0.282	38.298	0. 254	1.00	48.17
2249	N	ALA	A	92	0.098	36.113	0.648	1.00	56.37
2250	CA	ALA	A	92	0.044	36.326	2.080	1.00	56.37
2251	CB	ALA	A	92	-1.329	36.039	2.579	1.00	37.31
2252	C	ALA	A	92	1.033	35.422	2.769	1.00	56.37
2253	O	ALA	A	92	1.202	34.266	2.381	1.00	56.37
2254	N	SER	A	93	1.695	35.939	3.794	1.00	55.78
2255	CA	SER	A	93	2.665	35.146	4.535	1.00	55.78
2256	CB	SER	A	93	3.171	35.909	5.763	1.00	74.91
2257	OG	SER	A	93	2.111	36.461	6.531	1.00	74.91
2258	C	SER	A	93	1.912	33.919	4.956	1.00	55.78
2259	O	SER	A	93	2.205	32.828	4.501	1.00	55.78
2260	N	ALA	A	94	0.904	34.112	5.796	1.00	63.55
2261	CA	ALA	A	94	0.070	33.021	6.287	1.00	63.55
2262	CB	ALA	A	94	0.410	32.712	7.734	1.00	137.30
2263	C	ALA	A	94	-1.392	33.445	6.162	1.00	63.55
2264	O	ALA	A	94	-1.713	34.616	6.341	1.00	63.55
2265	N	GLU	A	95	-2.283	32.501	5.856	1.00	58.25
2266	CA	GLU	A	95	-3.702	32.826	5.684	1.00	58.25
2267	CB	GLU	A	95	-4.344	31.866	4.701	1.00	138.90
2268	CG	GLU	A	95	-3.695	31.890	3.337	1.00	138.90
2269	CD	GLU	A	85	-4.541	31.214	2.269	1.00	138.90
2270	OE1	GLU	A	95	-4.085	31.137	1.108	1.00	138.90
2271	OE2	GLU	A	95	-5.664	30.763	2.584	1.00	138.90
2272	C	GLU	A	95	-4.494	32.844	6.979	1.00	58.25
2273	O	GLU	A	95	-5.600	33.381	7.016	1.00	58.25
2274	N	VAL	A	96	-3.934	32.267	8.040	1.00	62.67
2275	CA	VAL	A	96	-4.584	32.253	9.353	1.00	62.67
2276	CB	VAL	A	96	-5.180	30.912	9.637	1.00	62.13
2277	CG1	VAL	A	96	-6.169	31.021	10.762	1.00	62.13
2278	CG2	VAL	A	96	-5.835	30.401	8.402	1.00	62.13
2279	C	VAL	A	96	-3.512	32.568	10.386	1.00	62.67
2280	O	VAL	A	96	-2.422	31.999	10.335	1.00	62.67
2281	N	VAL	A	97	-3.829	33.449	11.333	1.00	50.85
2282	CA	VAL	A	97	-2.833	33.902	12.289	1.00	50.55
2283	CB	VAL	A	97	-2.307	35.276	11.860	1.00	70.57
2284	CG1	VAL	A	97	-1.069	35.609	12.633	1.00	70.57
2285	CG2	VAL	A	97	-2.063	35.319	10.372	1.00	70.57
2286	C	VAL	A	97	-3.285	34.077	13.723	1.00	50.85
2287	O	VAL	A	97	-4.373	34.653	13.953	1.00	50.85
2288	N	MET	A	98	-2.449	33.629	14.673	1.00	73.49
2289	CA	MET	A	98	-2.749	33.780	16.096	1.00	73.49
2290	CB	MET	A	98	-1.766	32.956	16.916	1.00	225.45
2291	CG	MET	A	98	-1.855	31.478	16.645	1.00	228.45
2292	SD	MET	A	98	-3.227	30.766	17.530	1.00	228.45
2293	CE	MET	A	98	-2.529	30.766	19.195	1.00	228.45
2294	C	MET	A	98	-2.617	35.276	16.477	1.00	73.49
2295	O	MET	A	98	-1.636	35.921	16.109	1.00	73.49
2296	N	GLU	A	99	-3.595	35.826	17.202	1.00	97.63
2297	CA	GLU	A	99	-3.546	37.228	17.603	1.00	97.63
2298	CB	GLU	A	99	-4.562	37.499	18.710	1.00	188.19
2299	CG	GLU	A	99	-4.954	38.958	18.826	1.00	188.19
2300	CD	GLU	A	99	-5.707	39.259	20.106	1.00	188.19
2301	OE1	GLU	A	99	-6.524	38.412	20.529	1.00	188.19
2302	OE2	GLU	A	99	-5.492	40.347	20.682	1.00	188.19
2303	C	GLU	A	99	-2.146	37.510	18.128	1.00	97.63
2304	O	GLU	A	99	-1.651	36.783	18.987	1.00	97.63

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	2305	N	GLY	A	100	-1.492	38.538	17.594	1.00	88.99
	2306	CA	GLY	A	100	-0.159	38.881	18.066	1.00	88.99
	2307	C	GLY	A	100	0.992	38.577	17.130	1.00	88.99
	2308	O	GLY	A	100	2.071	39.135	17.293	1.00	88.99
5	2309	N	GLN	A	101	0.777	37.699	16.154	1.00	57.71
	2310	CA	GLN	A	101	1.820	37.329	15.192	1.00	57.71
	2311	CB	GLN	A	101	1.568	35.933	14.652	1.00	91.13
	2312	CG	GLN	A	101	1.663	34.861	15.708	1.00	91.13
	2313	CD	GLN	A	101	2.932	34.976	16.532	1.00	91.13
10	2314	OE1	GLN	A	101	3.038	35.828	17.420	1.00	91.13
	2315	NE2	GLN	A	101	3.912	34.131	16.230	1.00	91.13
	2316	C	GLN	A	101	1.973	38.281	14.017	1.00	57.71
	2317	O	GLN	A	101	1.117	39.124	13.763	1.00	57.71
	2318	N	PRO	A	102	3.070	38.153	13.266	1.00	73.79
15	2319	CD	PRO	A	102	4.201	37.220	13.403	1.00	74.96
	2320	CA	PRO	A	102	3.264	39.049	12.130	1.00	73.79
	2321	CB	PRO	A	102	4.760	38.932	11.873	1.00	74.96
	2322	CG	PRO	A	102	5.018	37.499	12.139	1.00	74.96
	2323	C	PRO	A	102	2.425	38.610	10.940	1.00	73.79
20	2324	O	PRO	A	102	2.053	37.446	10.831	1.00	73.79
	2325	N	LEU	A	103	2.125	39.551	10.054	1.00	77.13
	2326	CA	LEU	A	103	1.345	39.258	8.862	1.00	77.13
	2327	CB	LEU	A	103	-0.101	39.627	9.094	1.00	77.95
	2328	CG	LEU	A	103	-0.892	39.326	7.831	1.00	77.95
25	2329	CD1	LEU	A	103	-0.843	37.836	7.584	1.00	77.95
	2330	CD2	LEU	A	103	-2.324	39.799	7.975	1.00	77.95
	2331	C	LEU	A	103	1.850	40.060	7.680	1.00	77.13
	2332	O	LEU	A	103	1.892	41.280	7.769	1.00	77.13
	2333	N	PHE	A	104	2.226	39.404	6.580	1.00	65.06
30	2334	CA	PHE	A	104	2.708	40.147	5.410	1.00	65.06
	2335	CB	PHE	A	104	4.175	39.821	5.102	1.00	119.06
	2336	CG	PHE	A	104	5.118	40.096	6.246	1.00	119.06
	2337	CD1	PHE	A	104	5.209	39.208	7.312	1.00	119.06
	2338	CD2	PHE	A	104	5.926	41.237	6.255	1.00	119.06
35	2339	CE1	PHE	A	104	6.086	39.443	8.379	1.00	119.06
	2340	CE2	PHE	A	104	6.811	41.486	7.321	1.00	119.06
	2341	CZ	PHE	A	104	6.891	40.585	8.382	1.00	119.06
	2342	C	PHE	A	104	1.869	39.886	4.164	1.00	65.06
	2343	O	PHE	A	104	1.640	38.741	3.816	1.00	65.06
40	2344	N	LEU	A	105	1.373	40.944	3.519	1.00	48.39
	2345	CA	LEU	A	105	0.597	40.795	2.282	1.00	48.39
	2346	CB	LEU	A	105	-0.708	41.544	2.354	1.00	38.52
	2347	CG	LEU	A	105	-1.516	41.145	3.570	1.00	38.52
	2348	CD1	LEU	A	105	-2.952	41.785	3.515	1.00	38.52
45	2349	CD2	LEU	A	105	-1.587	39.647	3.571	1.00	38.52
	2350	C	LEU	A	105	1.445	41.417	1.205	1.00	48.39
	2351	O	LEU	A	105	2.137	42.397	1.461	1.00	48.39
	2352	N	ARG	A	106	1.385	40.872	0.001	1.00	64.12
	2353	CA	ARG	A	106	2.198	41.394	-1.074	1.00	64.12
50	2354	CB	ARG	A	106	3.424	40.501	-1.232	1.00	100.28
	2355	CG	ARG	A	106	4.313	40.873	-2.370	1.00	100.28
	2356	CD	ARG	A	106	5.351	39.801	-2.607	1.00	100.28
	2357	NE	ARG	A	106	6.190	40.124	-3.755	1.00	100.28
	2358	CZ	ARG	A	106	6.892	39.234	-4.443	1.00	100.28
55	2359	NH1	ARG	A	106	6.854	37.957	-4.100	1.00	100.28
	2360	NH2	ARG	A	106	7.619	39.623	-5.484	1.00	100.28
	2361	C	ARG	A	106	1.416	41.451	-2.380	1.00	64.12
	2362	O	ARG	A	106	0.842	40.444	-2.799	1.00	64.12
	2363	N	CYS	A	107	1.349	42.619	-3.018	1.00	99.13
60	2364	CA	CYS	A	107	0.651	42.685	-4.301	1.00	99.13
	2365	C	CYS	A	107	1.710	42.307	-5.317	1.00	99.13
	2366	O	CYS	A	107	2.639	43.059	-5.575	1.00	99.13
	2367	CB	CYS	A	107	0.113	44.075	-4.597	1.00	103.70
	2368	SG	CYS	A	107	-1.146	44.090	-5.916	1.00	103.70
65	2369	N	HIS	A	108	1.573	41.112	-5.866	1.00	72.29
	2370	CA	HIS	A	108	2.530	40.575	-6.804	1.00	72.29
	2371	CB	HIS	A	108	2.799	39.131	-6.429	1.00	116.05
	2372	CG	HIS	A	108	3.921	38.508	-7.191	1.00	116.05
	2373	CD2	HIS	A	108	3.973	37.391	-7.950	1.00	116.05
70	2374	ND1	HIS	A	108	5.195	39.028	-7.190	1.00	116.05

	2375	CE1	HIS	A	108	5.986	38.256	-7.913	1.00	116.05
	2376	NE2	HIS	A	108	5.268	37.255	-8.385	1.00	116.05
	2377	C	HIS	A	108	2.119	40.651	-8.271	1.00	72.29
	2378	O	HIS	A	108	1.045	40.176	-8.674	1.00	72.29
5	2379	N	GLY	A	109	2.999	41.242	-9.070	1.00	118.98
	2380	CA	GLY	A	109	2.735	41.367	-10.485	1.00	118.98
	2381	C	GLY	A	109	3.202	40.136	-11.231	1.00	118.98
	2382	O	GLY	A	109	4.083	39.410	-10.772	1.00	118.98
	2383	N	TRP	A	110	2.603	39.894	-12.389	1.00	106.09
10	2384	CA	TRP	A	110	2.968	38.751	-13.202	1.00	106.09
	2385	CB	TRP	A	110	2.016	38.629	-14.395	1.00	134.90
	2386	CG	TRP	A	110	2.418	37.581	-15.361	1.00	134.90
	2387	CD2	TRP	A	110	1.980	36.223	-15.380	1.00	134.90
	2388	CE2	TRP	A	110	2.657	35.576	-16.431	1.00	134.90
15	2389	CE3	TRP	A	110	1.072	35.481	-14.604	1.00	134.90
	2390	CD1	TRP	A	110	3.314	37.707	-16.370	1.00	134.90
	2391	NE1	TRP	A	110	3.466	36.509	-17.021	1.00	134.90
	2392	CZ2	TRP	A	110	2.464	34.224	-16.732	1.00	134.90
	2393	CZ3	TRP	A	110	0.879	34.132	-14.905	1.00	134.90
20	2394	CH2	TRP	A	110	1.575	33.521	-15.958	1.00	134.90
	2395	C	TRP	A	110	4.399	38.899	-13.683	1.00	106.09
	2396	O	TRP	A	110	4.916	40.008	-13.825	1.00	106.09
	2397	N	ARG	A	111	5.043	37.764	-13.918	1.00	87.25
	2398	CA	ARG	A	111	6.426	37.750	-14.392	1.00	87.25
25	2399	CB	ARG	A	111	6.468	38.086	-15.858	1.00	235.25
	2400	CG	ARG	A	111	6.316	36.881	-16.692	1.00	235.25
	2401	CD	ARG	A	111	6.642	37.245	-18.072	1.00	235.25
	2402	NE	ARG	A	111	7.428	36.197	-18.691	1.00	235.25
	2403	CZ	ARG	A	111	8.674	35.887	-18.358	1.00	235.25
30	2404	NH1	ARG	A	111	9.295	36.552	-17.392	1.00	235.25
	2405	NH2	ARG	A	111	9.290	34.895	-18.988	1.00	235.25
	2406	C	ARG	A	111	7.358	38.697	-13.665	1.00	87.25
	2407	O	ARG	A	111	8.402	39.105	-14.191	1.00	87.25
	2408	N	ASN	A	112	6.964	39.048	-12.453	1.00	105.23
35	2409	CA	ASN	A	112	7.744	39.942	-11.633	1.00	105.23
	2410	CB	ASN	A	112	9.121	39.353	-11.375	1.00	116.08
	2411	CG	ASN	A	112	9.735	39.907	-10.118	1.00	116.08
	2412	OD1	ASN	A	112	9.369	41.000	-9.660	1.00	116.08
	2413	ND2	ASN	A	112	10.668	39.166	-9.544	1.00	116.08
40	2414	C	ASN	A	112	7.905	41.345	-12.218	1.00	105.23
	2415	O	ASN	A	112	8.852	42.055	-11.885	1.00	105.23
	2416	N	TRP	A	113	6.992	41.753	-13.089	1.00	124.66
	2417	CA	TRP	A	113	7.095	43.088	-13.645	1.00	124.66
	2418	CB	TRP	A	113	6.019	43.344	-14.688	1.00	167.38
45	2419	CG	TRP	A	113	6.315	42.730	-15.979	1.00	167.38
	2420	CD2	TRP	A	113	5.379	42.134	-16.868	1.00	167.38
	2421	CE2	TRP	A	113	6.091	41.718	-18.006	1.00	167.38
	2422	CE3	TRP	A	113	3.997	41.914	-16.816	1.00	167.38
	2423	CD1	TRP	A	113	7.533	42.658	-16.592	1.00	167.38
50	2424	NE1	TRP	A	113	7.406	42.049	-17.813	1.00	167.38
	2425	CZ2	TRP	A	113	5.475	41.093	-19.080	1.00	167.38
	2426	CZ3	TRP	A	113	3.383	41.293	-17.886	1.00	167.38
	2427	CH2	TRP	A	113	4.126	40.886	-19.004	1.00	167.38
	2428	C	TRP	A	113	6.939	44.106	-12.540	1.00	124.66
55	2429	O	TRP	A	113	6.964	43.768	-11.357	1.00	124.66
	2430	N	ASP	A	114	6.773	45.359	-12.937	1.00	183.83
	2431	CA	ASP	A	114	6.603	46.430	-11.981	1.00	183.83
	2432	CB	ASP	A	114	7.598	47.558	-12.258	1.00	145.30
	2433	CG	ASP	A	114	8.978	47.269	-11.692	1.00	145.30
60	2434	OD1	ASP	A	114	9.077	47.087	-10.459	1.00	145.30
	2435	OD2	ASP	A	114	9.957	47.225	-12.473	1.00	145.30
	2436	C	ASP	A	114	5.188	46.956	-12.034	1.00	183.83
	2437	O	ASP	A	114	4.598	47.106	-13.108	1.00	183.83
	2438	N	VAL	A	115	4.645	47.216	-10.853	1.00	117.62
65	2439	CA	VAL	A	115	3.294	47.740	-10.735	1.00	117.82
	2440	CB	VAL	A	115	2.421	46.835	-9.879	1.00	77.28
	2441	CG1	VAL	A	115	0.971	47.248	-10.008	1.00	77.28
	2442	CG2	VAL	A	115	2.616	45.409	-10.302	1.00	77.28
	2443	C	VAL	A	115	3.329	49.116	-10.089	1.00	117.62
70	2444	O	VAL	A	115	4.142	49.377	-9.191	1.00	117.62

	2445	N	TYR	A	116	2.444	49.995	-10.553	1.00	77.55
	2446	CA	TYR	A	116	2.380	51.344	-10.021	1.00	77.55
	2447	CB	TYR	A	116	2.831	52.352	-11.086	1.00	167.00
	2448	CG	TYR	A	116	4.271	52.172	-11.532	1.00	167.00
5	2449	CD1	TYR	A	116	4.581	51.453	-12.676	1.00	167.00
	2450	CE1	TYR	A	116	5.909	51.265	-13.071	1.00	167.00
	2451	CD2	TYR	A	116	5.325	52.703	-10.789	1.00	167.00
	2452	CE2	TYR	A	116	6.653	52.519	-11.173	1.00	167.00
	2453	CZ	TYR	A	116	6.937	51.800	-12.312	1.00	167.00
10	2454	OH	TYR	A	116	8.246	51.606	-12.687	1.00	167.00
	2455	C	TYR	A	116	0.984	51.699	-9.519	1.00	77.55
	2456	O	TYR	A	116	0.023	50.951	-9.742	1.00	77.55
	2457	N	LYS	A	117	0.879	52.842	-8.840	1.00	94.85
	2458	CA	LYS	A	117	-0.399	53.292	-8.310	1.00	94.85
15	2459	CB	LYS	A	117	-1.300	53.834	-9.423	1.00	193.46
	2460	CG	LYS	A	117	-1.084	55.291	-9.786	1.00	193.46
	2461	CD	LYS	A	117	-2.284	55.824	-10.563	1.00	193.46
	2462	CE	LYS	A	117	-3.569	55.726	-9.735	1.00	193.46
	2463	NZ	LYS	A	117	-4.780	56.210	-10.464	1.00	193.46
20	2464	C	LYS	A	117	-1.099	52.125	-7.629	1.00	94.85
	2465	O	LYS	A	117	-2.226	51.770	-7.977	1.00	94.85
	2466	N	VAL	A	118	-0.422	51.530	-6.655	1.00	105.41
	2467	CA	VAL	A	118	-0.979	50.402	-5.927	1.00	105.41
	2468	CB	VAL	A	118	0.122	49.503	-5.445	1.00	73.04
25	2469	CG1	VAL	A	118	-0.314	48.777	-4.205	1.00	73.04
	2470	CG2	VAL	A	118	0.455	48.521	-6.514	1.00	73.04
	2471	C	VAL	A	118	-1.862	50.736	-4.723	1.00	105.41
	2472	O	VAL	A	118	-1.527	51.582	-3.894	1.00	105.41
	2473	N	ILE	A	119	-2.971	50.020	-4.607	1.00	71.97
30	2474	CA	ILE	A	119	-3.902	50.248	-3.518	1.00	71.97
	2475	CB	ILE	A	119	-5.125	51.002	-4.016	1.00	77.41
	2476	CG2	ILE	A	119	-6.037	51.319	-2.866	1.00	77.41
	2477	CG1	ILE	A	119	-4.687	52.285	-4.705	1.00	77.41
	2478	CD1	ILE	A	119	-5.804	52.949	-5.467	1.00	77.41
35	2479	C	ILE	A	119	-4.395	48.928	-2.961	1.00	71.97
	2480	O	ILE	A	119	-4.954	48.146	-3.701	1.00	71.97
	2481	N	TYR	A	120	-4.193	48.654	-1.679	1.00	64.29
	2482	CA	TYR	A	120	-4.698	47.403	-1.117	1.00	64.29
	2483	CB	TYR	A	120	-3.867	46.908	0.059	1.00	49.60
40	2484	CG	TYR	A	120	-2.521	46.438	-0.297	1.00	49.60
	2485	CD1	TYR	A	120	-1.472	47.324	-0.395	1.00	49.60
	2486	CE1	TYR	A	120	-0.195	46.897	-0.736	1.00	49.60
	2487	CD2	TYR	A	120	-2.292	45.109	-0.546	1.00	49.60
	2488	CE2	TYR	A	120	-1.026	44.650	-0.901	1.00	49.60
45	2489	CZ	TYR	A	120	0.020	45.548	-0.992	1.00	49.60
	2490	OH	TYR	A	120	1.268	45.095	-1.339	1.00	49.60
	2491	C	TYR	A	120	-6.069	47.679	-0.580	1.00	64.29
	2492	O	TYR	A	120	-6.313	48.764	-0.069	1.00	64.29
	2493	N	TYR	A	121	-6.945	46.686	-0.658	1.00	62.29
50	2494	CA	TYR	A	121	-8.299	46.838	-0.154	1.00	62.29
	2495	CB	TYR	A	121	-9.315	46.752	-1.302	1.00	87.89
	2496	CG	TYR	A	121	-9.308	47.900	-2.293	1.00	87.89
	2497	CD1	TYR	A	121	-8.219	48.119	-3.126	1.00	87.89
	2498	CE1	TYR	A	121	-8.232	49.147	-4.073	1.00	87.89
55	2499	CD2	TYR	A	121	-10.422	48.745	-2.424	1.00	87.89
	2500	CE2	TYR	A	121	-10.450	49.776	-3.368	1.00	87.89
	2501	CZ	TYR	A	121	-9.351	49.970	-4.193	1.00	37.89
	2502	OH	TYR	A	121	-9.383	50.966	-5.156	1.00	87.89
	2503	C	TYR	A	121	-8.647	45.772	0.883	1.00	62.29
60	2504	O	TYR	A	121	-8.275	44.598	0.723	1.00	62.29
	2505	N	LYS	A	122	-9.349	46.180	1.943	1.00	53.98
	2506	CA	LYS	A	122	-9.794	45.238	2.957	1.00	53.98
	2507	CB	LYS	A	122	-9.069	45.436	4.278	1.00	98.53
	2508	CG	LYS	A	122	-9.499	44.427	5.329	1.00	98.53
65	2509	CD	LYS	A	122	-9.038	44.809	6.719	1.00	98.53
	2510	CE	LYS	A	122	-9.644	43.912	7.774	1.00	98.53
	2511	NZ	LYS	A	122	-9.317	44.426	9.120	1.00	98.53
	2512	C	LYS	A	122	-11.291	45.452	3.158	1.00	53.98
	2513	O	LYS	A	122	-11.720	46.526	3.569	1.00	53.98
70	2514	N	ASP	A	123	-12.081	44.429	2.841	1.00	82.84

	2515	CA	ASP	A	123	-13.530	44.491	2.976	1.00	82.84
	2516	CB	ASP	A	123	-13.926	44.624	4.449	1.00	104.85
	2517	CG	ASP	A	123	-13.786	43.313	5.204	1.00	104.85
	2518	OD1	ASP	A	123	-14.244	42.269	4.680	1.00	104.85
5	2519	OD2	ASP	A	123	-13.228	43.321	6.324	1.00	104.85
	2520	C	ASP	A	123	-14.140	45.620	2.158	1.00	82.84
	2521	O	ASP	A	123	-15.013	46.350	2.638	1.00	82.84
	2522	N	GLY	A	124	-13.677	45.743	0.915	1.00	89.57
	2523	CA	GLY	A	124	-14.179	46.772	0.018	1.00	89.57
10	2524	C	GLY	A	124	-13.699	48.197	0.279	1.00	89.57
	2525	O	GLY	A	124	-13.981	49.093	-0.528	1.00	89.57
	2526	N	GLU	A	125	-12.978	48.412	1.382	1.00	81.16
	2527	CA	GLU	A	125	-12.476	49.746	1.745	1.00	81.16
	2528	CB	GLU	A	125	-12.470	49.925	3.274	1.00	176.94
15	2529	CG	GLU	A	125	-13.834	49.988	3.958	1.00	176.94
	2530	CD	GLU	A	125	-14.499	51.350	3.844	1.00	176.94
	2531	OE1	GLU	A	125	-13.931	52.343	4.352	1.00	176.94
	2532	OE2	GLU	A	125	-15.595	51.428	3.251	1.00	176.94
	2533	C	GLU	A	125	-11.055	50.008	1.238	1.00	81.16
20	2534	O	GLU	A	125	-10.223	49.116	1.229	1.00	81.16
	2535	N	ALA	A	126	-10.772	51.228	0.815	1.00	92.74
	2536	CA	ALA	A	126	-9.424	51.546	0.375	1.00	92.74
	2537	CB	ALA	A	126	-9.379	52.967	-0.145	1.00	165.28
	2538	C	ALA	A	126	-8.592	51.410	1.650	1.00	92.74
25	2539	O	ALA	A	126	-9.083	51.719	2.731	1.00	92.74
	2540	N	LEU	A	127	-7.347	50.957	1.550	1.00	58.95
	2541	CA	LEU	A	127	-6.544	50.778	2.749	1.00	58.95
	2542	CB	LEU	A	127	-6.333	49.305	3.037	1.00	73.14
	2543	CG	LEU	A	127	-6.046	49.150	4.528	1.00	73.14
30	2544	CD1	LEU	A	127	-7.224	49.745	5.285	1.00	73.14
	2545	CD2	LEU	A	127	-5.840	47.693	4.917	1.00	73.14
	2546	C	LEU	A	127	-5.195	51.457	2.764	1.00	58.95
	2547	O	LEU	A	127	-4.910	52.212	3.691	1.00	58.95
	2548	N	LYS	A	128	-4.344	51.153	1.788	1.00	77.17
35	2549	CA	LYS	A	128	-3.028	51.788	1.690	1.00	77.17
	2550	CB	LYS	A	128	-1.920	50.862	2.197	1.00	133.78
	2551	CG	LYS	A	128	-2.041	50.465	3.656	1.00	133.78
	2552	CD	LYS	A	128	-1.716	51.601	4.605	1.00	133.78
	2553	CE	LYS	A	128	-1.741	51.120	6.052	1.00	133.78
40	2554	NZ	LYS	A	128	-1.293	52.157	7.033	1.00	133.78
	2555	C	LYS	A	128	-2.788	52.130	0.212	1.00	77.17
	2556	O	LYS	A	128	-3.348	51.493	-0.675	1.00	77.17
	2557	N	TYR	A	129	-1.973	53.142	-0.063	1.00	64.91
	2558	CA	TYR	A	129	-1.693	53.519	-1.444	1.00	64.91
45	2559	CB	TYR	A	129	-2.633	54.637	-1.882	1.00	122.39
	2560	CG	TYR	A	129	-2.100	55.390	-3.080	1.00	122.39
	2561	CD1	TYR	A	129	-2.232	54.874	-4.366	1.00	122.39
	2562	CE1	TYR	A	129	-1.702	55.539	-5.465	1.00	122.39
	2563	CD2	TYR	A	129	-1.416	56.599	-2.919	1.00	122.39
50	2564	CE2	TYR	A	129	-0.875	57.273	-4.012	1.00	122.39
	2565	CZ	TYR	A	129	-1.024	56.738	-5.282	1.00	122.39
	2566	OH	TYR	A	129	-0.508	57.402	-6.370	1.00	122.39
	2567	C	TYR	A	129	-0.244	53.978	-1.679	1.00	64.91
	2568	O	TYR	A	129	0.320	54.739	-0.885	1.00	64.91
55	2569	N	TRP	A	130	0.348	53.530	-2.787	1.00	121.28
	2570	CA	TRP	A	130	1.713	53.914	-3.125	1.00	121.28
	2571	CB	TRP	A	130	2.715	52.874	-2.627	1.00	194.88
	2572	CG	TRP	A	130	2.557	52.464	-1.196	1.00	194.88
	2573	CD2	TRP	A	130	3.398	52.848	-0.100	1.00	194.88
60	2574	CE2	TRP	A	130	2.909	52.182	1.049	1.00	194.88
	2575	CE3	TRP	A	130	4.508	53.694	0.023	1.00	194.88
	2576	CD1	TRP	A	130	1.629	51.608	-0.683	1.00	194.88
	2577	NE1	TRP	A	130	1.833	51.431	0.666	1.00	194.88
	2578	CZ2	TRP	A	130	3.500	52.334	2.309	1.00	194.88
65	2579	CZ3	TRP	A	130	5.096	53.847	1.280	1.00	194.88
	2580	CH2	TRP	A	130	4.592	53.163	2.403	1.00	194.88
	2581	C	TRP	A	130	1.907	54.064	-4.627	1.00	121.28
	2582	O	TRP	A	130	1.075	53.627	-5.422	1.00	121.28
	2583	N	TYR	A	131	3.015	54.685	-5.015	1.00	100.84
70	2584	CA	TYR	A	131	3.304	54.849	-6.426	1.00	100.84

	2585	CB	TYR	A	131	4.202	56.059	-6.683	1.00	199.69
	2586	CG	TYR	A	131	4.299	56.369	-8.155	1.00	199.69
	2587	CD1	TYR	A	131	3.223	56.944	-8.830	1.00	199.69
	2588	CE1	TYR	A	131	3.246	57.115	-10.206	1.00	199.69
5	2589	CD2	TYR	A	131	5.414	55.982	-8.899	1.00	199.69
	2590	CE2	TYR	A	131	5.448	56.148	-10.281	1.00	199.69
	2591	CZ	TYR	A	131	4.357	56.712	-10.926	1.00	199.69
	2592	OH	TYR	A	131	4.364	56.843	-12.295	1.00	199.69
	2593	C	TYR	A	131	4.029	53.572	-6.818	1.00	100.84
10	2594	O	TYR	A	131	3.397	52.644	-7.326	1.00	100.84
	2595	N	GLU	A	132	5.351	53.543	-6.624	1.00	218.16
	2596	CA	GLU	A	132	6.122	52.331	-6.894	1.00	218.16
	2597	CB	GLU	A	132	7.629	52.547	-6.666	1.00	249.55
	2598	CG	GLU	A	132	8.382	53.317	-7.762	1.00	249.55
15	2599	CD	GLU	A	132	9.480	52.482	-8.422	1.00	249.55
	2600	OE1	GLU	A	132	9.903	51.469	-7.822	1.00	249.55
	2601	OE2	GLU	A	132	9.922	52.848	-9.533	1.00	249.55
	2602	C	GLU	A	132	5.531	51.536	-5.747	1.00	218.16
	2603	O	GLU	A	132	5.514	52.022	-4.616	1.00	218.16
20	2604	N	ASN	A	133	5.032	50.334	-6.012	1.00	155.99
	2605	CA	ASN	A	133	4.388	49.588	-4.939	1.00	155.99
	2606	CB	ASN	A	133	3.656	48.353	-5.472	1.00	108.04
	2607	CG	ASN	A	133	4.538	47.157	-5.575	1.00	108.04
	2608	OD1	ASN	A	133	5.620	47.230	-6.143	1.00	108.04
25	2609	ND2	ASN	A	133	4.085	46.035	-5.035	1.00	108.04
	2610	C	ASN	A	133	5.244	49.194	-3.759	1.00	155.99
	2611	O	ASN	A	133	6.458	49.376	-3.734	1.00	155.99
	2612	N	HIS	A	134	4.560	48.629	-2.779	1.00	115.35
	2613	CA	HIS	A	134	5.153	48.235	-1.520	1.00	115.35
30	2614	CB	HIS	A	134	4.782	49.305	-0.489	1.00	200.02
	2615	CG	HIS	A	134	5.436	49.129	0.842	1.00	200.02
	2616	CD2	HIS	A	134	4.912	48.883	2.067	1.00	200.02
	2617	ND1	HIS	A	134	6.799	49.213	1.016	1.00	200.02
	2618	CE1	HIS	A	134	7.088	49.035	2.293	1.00	200.02
35	2619	NE2	HIS	A	134	5.961	48.840	2.951	1.00	200.02
	2620	C	HIS	A	134	4.596	46.874	-1.114	1.00	115.35
	2621	O	HIS	A	134	4.008	46.161	-1.934	1.00	115.35
	2622	N	ASN	A	135	4.781	46.524	0.153	1.00	81.38
	2623	CA	ASN	A	135	4.298	45.263	0.675	1.00	81.38
40	2624	CB	ASN	A	135	5.426	44.243	0.654	1.00	168.37
	2625	CG	ASN	A	135	5.832	43.891	-0.754	1.00	168.37
	2626	OD1	ASN	A	135	4.964	43.656	-1.596	1.00	168.37
	2627	ND2	ASN	A	135	7.134	43.839	-1.029	1.00	168.37
	2628	C	ASN	A	135	3.748	45.431	2.073	1.00	81.38
45	2629	O	ASN	A	135	4.455	45.219	3.042	1.00	81.38
	2630	N	ILE	A	136	2.481	45.817	2.168	1.00	68.07
	2631	CA	ILE	A	136	1.826	46.032	3.456	1.00	68.07
	2632	CB	ILE	A	136	0.288	46.019	3.287	1.00	68.88
	2633	CG2	ILE	A	136	-0.135	44.814	2.531	1.00	86.88
50	2634	CG1	ILE	A	136	-0.397	46.040	4.638	1.00	86.88
	2635	CD1	ILE	A	136	-1.885	46.136	4.514	1.00	86.88
	2636	C	ILE	A	136	2.277	44.997	4.482	1.00	68.07
	2637	O	ILE	A	136	2.085	43.801	4.301	1.00	68.07
	2638	N	SER	A	137	2.904	45.484	5.550	1.00	113.35
55	2639	CA	SER	A	137	3.422	44.631	6.606	1.00	113.35
	2640	CB	SER	A	137	4.932	44.788	6.686	1.00	73.04
	2641	OG	SER	A	137	5.433	44.258	7.891	1.00	73.04
	2642	C	SER	A	137	2.808	44.903	7.974	1.00	113.35
	2643	O	SER	A	137	2.469	46.029	8.304	1.00	113.35
60	2644	N	ILE	A	138	2.688	43.856	8.777	1.00	71.19
	2645	CA	ILE	A	138	2.116	43.961	10.117	1.00	71.19
	2646	CB	ILE	A	138	0.715	43.413	10.147	1.00	41.44
	2647	CG2	ILE	A	138	0.257	43.304	11.582	1.00	41.44
	2648	CG1	ILE	A	138	-0.212	44.297	9.318	1.00	41.44
65	2649	CD1	ILE	A	138	-1.531	43.627	9.019	1.00	41.44
	2650	C	ILE	A	138	2.922	43.170	11.146	1.00	71.19
	2651	O	ILE	A	138	3.093	41.954	11.012	1.00	71.19
	2652	N	THR	A	139	3.397	43.856	12.185	1.00	108.53
	2653	CA	THR	A	139	4.195	43.216	13.234	1.00	108.53
70	2654	CB	THR	A	139	5.001	44.260	14.012	1.00	232.49

	2655	OG1	THR	A	139	4.127	45.304	14.460	1.00	232.49
	2656	CG2	THR	A	139	6.080	44.854	13.121	1.00	232.49
	2657	C	THR	A	139	3.291	42.456	14.192	1.00	108.53
	2658	O	THR	A	139	3.199	41.235	14.125	1.00	108.53
5	2659	N	ASN	A	140	2.632	43.192	15.083	1.00	125.42
	2660	CA	ASN	A	140	1.699	42.621	16.050	1.00	125.42
	2661	CB	ASN	A	140	1.662	43.455	17.328	1.00	148.98
	2662	CG	ASN	A	140	0.819	42.967	18.305	1.00	148.98
	2663	OD1	ASN	A	140	-0.533	42.738	17.950	1.00	148.98
10	2664	ND2	ASN	A	140	1.024	42.828	19.558	1.00	148.98
	2665	C	ASN	A	140	0.335	42.677	15.375	1.00	125.42
	2666	O	ASN	A	140	-0.149	43.763	15.030	1.00	125.42
	2667	N	ALA	A	141	-0.291	41.518	15.203	1.00	57.61
	2668	CA	ALA	A	141	-1.569	41.462	14.527	1.00	57.61
15	2669	CB	ALA	A	141	-1.605	40.246	13.644	1.00	27.12
	2670	C	ALA	A	141	-2.785	41.468	15.439	1.00	57.61
	2671	O	ALA	A	141	-2.895	40.661	16.364	1.00	57.61
	2672	N	THR	A	142	-3.713	42.373	15.149	1.00	70.60
	2673	CA	THR	A	142	-4.939	42.481	15.912	1.00	70.60
20	2674	CB	THR	A	142	-5.488	43.903	15.811	1.00	136.27
	2675	OG1	THR	A	142	-4.440	44.833	16.136	1.00	136.27
	2676	CG2	THR	A	142	-6.643	44.104	16.773	1.00	136.27
	2677	C	THR	A	142	-5.937	41.478	15.334	1.00	70.60
	2678	O	THR	A	142	-5.666	40.852	14.311	1.00	70.60
25	2679	N	VAL	A	143	-7.066	41.285	16.001	1.00	71.67
	2680	CA	VAL	A	143	-8.057	40.355	15.489	1.00	71.67
	2681	CB	VAL	A	143	-8.949	39.782	16.610	1.00	65.94
	2682	CG1	VAL	A	143	-9.785	40.880	17.217	1.00	65.94
	2683	CG2	VAL	A	143	-9.848	38.672	16.047	1.00	65.94
30	2684	C	VAL	A	143	-8.934	41.126	14.518	1.00	71.67
	2685	O	VAL	A	143	-9.679	40.552	13.726	1.00	71.67
	2686	N	GLU	A	144	-8.842	42.442	14.579	1.00	71.12
	2687	CA	GLU	A	144	-9.650	43.260	13.699	1.00	71.12
	2688	CB	GLU	A	144	-9.747	44.691	14.235	1.00	228.43
35	2689	CG	GLU	A	144	-10.475	44.796	15.566	1.00	228.43
	2690	CD	GLU	A	144	-9.558	45.204	16.699	1.00	228.43
	2691	OE1	GLU	A	144	-8.966	46.296	16.611	1.00	228.43
	2692	OE2	GLU	A	144	-9.428	44.440	17.676	1.00	228.43
	2693	C	GLU	A	144	-9.068	43.250	12.301	1.00	71.12
40	2694	O	GLU	A	144	-9.732	43.609	11.338	1.00	71.12
	2695	N	ASP	A	145	-7.821	42.820	12.194	1.00	58.24
	2696	CA	ASP	A	145	-7.146	42.754	10.900	1.00	58.24
	2697	CB	ASP	A	145	-5.645	42.541	11.091	1.00	106.20
	2698	CG	ASP	A	145	-4.945	43.784	11.606	1.00	106.20
45	2699	OD1	ASP	A	145	-5.013	44.817	10.911	1.00	106.20
	2700	OD2	ASP	A	145	-4.329	43.733	12.696	1.00	106.20
	2701	C	ASP	A	145	-7.705	41.643	10.018	1.00	58.24
	2702	O	ASP	A	145	-7.434	41.608	8.819	1.00	58.24
	2703	N	SER	A	146	-8.490	40.744	10.607	1.00	85.01
50	2704	CA	SER	A	146	-9.077	39.652	9.848	1.00	85.01
	2705	CB	SER	A	146	-9.781	38.669	10.789	1.00	118.46
	2706	OG	SER	A	146	-8.854	38.089	11.691	1.00	118.46
	2707	C	SER	A	146	-10.052	40.266	8.855	1.00	85.01
	2708	O	SER	A	146	-10.741	41.227	9.168	1.00	85.01
55	2709	N	GLY	A	147	-10.081	39.735	7.644	1.00	64.55
	2710	CA	GLY	A	147	-10.972	40.264	6.632	1.00	64.55
	2711	C	GLY	A	147	-10.649	39.664	5.277	1.00	64.55
	2712	O	GLY	A	147	-9.963	38.628	5.214	1.00	64.55
	2713	N	THR	A	148	-11.147	40.285	4.201	1.00	54.60
60	2714	CA	THR	A	148	-10.881	39.795	2.841	1.00	54.60
	2715	CB	THR	A	148	-12.159	39.339	2.143	1.00	77.82
	2716	OG1	THR	A	148	-12.541	40.316	1.193	1.00	77.82
	2717	CG2	THR	A	148	-13.272	39.179	3.148	1.00	77.82
	2718	C	THR	A	148	-10.204	40.891	2.029	1.00	54.60
65	2719	O	THR	A	148	-10.789	41.941	1.746	1.00	54.60
	2720	N	TYR	A	149	-8.958	40.639	1.661	1.00	38.49
	2721	CA	TYR	A	149	-8.181	41.622	0.950	1.00	38.49
	2722	CB	TYR	A	149	-6.775	41.604	1.518	1.00	47.71
	2723	CG	TYR	A	149	-6.654	41.954	2.987	1.00	47.71
70	2724	CD1	TYR	A	149	-7.128	41.123	3.982	1.00	47.71

	2725	CE1	TYR	A	149	-6.952	41.468	5.327	1.00	47.71
	2726	CD2	TYR	A	149	-6.010	43.124	3.370	1.00	47.71
	2727	CE2	TYR	A	149	-5.832	43.470	4.691	1.00	47.71
5	2728	CZ	TYR	A	149	-6.297	42.656	5.669	1.00	47.71
	2729	OH	TYR	A	149	-6.098	43.066	6.973	1.00	47.71
	2730	C	TYR	A	149	-8.098	41.368	-0.543	1.00	38.49
	2731	O	TYR	A	149	-8.451	40.272	-1.006	1.00	38.49
	2732	N	TYR	A	150	-7.639	42.382	-1.279	1.00	53.38
	2733	CA	TYR	A	150	-7.385	42.305	-2.716	1.00	53.38
10	2734	CB	TYR	A	150	-8.681	42.142	-3.520	1.00	86.43
	2735	CG	TYR	A	150	-9.564	43.353	-3.735	1.00	86.43
	2736	CD1	TYR	A	150	-9.167	44.393	-4.563	1.00	86.43
	2737	CE1	TYR	A	150	-9.992	45.488	-4.795	1.00	86.43
	2738	CD2	TYR	A	150	-10.816	43.436	-3.142	1.00	86.43
15	2739	CE2	TYR	A	150	-11.652	44.522	-3.365	1.00	86.43
	2740	CZ	TYR	A	150	-11.234	45.547	-4.190	1.00	86.43
	2741	OH	TYR	A	150	-12.049	46.642	-4.381	1.00	86.43
	2742	C	TYR	A	150	-6.653	43.598	-3.028	1.00	53.38
	2743	O	TYR	A	150	-6.726	44.536	-2.225	1.00	53.38
20	2744	N	CYS	A	151	-5.900	43.660	-4.127	1.00	73.39
	2745	CA	CYS	A	151	-5.179	44.894	-4.462	1.00	73.39
	2746	C	CYS	A	151	-5.388	45.311	-5.900	1.00	73.39
	2747	O	CYS	A	151	-5.741	44.487	-6.721	1.00	73.39
	2748	CB	CYS	A	151	-3.680	44.745	-4.197	1.00	73.27
25	2749	SG	CYS	A	151	-2.861	43.358	-5.059	1.00	73.27
	2750	N	THR	A	152	-5.177	46.593	-6.192	1.00	98.75
	2751	CA	THR	A	152	-5.335	47.121	-7.537	1.00	98.75
	2752	CB	THR	A	152	-6.478	48.154	-7.602	1.00	109.76
	2753	OG1	THR	A	152	-6.138	49.310	-6.821	1.00	109.76
30	2754	CG2	THR	A	152	-7.746	47.558	-7.048	1.00	109.76
	2755	C	THR	A	152	-4.025	47.793	-7.905	1.00	98.75
	2756	O	THR	A	152	-3.329	48.322	-7.032	1.00	98.75
	2757	N	GLY	A	153	-3.681	47.764	-9.188	1.00	91.16
	2758	CA	GLY	A	153	-2.444	48.385	-9.622	1.00	91.16
35	2759	C	GLY	A	153	-2.392	48.562	-11.122	1.00	91.16
	2760	O	GLY	A	153	-3.163	47.947	-11.843	1.00	91.16
	2761	N	LYS	A	154	-1.488	49.409	-11.597	1.00	71.11
	2762	CA	LYS	A	154	-1.359	49.643	-13.023	1.00	71.11
	2763	CB	LYS	A	154	-1.229	51.140	-13.299	1.00	173.07
40	2764	CG	LYS	A	154	-1.235	51.523	-14.769	1.00	173.07
	2765	CD	LYS	A	154	-1.155	53.036	-14.911	1.00	173.07
	2766	CE	LYS	A	154	-1.050	53.490	-16.359	1.00	173.07
	2767	NZ	LYS	A	154	-0.857	54.960	-16.420	1.00	173.07
	2768	C	LYS	A	154	-0.120	48.907	-13.500	1.00	71.11
45	2769	O	LYS	A	154	0.963	49.009	-12.900	1.00	71.11
	2770	N	VAL	A	155	-0.289	48.128	-14.563	1.00	155.85
	2771	CA	VAL	A	155	0.813	47.372	-15.153	1.00	155.85
	2772	CB	VAL	A	155	0.510	45.884	-15.201	1.00	196.06
	2773	CG1	VAL	A	155	1.673	45.144	-15.841	1.00	196.06
50	2774	CG2	VAL	A	155	0.273	45.373	-13.809	1.00	196.06
	2775	C	VAL	A	155	0.960	47.894	-16.560	1.00	155.85
	2776	O	VAL	A	155	-0.013	47.951	-17.309	1.00	155.85
	2777	N	TRP	A	156	2.187	48.251	-16.912	1.00	136.77
	2778	CA	TRP	A	156	2.437	48.821	-18.215	1.00	136.77
55	2779	CB	TRP	A	156	1.888	47.941	-19.308	1.00	169.17
	2780	CG	TRP	A	156	2.584	46.701	-19.394	1.00	169.17
	2781	CD2	TRP	A	156	3.991	46.538	-19.596	1.00	169.17
	2782	CE2	TRP	A	156	4.260	45.184	-19.532	1.00	169.17
	2783	CE3	TRP	A	156	5.037	47.423	-19.855	1.00	169.17
60	2784	CD1	TRP	A	156	2.066	45.478	-19.202	1.00	169.17
	2785	NE1	TRP	A	156	3.053	44.565	-19.283	1.00	169.17
	2786	CZ2	TRP	A	156	5.536	44.634	-19.734	1.00	169.17
	2787	CZ3	TRP	A	156	6.293	46.924	-20.012	1.00	169.17
65	2788	CH2	TRP	A	156	6.542	45.522	-19.971	1.00	169.17
	2789	C	TRP	A	156	1.664	50.102	-18.251	1.00	136.77
	2790	O	TRP	A	156	2.130	51.132	-17.775	1.00	136.77
	2791	N	GLN	A	157	0.445	50.004	-18.777	1.00	192.06
	2792	CA	GLN	A	157	-0.395	51.166	-18.902	1.00	192.06
70	2793	CB	GLN	A	157	-0.133	51.791	-20.263	1.00	249.57
	2794	CG	GLN	A	157	1.231	52.449	-20.291	1.00	249.57

	2795	CD	GLN	A	157	1.374	53.420	-19.126	1.00	249.57
	2796	OE1	GLN	A	157	0.539	54.293	-18.950	1.00	249.57
	2797	NE2	GLN	A	157	2.428	53.271	-18.339	1.00	249.57
	2798	C	GLN	A	157	-1.873	50.913	-18.673	1.00	192.06
5	2799	O	GLN	A	157	-2.717	51.753	-18.989	1.00	192.06
	2800	N	LEU	A	158	-2.181	49.753	-18.108	1.00	96.98
	2801	CA	LEU	A	158	-3.565	49.394	-17.813	1.00	96.98
	2802	CB	LEU	A	158	-4.018	48.234	-18.697	1.00	92.50
	2803	CG	LEU	A	158	-4.362	48.530	-20.148	1.00	92.50
10	2804	CD1	LEU	A	158	-5.577	47.691	-20.496	1.00	92.50
	2805	CD2	LEU	A	158	-4.695	50.015	-20.343	1.00	92.50
	2806	C	LEU	A	158	-3.758	49.028	-16.345	1.00	96.98
	2807	O	LEU	A	158	-2.821	48.596	-15.661	1.00	96.98
	2808	N	ASP	A	159	-4.983	49.216	-15.869	1.00	119.40
15	2809	CA	ASP	A	159	-5.330	48.925	-14.485	1.00	119.40
	2810	CB	ASP	A	159	-6.442	49.875	-14.018	1.00	201.99
	2811	CG	ASP	A	159	-6.096	51.345	-14.236	1.00	201.99
	2812	OD1	ASP	A	159	-5.103	51.832	-13.651	1.00	201.99
	2813	OD2	ASP	A	159	-6.823	52.018	-15.000	1.00	201.99
20	2814	C	ASP	A	159	-5.793	47.473	-14.334	1.00	119.40
	2815	O	ASP	A	159	-6.417	46.919	-15.235	1.00	119.40
	2816	N	TYR	A	160	-5.475	46.860	-13.197	1.00	117.93
	2817	CA	TYR	A	160	-5.875	45.481	-12.929	1.00	117.93
	2818	CB	TYR	A	160	-4.769	44.503	-13.308	1.00	127.75
25	2819	CG	TYR	A	160	-4.261	44.648	-14.715	1.00	127.75
	2820	CD1	TYR	A	160	-3.184	45.483	-14.997	1.00	127.75
	2821	CE1	TYR	A	160	-2.707	45.625	-16.277	1.00	127.75
	2822	CD2	TYR	A	160	-4.855	43.952	-15.766	1.00	127.75
	2823	CE2	TYR	A	160	-4.386	44.087	-17.061	1.00	127.75
30	2824	CZ	TYR	A	160	-3.309	44.932	-17.297	1.00	127.75
	2825	OH	TYR	A	160	-2.808	45.145	-18.541	1.00	127.75
	2826	C	TYR	A	160	-6.239	45.240	-11.471	1.00	117.93
	2827	O	TYR	A	160	-5.674	45.836	-10.557	1.00	117.93
	2828	N	GLU	A	161	-7.184	44.335	-11.275	1.00	99.07
35	2829	CA	GLU	A	161	-7.665	43.963	-9.960	1.00	99.07
	2830	CB	GLU	A	161	-9.179	44.113	-9.845	1.00	160.66
	2831	CG	GLU	A	161	-9.877	43.683	-8.681	1.00	160.66
	2832	CD	GLU	A	161	-11.290	44.226	-8.624	1.00	160.66
	2833	OE1	GLU	A	161	-12.117	43.690	-7.856	1.00	160.66
40	2834	OE2	GLU	A	161	-11.564	45.206	-9.350	1.00	160.66
	2835	C	GLU	A	161	-7.258	42.507	-9.699	1.00	99.07
	2836	O	GLU	A	161	-7.346	41.672	-10.598	1.00	99.07
	2837	N	SER	A	162	-6.806	42.206	-8.481	1.00	84.68
	2838	CA	SER	A	162	-6.378	40.856	-8.119	1.00	84.68
45	2839	CB	SER	A	162	-5.247	40.923	-7.102	1.00	134.29
	2840	OG	SER	A	162	-5.670	41.599	-5.932	1.00	134.29
	2841	C	SER	A	162	-7.520	40.029	-7.536	1.00	84.68
	2842	O	SER	A	162	-8.592	40.555	-7.230	1.00	84.68
	2843	N	GLU	A	163	-7.292	38.729	-7.382	1.00	56.84
50	2844	CA	GLU	A	163	-8.316	37.829	-6.842	1.00	56.84
	2845	CB	GLU	A	163	-7.885	36.370	-7.015	1.00	162.97
	2846	CG	GLU	A	163	-7.984	35.836	-8.438	1.00	162.97
	2847	CD	GLU	A	163	-9.417	35.601	-8.869	1.00	162.97
	2848	OE1	GLU	A	163	-10.122	34.835	-8.175	1.00	162.97
55	2849	OE2	GLU	A	163	-9.835	36.176	-9.900	1.00	162.97
	2850	C	GLU	A	163	-8.437	38.151	-5.368	1.00	56.84
	2851	O	GLU	A	163	-7.439	38.433	-4.720	1.00	56.84
	2852	N	PRO	A	164	-9.660	38.122	-4.805	1.00	48.99
	2853	CD	PRO	A	164	-10.959	37.760	-5.379	1.00	93.04
60	2854	CA	PRO	A	164	-9.789	38.423	-3.371	1.00	48.99
	2855	CB	PRO	A	164	-11.295	38.547	-3.196	1.00	93.04
	2856	CG	PRO	A	164	-11.814	37.544	-4.135	1.00	93.04
	2857	C	PRO	A	164	-9.201	37.307	-2.528	1.00	48.99
	2858	O	PRO	A	164	-9.101	36.160	-2.977	1.00	48.99
65	2859	N	LEU	A	165	-8.802	37.625	-1.303	1.00	69.69
	2860	CA	LEU	A	165	-8.236	36.609	-0.426	1.00	69.69
	2861	CB	LEU	A	165	-6.733	36.661	-0.465	1.00	37.26
	2862	CG	LEU	A	165	-6.041	35.774	0.560	1.00	37.26
	2863	CD1	LEU	A	165	-6.655	34.407	0.459	1.00	37.26
70	2864	CD2	LEU	A	165	-4.535	35.665	0.301	1.00	37.26

	2865	C	LEU	A	165	-8.661	36.800	1.000	1.00	69.69
	2866	O	LEU	A	165	-8.430	37.863	1.562	1.00	69.69
	2867	N	ASN	A	166	-9.272	35.777	1.585	1.00	67.70
	2868	CA	ASN	A	166	-9.725	35.861	2.962	1.00	67.70
5	2869	CB	ASN	A	166	-10.806	34.849	3.224	1.00	76.12
	2870	CG	ASN	A	166	-12.182	35.396	2.998	1.00	76.12
	2871	OD1	ASN	A	166	-12.414	36.571	3.171	1.00	76.12
	2872	ND2	ASN	A	166	-13.106	34.519	2.633	1.00	76.12
	2873	C	ASN	A	166	-8.606	35.605	3.943	1.00	67.70
10	2874	O	ASN	A	166	-7.724	34.792	3.687	1.00	67.70
	2875	N	ILE	A	167	-8.665	36.273	5.090	1.00	54.98
	2876	CA	ILE	A	167	-7.634	36.127	6.105	1.00	54.98
	2877	CB	ILE	A	167	-6.686	37.292	6.049	1.00	41.48
	2878	CG2	ILE	A	167	-5.883	37.357	7.277	1.00	41.48
15	2879	CG1	ILE	A	167	-5.770	37.131	4.855	1.00	41.48
	2880	CD1	ILE	A	167	-4.655	38.164	4.815	1.00	41.48
	2881	C	ILE	A	167	-8.248	36.093	7.478	1.00	54.98
	2882	O	ILE	A	167	-9.113	36.914	7.783	1.00	54.98
	2883	N	THR	A	168	-7.820	35.163	8.317	1.00	55.70
20	2884	CA	THR	A	168	-8.391	35.122	9.642	1.00	55.70
	2885	CB	THR	A	168	-9.241	33.875	9.837	1.00	71.33
	2886	OG1	THR	A	168	-10.289	33.866	8.860	1.00	71.33
	2887	CG2	THR	A	168	-9.857	33.869	11.209	1.00	71.33
	2888	C	THR	A	168	-7.339	35.171	10.697	1.00	55.70
25	2889	O	THR	A	168	-6.295	34.539	10.587	1.00	55.70
	2890	N	VAL	A	169	-7.618	35.950	11.724	1.00	64.35
	2891	CA	VAL	A	169	-6.725	36.090	12.863	1.00	64.35
	2892	CB	VAL	A	169	-6.370	37.560	13.087	1.00	77.36
	2893	CG1	VAL	A	169	-5.895	37.772	14.468	1.00	77.36
30	2894	CG2	VAL	A	169	-5.314	37.978	12.128	1.00	77.36
	2895	C	VAL	A	169	-7.539	35.567	14.048	1.00	64.35
	2896	O	VAL	A	169	-8.510	36.203	14.463	1.00	64.35
	2897	N	ILE	A	170	-7.175	34.395	14.562	1.00	76.83
	2898	CA	ILE	A	170	-7.889	33.797	15.690	1.00	76.83
35	2899	CB	ILE	A	170	-7.898	32.250	15.590	1.00	133.66
	2900	CG2	ILE	A	170	-8.437	31.821	14.237	1.00	133.66
	2901	CG1	ILE	A	170	-6.482	31.697	15.761	1.00	133.66
	2902	CD1	ILE	A	170	-6.386	30.180	15.647	1.00	133.66
	2903	C	ILE	A	170	-7.196	34.228	16.976	1.00	76.83
40	2904	O	ILE	A	170	-6.164	34.887	16.922	1.00	76.83
	2905	N	LYS	A	171	-7.757	33.870	18.127	1.00	125.94
	2906	CA	LYS	A	171	-7.152	34.252	19.397	1.00	125.94
	2907	CB	LYS	A	171	-8.004	35.328	20.069	1.00	198.00
	2908	CG	LYS	A	171	-9.449	34.922	20.293	1.00	198.00
45	2909	CD	LYS	A	171	-10.354	36.141	20.399	1.00	198.00
	2910	CE	LYS	A	171	-9.952	37.059	21.546	1.00	198.00
	2911	NZ	LYS	A	171	-10.825	38.268	21.607	1.00	198.00
	2912	C	LYS	A	171	-6.957	33.072	20.338	1.00	125.94
	2913	O	LYS	A	171	-6.326	33.204	21.388	1.00	125.94
50	2914	C1	NAG	A	221	13.561	29.146	-11.328	1.00	244.51
	2915	C2	NAG	A	221	13.758	30.631	-11.596	1.00	244.51
	2916	N2	NAG	A	221	12.475	31.303	-11.575	1.00	244.51
	2917	C7	NAG	A	221	12.407	32.594	-11.273	1.00	244.51
	2918	O7	NAG	A	221	13.396	33.270	-10.988	1.00	244.51
55	2919	C8	NAG	A	221	11.0c.J	33.233	-11.281	1.00	244.51
	2920	C3	NAG	A	221	14.405	30.847	-12.952	1.00	244.51
	2921	O3	NAG	A	221	14.740	32.219	-13.099	1.00	244.51
	2922	C4	NAG	A	221	15.661	29.997	-13.135	1.00	244.51
	2923	O4	NAG	A	221	16.044	30.091	-14.520	1.00	244.51
60	2924	C5	NAG	A	221	15.375	28.530	-12.759	1.00	244.51
	2925	O5	NAG	A	221	14.809	28.456	-11.436	1.00	244.51
	2926	C6	NAG	A	221	16.622	27.665	-12.740	1.00	244.51
	2927	O6	NAG	A	221	17.566	28.140	-11.790	1.00	244.51
	2928	C1	NAG	A	222	17.330	29.723	-14.890	1.00	195.02
65	2929	C2	NAG	A	222	17.910	30.770	-15.864	1.00	195.02
	2930	N2	NAG	A	222	17.966	32.078	-15.229	1.00	195.02
	2931	C7	NAG	A	222	19.134	32.692	-15.052	1.00	195.02
	2932	O7	NAG	A	222	20.210	32.206	-15.404	1.00	195.02
	2933	C8	NAG	A	222	19.106	34.055	-14.383	1.00	195.02
70	2934	C3	NAG	A	222	17.061	30.835	-17.148	1.00	195.02

	2935	O3	NAG	A	222	17.694	31.675	-18.105	1.00	195.02
	2936	C4	NAG	A	222	16.869	29.431	-17.744	1.00	195.02
	2937	O4	NAG	A	222	15.938	29.494	-18.814	1.00	195.02
	2938	C5	NAG	A	222	16.356	28.454	-16.676	1.00	195.02
5	2939	O5	NAG	A	222	17.249	28.441	-15.538	1.00	195.02
	2940	C6	NAG	A	222	16.248	27.029	-17.174	1.00	195.02
	2941	O6	NAG	A	222	15.013	26.448	-16.789	1.00	195.02
	2942	C1	NAG	A	242	-3.473	17.670	-6.472	1.00	81.55
	2943	C2	NAG	A	242	-3.080	17.582	-7.921	1.00	81.55
10	2944	N2	NAG	A	242	-1.712	17.148	-8.025	1.00	81.55
	2945	C7	NAG	A	242	-1.420	16.075	-8.748	1.00	81.55
	2946	O7	NAG	A	242	-2.270	15.414	-9.324	1.00	81.55
	2947	C8	NAG	A	242	0.033	15.657	-8.846	1.00	81.55
	2948	C3	NAG	A	242	-3.225	18.933	-8.583	1.00	81.55
15	2949	O3	NAG	A	242	-2.918	18.814	-9.969	1.00	81.55
	2950	C4	NAG	A	242	-4.642	19.456	-8.403	1.00	81.55
	2951	O4	NAG	A	242	-4.712	20.825	-8.846	1.00	81.55
	2952	C5	NAG	A	242	-5.062	19.392	-6.945	1.00	81.55
	2953	O5	NAG	A	242	-4.830	18.086	-6.394	1.00	81.55
20	2954	C6	NAG	A	242	-6.547	19.630	-6.824	1.00	81.55
	2955	O6	NAG	A	242	-6.826	20.697	-5.933	1.00	81.55
	2956	C1	NAG	A	243	-5.536	21.071	-9.934	1.00	123.88
	2957	C2	NAG	A	243	-6.020	22.528	-9.929	1.00	123.88
	2958	N2	NAG	A	243	-6.814	22.800	-8.743	1.00	123.88
25	2959	C7	NAG	A	243	-6.607	23.908	-8.041	1.00	123.88
	2960	O7	NAG	A	243	-5.746	24.727	-8.337	1.00	123.88
	2961	C8	NAG	A	243	-7.482	24.135	-6.820	1.00	123.88
	2962	C3	NAG	A	243	-6.875	22.766	-11.173	1.00	123.88
	2963	O3	NAG	A	243	-7.276	24.126	-11.231	1.00	123.88
30	2964	C4	NAG	A	243	-6.109	22.379	-12.449	1.00	123.88
	2965	O4	NAG	A	243	-7.002	22.470	-13.597	1.00	123.88
	2966	C5	NAG	A	243	-5.608	20.937	-12.312	1.00	123.88
	2967	O5	NAG	A	243	-4.793	20.809	-11.132	1.00	123.88
	2968	C6	NAG	A	243	-4.789	20.444	-13.485	1.00	123.88
35	2969	O6	NAG	A	243	-3.560	21.141	-13.577	1.00	123.88
	2970	C1	MAN	A	244	-6.640	23.134	-14.739	1.00	177.21
	2971	C2	MAN	A	244	-6.289	24.639	-14.645	1.00	177.21
	2972	O2	MAN	A	244	-4.892	24.794	-14.586	1.00	177.21
	2973	C3	MAN	A	244	-6.845	25.182	-15.998	1.00	177.21
40	2974	O3	MAN	A	244	-6.636	26.575	-16.149	1.00	177.21
	2975	C4	MAN	A	244	-6.314	24.396	-17.244	1.00	177.21
	2976	O4	MAN	A	244	-6.840	24.954	-18.451	1.00	177.21
	2977	C5	MAN	A	244	-6.779	22.928	-17.096	1.00	177.21
	2978	O5	MAN	A	244	-6.232	22.337	-15.891	1.00	177.21
45	2979	C6	MAN	A	244	-6.487	22.037	-18.309	1.00	177.21
	2980	O6	MAN	A	244	-5.159	21.562	-18.301	1.00	177.21
	2981	C1	NAG	A	250	18.849	18.682	-1.016	1.00	245.89
	2982	C2	NAG	A	250	19.989	19.613	-0.566	1.00	245.89
	2983	N2	NAG	A	250	20.115	19.601	0.880	1.00	245.89
50	2984	C7	NAG	A	250	21.178	19.048	1.458	1.00	245.89
	2985	O7	NAG	A	250	22.091	18.518	0.819	1.00	245.89
	2986	C8	NAG	A	250	21.237	19.081	2.980	1.00	245.89
	2987	C3	NAG	A	250	19.696	21.039	-1.050	1.00	245.89
	2988	O3	NAG	A	250	20.782	21.896	-0.728	1.00	245.89
55	2989	C4	NAG	A	250	19.457	21.047	-2.564	1.00	245.89
	2990	O4	NAG	A	250	19.058	22.347	-2.977	1.00	245.89
	2991	C5	NAG	A	250	18.367	20.028	-2.935	1.00	245.89
	2992	O5	NAG	A	250	18.721	18.715	-2.444	1.00	245.89
	2993	C6	NAG	A	250	18.165	19.903	-4.436	1.00	245.89
60	2994	O6	NAG	A	250	17.400	18.748	-4.760	1.00	245.89
	2995	C1	NAG	A	274	2.176	9.666	16.692	1.00	235.37
	2996	C2	NAG	A	274	1.514	10.512	17.789	1.00	235.37
	2997	N2	NAG	A	274	2.519	11.269	18.514	1.00	235.37
	2998	C7	NAG	A	274	2.186	12.397	19.137	1.00	235.37
65	2999	O7	NAG	A	274	1.042	12.855	19.128	1.00	235.37
	3000	C8	NAG	A	274	3.289	13.134	19.882	1.00	235.37
	3001	C3	NAG	A	274	0.750	9.604	18.761	1.00	235.37
	3002	O3	NAG	A	274	0.023	10.398	19.687	1.00	235.37
	3003	C4	NAG	A	274	-0.216	8.687	18.005	1.00	235.37
70	3004	O4	NAG	A	274	-0.794	7.758	18.909	1.00	235.37

	3005	C5	NAG A	274	0.534	7.934	16.800	1.00	235.37
	3006	O5	NAG A	274	1.187	8.871	16.018	1.00	235.37
	3007	C6	NAG A	274	-0.384	7.085	16.044	1.00	235.37
	3008	O6	NAG A	274	0.294	6.598	14.895	1.00	235.37
5	3009	C1	NAG A	335	7.685	42.617	-1.591	1.00	248.30
	3010	C2	NAG A	335	8.870	42.060	-0.765	1.00	248.30
	3011	N2	NAG A	335	8.767	42.587	0.583	1.00	248.30
	3012	C7	NAG A	335	8.573	41.777	1.618	1.00	248.30
	3013	O7	NAG A	335	8.483	40.553	1.511	1.00	248.30
10	3014	C8	NAG A	335	8.472	42.430	2.987	1.00	248.30
	3015	C3	NAG A	335	10.258	42.417	-1.325	1.00	248.30
	3016	O3	NAG A	335	11.229	41.541	-0.771	1.00	248.30
	3017	C4	NAG A	335	10.290	42.300	-2.841	1.00	248.30
	3018	O4	NAG A	335	11.560	42.706	-3.329	1.00	248.30
15	3019	C5	NAG A	335	9.195	43.189	-3.414	1.00	248.30
	3020	O5	NAG A	335	7.904	42.673	-3.021	1.00	248.30
	3021	C6	NAG A	335	9.222	43.210	-4.935	1.00	248.30
	3022	O6	NAG A	335	9.423	44.524	-5.434	1.00	248.30
	3023	C1	NAG A	340	0.521	43.731	20.574	1.00	249.48
20	3024	C2	NAG A	340	-0.261	42.929	21.588	1.00	249.48
	3025	N2	NAG A	340	-1.284	42.144	20.930	1.00	249.48
	3026	C7	NAG A	340	-1.377	40.843	21.191	1.00	249.48
	3027	O7	NAG A	340	-0.627	40.266	21.988	1.00	249.48
	3028	C8	NAG A	340	-2.460	40.060	20.472	1.00	249.48
25	3029	C3	NAG A	340	-0.877	43.866	22.605	1.00	249.48
	3030	O3	NAG A	340	-1.567	43.103	23.596	1.00	249.48
	3031	C4	NAG A	340	0.234	44.689	23.266	1.00	249.48
	3032	O4	NAG A	340	-0.370	45.703	24.068	1.00	249.48
	3033	C5	NAG A	340	1.188	45.334	22.220	1.00	249.48
30	3034	O5	NAG A	340	1.601	44.382	21.233	1.00	249.48
	3035	C6	NAG A	340	2.460	45.780	22.881	1.00	249.48
	3036	O6	NAG A	340	3.548	45.816	21.985	1.00	249.48
	3037	C1	NAG A	366	-14.447	34.952	2.337	1.00	170.79
	3038	C2	NAG A	366	-15.009	34.055	1.250	1.00	170.79
35	3039	N2	NAG A	366	-14.171	34.149	0.073	1.00	170.79
	3040	C7	NAG A	366	-13.171	33.289	-0.105	1.00	170.79
	3041	O7	NAG A	366	-12.912	32.383	0.691	1.00	170.79
	3042	C8	NAG A	366	-12.329	33.454	-1.361	1.00	170.79
	3043	C3	NAG A	366	-16.425	34.482	0.910	1.00	170.79
40	3044	O3	NAG A	366	-16.997	33.542	0.014	1.00	170.79
	3045	C4	NAG A	366	-17.290	34.565	2.168	1.00	170.79
	3046	O4	NAG A	366	-18.549	35.187	1.824	1.00	170.79
	3047	C5	NAG A	366	-16.584	35.380	3.275	1.00	170.79
	3048	O5	NAG A	366	-15.258	34.873	3.503	1.00	170.79
45	3049	C6	NAG A	366	-17.297	35.315	4.613	1.00	170.79
	3050	O6	NAG A	366	-16.620	36.092	5.592	1.00	170.79
	3051	C1	NAG A	367	-19.711	34.493	2.163	1.00	247.02
	3052	C2	NAG A	367	-20.892	35.462	2.268	1.00	247.02
	3053	N2	NAG A	367	-20.619	36.488	3.255	1.00	247.02
50	3054	C7	NAG A	367	-20.363	37.730	2.856	1.00	247.02
	3055	O7	NAG A	367	-20.347	38.061	1.668	1.00	247.02
	3056	C8	NAG A	367	-20.084	38.762	3.937	1.00	247.02
	3057	C3	NAG A	367	-22.151	34.676	2.640	1.00	247.02
	3058	O3	NAG A	367	-23.265	35.554	2.696	1.00	247.02
55	3059	C4	NAG A	367	-22.395	33.586	1.591	1.00	247.02
	3060	O4	NAG A	367	-23 511	32.793	1.970	1.00	247.02
	3061	C5	NAG A	367	-21.148	32.698	1.448	1.00	247.02
	3062	O5	NAG A	367	-19.981	33.508	1.147	1.00	247.02
	3063	C6	NAG A	367	-21.291	31.682	0.332	1.00	247.02
60	3064	O6	NAG A	367	-20.416	31.974	-0.749	1.00	247.02
	3065	CB	LYS B	4	28.538	57.342	22.861	1.00	248.35
	3066	CG	LYS B	4	28.723	58.799	22.474	1.00	248.35
	3067	CD	LYS B	4	28.723	59.692	23.702	1.00	248.35
	3068	CE	LYS B	4	28.914	61.151	23.330	1.00	248.35
65	3069	NZ	LYS B	4	28.914	62.022	24.537	1.00	248.35
	3070	C	LYS B	4	29.934	56.599	20.941	1.00	249.33
	3071	O	LYS B	4	30.913	57.081	21.514	1.00	249.33
	3072	N	LYS B	4	28.491	54.970	22.165	1.00	249.33
	3073	CA	LYS B	4	28.619	56.377	21.683	1.00	249.33
70	3074	N	PRO B	5	29.974	56.244	19.648	1.00	115.49

	3075	CD	PRO	B	5	28.994	55.392	18.958	1.00	70.51
	3076	CA	PRO	B	5	31.186	56.414	18.835	1.00	115.49
	3077	CB	PRO	B	5	31.037	55.337	17.765	1.00	70.51
	3078	CG	PRO	B	5	29.573	55.299	17.553	1.00	70.51
5	3079	C	PRO	B	5	31.329	57.807	18.247	1.00	115.49
	3080	O	PRO	B	5	30.350	58.537	18.126	1.00	115.49
	3081	N	LYS	B	6	32.553	58.174	17.885	1.00	105.72
	3082	CA	LYS	B	6	32.811	59.492	17.331	1.00	105.72
	3083	CB	LYS	B	6	33.258	60.458	18.449	1.00	206.94
10	3084	CG	LYS	B	6	33.432	61.901	17.991	1.00	206.94
	3085	CD	LYS	B	6	33.697	62.850	19.152	1.00	206.94
	3086	CE	LYS	B	6	33.826	64.287	18.654	1.00	206.94
	3087	NZ	LYS	B	6	34.006	65.275	19.759	1.00	206.94
	3088	C	LYS	B	6	33.857	59.429	16.222	1.00	105.72
15	3089	O	LYS	B	6	35.018	59.109	16.467	1.00	105.72
	3090	N	VAL	B	7	33.433	59.742	15.002	1.00	68.17
	3091	CA	VAL	B	7	34.317	59.728	13.843	1.00	68.17
	3092	CB	VAL	Ɔ	7	33.553	59.960	12.545	1.00	86.47
	3093	CG1	VAL	B	7	34.487	59.738	11.359	1.00	86.47
20	3094	CG2	VAL	B	7	32.346	59.072	12.479	1.00	86.47
	3095	C	VAL	B	7	35.401	60.796	13.845	1.00	68.17
	3096	O	VAL	B	7	35.094	61.988	13.803	1.00	68.17
	3097	N	SER	B	8	36.661	60.385	13.864	1.00	61.68
	3098	CA	SER	B	8	37.741	61.355	13.837	1.00	61.68
25	3099	CB	SER	B	8	38.836	60.969	14.842	1.00	135.50
	3100	OG	SER	B	8	39.289	59.647	14.622	1.00	135.50
	3101	C	SER	B	8	38.303	61.405	12.406	1.00	61.68
	3102	O	SER	B	8	38.019	60.525	11.594	1.00	61.68
	3103	N	LEU	B	9	39.092	62.435	12.106	1.00	91.60
30	3104	CA	LEU	B	9	39.699	62.594	10.790	1.00	91.60
	3105	CB	LEU	B	9	39.080	63.779	10.053	1.00	67.13
	3106	CG	LEU	B	9	37.601	63.806	9.688	1.00	67.13
	3107	CD1	LEU	B	9	37.378	64.735	8.524	1.00	67.13
	3108	CD2	LEU	B	9	37.167	62.435	9.291	1.00	67.13
35	3109	C	LEU	B	9	41.195	62.847	10.897	1.00	91.60
	3110	O	LEU	B	9	41.675	63.347	11.915	1.00	91.60
	3111	N	ASN	B	10	41.928	62.519	9.835	1.00	84.59
	3112	CA	ASN	B	10	43.369	62.742	9.800	1.00	84.59
	3113	CB	ASN	B	10	44.107	61.640	10.548	1.00	140.61
40	3114	CG	ASN	B	10	45.558	61.978	10.763	1.00	140.61
	3115	OD1	ASN	B	10	45.889	62.905	11.505	1.00	140.61
	3116	ND2	ASN	B	10	46.438	61.241	10.099	1.00	140.61
	3117	C	ASN	B	10	43.876	62.812	8.367	1.00	84.59
	3118	O	ASN	B	10	43.883	61.805	7.656	1.00	84.59
45	3119	N	PRO	B	11	44.310	64.010	7.917	1.00	77.61
	3120	CD	PRO	B	11	44.699	64.185	6.506	1.00	115.85
	3121	CA	PRO	B	11	44.370	65.289	8.638	1.00	77.61
	3122	CB	PRO	B	11	44.811	66.264	7.544	1.00	115.85
	3123	CG	PRO	B	11	45.560	65.394	6.570	1.00	115.85
50	3124	C	PRO	B	11	43.042	65.731	9.290	1.00	77.61
	3125	O	PRO	B	11	41.982	65.231	8.937	1.00	77.61
	3126	N	PRO	B	12	43.085	66.680	10.239	1.00	88.06
	3127	CD	PRO	B	12	44.279	67.378	10.753	1.00	174.82
	3128	CA	PRO	B	12	41.883	67.170	10.921	1.00	88.06
55	3129	CB	PRO	R	12	42.433	68.119	11.982	1.00	174.82
	3130	CG	PRO	B	12	43.854	67.699	12.148	1.00	174.82
	3131	C	PRO	B	12	40.993	67.939	9.924	1.00	88.06
	3132	O	PRO	B	12	39.781	68.071	10.108	1.00	88.06
	3133	N	TRP	B	13	41.623	68.464	8.880	1.00	96.43
60	3134	CA	TRP	B	13	40.932	69.239	7.859	1.00	96.43
	3135	CB	TRP	B	13	41.907	69.605	6.731	1.00	96.49
	3136	CG	TRP	B	13	43.190	70.134	7.232	1.00	96.49
	3137	CD2	TRP	B	13	43.376	70.974	8.358	1.00	96.49
	3138	CE2	TRP	B	13	44.757	71.168	8.509	1.00	96.49
65	3139	CE3	TRP	B	13	42.504	71.588	9.268	1.00	96.49
	3140	CD1	TRP	B	13	44.423	69.863	6.745	1.00	96.49
	3141	NE1	TRP	B	13	45.373	70.474	7.506	1.00	96.49
	3142	CZ2	TRP	B	13	45.298	71.947	9.532	1.00	96.49
	3143	CZ3	TRP	B	13	43.034	72.363	10.283	1.00	96.49
70	3144	CH2	TRP	B	13	44.424	72.536	10.410	1.00	96.49

	3145	C	TRP	B	13	39.742	68.497	7.281	1.00	96.43
	3146	O	TRP	B	13	39.882	67.403	6.738	1.00	96.43
	3147	N	ASN	B	14	38.567	69.102	7.407	1.00	72.14
	3148	CA	ASN	B	14	37.352	68.509	6.867	1.00	72.14
5	3149	CB	ASN	B	14	36.239	68.455	7.931	1.00	117.87
	3150	CG	ASN	B	14	35.712	69.812	8.309	1.00	117.87
	3151	OD1	ASN	B	14	36.462	70.695	8.718	1.00	117.87
	3152	ND2	ASN	B	14	34.407	69.984	8.184	1.00	117.87
	3153	C	ASN	B	14	36.858	69.201	5.588	1.00	72.14
10	3154	O	ASN	B	14	35.721	69.018	5.177	1.00	72.14
	3155	N	ARG	B	15	37.715	70.009	4.973	1.00	61.00
	3156	CA	ARG	B	15	37.399	70.653	3.701	1.00	61.00
	3157	CB	ARG	B	15	37.241	72.149	3.841	1.00	68.74
	3158	CG	ARG	B	15	36.513	72.569	5.064	1.00	68.74
15	3159	CD	ARG	B	15	36.354	74.075	5.045	1.00	68.74
	3160	NE	ARG	B	15	35.436	74.525	4.007	1.00	68.74
	3161	CZ	ARG	B	15	35.531	75.714	3.429	1.00	68.74
	3162	NH1	ARG	B	15	36.501	76.533	3.794	1.00	68.74
	3163	NH2	ARG	B	15	34.660	76.093	2.498	1.00	68.74
20	3164	C	ARG	B	15	38.662	70.393	2.900	1.00	61.00
	3165	O	ARG	B	15	39.707	70.950	3.199	1.00	61.00
	3166	N	ILE	B	16	38.587	69.540	1.895	1.00	73.69
	3167	CA	ILE	B	16	39.770	69.256	1.135	1.00	73.69
	3168	CB	ILE	B	16	40.194	67.833	1.339	1.00	63.86
25	3169	CG2	ILE	B	16	40.624	67.645	2.767	1.00	63.86
	3170	CG1	ILE	B	16	39.044	66.895	0.994	1.00	63.86
	3171	CD1	ILE	B	16	39.388	65.448	1.178	1.00	63.86
	3172	C	ILE	B	16	39.621	69.493	-0.340	1.00	73.69
	3173	O	ILE	B	16	38.516	69.651	-0.866	1.00	73.69
30	3174	N	PHE	B	17	40.770	69.491	-0.998	1.00	99.56
	3175	CA	PHE	B	17	40.889	69.696	-2.425	1.00	99.56
	3176	CB	PHE	B	17	42.282	70.211	-2.720	1.00	81.03
	3177	CG	PHE	B	17	42.400	71.703	-2.699	1.00	81.03
	3178	CD1	PHE	B	17	43.515	72.315	-2.128	1.00	81.03
35	3179	CD2	PHE	B	17	41.453	72.497	-3.344	1.00	81.03
	3180	CE1	PHE	B	17	43.685	73.688	-2.204	1.00	81.03
	3181	CE2	PHE	B	17	41.613	73.877	-3.428	1.00	81.03
	3182	CZ	PHE	B	17	42.733	74.475	-2.860	1.00	81.03
	3183	C	PHE	B	17	40.678	68.392	-3.169	1.00	99.56
40	3184	O	PHE	B	17	40.804	67.321	-2.591	1.00	99.56
	3185	N	LYS	B	18	40.374	68.484	-4.459	1.00	100.47
	3186	CA	LYS	B	18	40.160	67.302	-5.288	1.00	100.47
	3187	CB	LYS	B	18	39.700	67.733	-6.682	1.00	201.96
	3188	CG	LYS	B	18	39.302	66.601	-7.612	1.00	201.96
45	3189	CD	LYS	B	18	38.552	67.166	-8.809	1.00	201.96
	3190	CE	LYS	B	18	38.122	66.086	-9.776	1.00	201.96
	3191	NZ	LYS	B	18	39.299	65.382	-10.345	1.00	201.96
	3192	C	LYS	B	18	41.448	66.492	-5.394	1.00	100.47
	3193	O	LYS	B	18	42.518	67.028	-5.671	1.00	100.47
50	3194	N	GLY	B	19	41.362	65.197	-5.143	1.00	85.25
	3195	CA	GLY	B	19	42.547	64.371	-5.264	1.00	85.25
	3196	C	GLY	B	19	43.350	64.115	-4.008	1.00	85.25
	3197	O	GLY	B	19	44.237	63.274	-3.996	1.00	85.25
	3198	N	GLU	B	20	43.057	64.825	-2.937	1.00	70.09
55	3199	CA	GLU	B	20	43.804	64.606	-1.701	1.00	70.09
	3200	CB	GLU	B	20	43.005	65.846	-0.813	1.00	167.13
	3201	CG	GLU	B	20	44.020	67.133	-1.566	1.00	167.13
	3202	CD	GLU	B	20	44.034	68.357	-0.677	1.00	167.13
	3203	OE1	GLU	B	20	43.009	68.622	-0.013	1.00	167.13
60	3204	OE2	GLU	B	20	45.070	69.056	-0.655	1.00	167.13
	3205	C	GLU	B	20	43.296	63.356	-0.967	1.00	70.09
	3206	O	GLU	B	20	42.273	62.769	-1.368	1.00	70.09
	3207	N	ASN	B	21	44.002	62.935	0.086	1.00	77.36
	3208	CA	ASN	B	21	43.579	61.747	0.830	1.00	77.36
65	3209	CB	ASN	B	21	44.626	60.630	0.802	1.00	155.50
	3210	CG	ASN	B	21	45.285	60.472	-0.537	1.00	155.50
	3211	OD1	ASN	B	21	44.634	60.520	-1.585	1.00	155.50
	3212	ND2	ASN	B	21	46.598	60.265	-0.490	1.00	155.50
	3213	C	ASN	B	21	43.300	62.066	2.287	1.00	77.36
70	3214	O	ASN	B	21	43.997	62.877	2.892	1.00	77.36

	3215	N	VAL	B	22	42.286	61.409	2.848	1.00	68.07
	3216	CA	VAL	B	22	41.899	61.602	4.241	1.00	68.07
	3217	CB	VAL	B	22	40.732	62.572	4.364	1.00	74.66
5	3218	CG1	VAL	B	22	39.514	62.023	3.658	1.00	74.66
	3219	CG2	VAL	B	22	40.438	62.807	5.811	1.00	74.66
	3220	C	VAL	B	22	41.469	60.270	4.829	1.00	68.07
	3221	O	VAL	B	22	40.964	59.391	4.120	1.00	68.07
	3222	N	THR	B	23	41.646	60.123	6.132	1.00	73.02
	3223	CA	THR	B	23	41.316	58.865	6.791	1.00	73.02
10	3224	CB	THR	B	23	42.576	58.274	7.428	1.00	107.36
	3225	OG1	THR	B	23	43.602	58.155	6.435	1.00	107.36
	3226	CG2	THR	B	23	42.288	56.919	8.018	1.00	107.36
	3227	C	THR	B	23	40.278	59.057	7.885	1.00	73.02
	3228	O	THR	B	23	40.446	59.918	8.739	1.00	73.02
15	3229	N	LEU	B	24	39.211	58.261	7.888	1.00	82.14
	3230	CA	LEU	B	24	38.180	58.423	8.920	1.00	82.14
	3231	CB	LEU	B	24	36.771	58.497	8.323	1.00	67.63
	3232	CG	LEU	B	24	36.534	59.233	6.996	1.00	67.63
	3233	CD1	LEU	B	24	35.063	59.448	6.787	1.00	67.63
20	3234	CD2	LEU	B	24	37.249	60.554	6.987	1.00	67.63
	3235	C	LEU	B	24	38.205	57.286	9.904	1.00	82.14
	3236	O	LEU	B	24	37.732	56.195	9.615	1.00	82.14
	3237	N	THR	B	25	38.735	57.551	11.086	1.00	78.19
	3238	CA	THR	B	25	38.817	56.519	12.099	1.00	78.19
25	3239	CB	THR	B	25	40.047	56.755	12.971	1.00	154.05
	3240	OG1	THR	B	25	41.200	56.846	12.124	1.00	154.05
	3241	CG2	THR	B	25	40.231	55.618	13.949	1.00	154.05
	3242	C	THR	B	25	37.554	56.489	12.941	1.00	78.19
	3243	O	THR	B	25	37.022	57.532	13.310	1.00	78.19
30	3244	N	CYS	B	26	37.044	55.296	13.210	1.00	82.94
	3245	CA	CYS	B	26	35.860	55.184	14.049	1.00	82.94
	3246	C	CYS	B	26	36.280	55.187	15.510	1.00	82.94
	3247	O	CYS	B	26	37.254	54.549	15.896	1.00	82.94
	3248	CB	CYS	B	26	35.094	53.908	13.763	1.00	125.46
35	3249	SG	CYS	B	26	33.481	53.869	14.604	1.00	125.46
	3250	N	ASN	B	27	35.535	55.931	16.309	1.00	247.26
	3251	CA	ASN	B	27	35.784	56.058	17.730	1.00	247.26
	3252	CB	ASN	B	27	34.500	55.740	18.470	1.00	240.69
	3253	CG	ASN	B	27	34.506	56.280	19.864	1.00	240.69
40	3254	OD1	ASN	B	27	35.033	57.371	20.107	1.00	240.69
	3255	ND2	ASN	B	27	33.909	55.541	20.797	1.00	240.69
	3256	C	ASN	B	27	36.922	55.201	18.289	1.00	247.26
	3257	O	ASN	B	27	36.702	54.072	18.722	1.00	247.26
	3258	N	GLY	B	28	38.135	55.748	18.286	1.00	195.90
45	3259	CA	GLY	B	28	39.286	55.021	18.792	1.00	195.90
	3260	C	GLY	B	28	40.518	55.841	18.506	1.00	195.90
	3261	O	GLY	B	28	40.788	56.161	17.355	1.00	195.90
	3262	N	ASN	B	29	41.274	56.181	19.541	1.00	230.48
	3263	CA	ASN	B	29	42.456	57.003	19.352	1.00	230.48
50	3264	CB	ASN	B	29	42.882	57.612	20.690	1.00	249.51
	3265	CG	ASN	B	29	43.919	58.710	20.527	1.00	249.51
	3266	OD1	ASN	B	29	44.154	59.198	19.421	1.00	249.51
	3267	ND2	ASN	B	29	44.534	59.115	21.634	1.00	249.51
	3268	C	ASN	B	29	43.644	56.302	18.699	1.00	230.48
55	3269	O	ASN	B	29	44.198	56.804	17.716	1.00	230.48
	3270	N	ASN	B	30	44.040	55.149	19.229	1.00	218.47
	3271	CA	ASN	B	30	45.185	54.441	18.667	1.00	218.47
	3272	CB	ASN	B	30	46.364	54.509	19.631	1.00	238.45
	3273	CG	ASN	B	30	46.841	55.909	19.854	1.00	238.45
60	3274	OD1	ASN	B	30	46.936	56.337	20.986	1.00	238.45
	3275	ND2	ASN	B	30	47.139	56.635	18.778	1.00	238.45
	3276	C	ASN	B	30	44.936	52.990	18.293	1.00	218.47
	3277	O	ASN	B	30	44.881	52.646	17.109	1.00	218.47
	3278	N	PHE	B	31	44.779	52.137	19.300	1.00	249.37
65	3279	CA	PHE	B	31	44.573	50.724	19.037	1.00	249.37
	3280	CB	PHE	B	31	45.620	49.901	19.799	1.00	234.42
	3281	CG	PHE	B	31	47.045	50.311	19.513	1.00	234.42
	3282	CD1	PHE	B	31	47.600	51.429	20.131	1.00	234.42
	3283	CD2	PHE	B	31	47.822	49.594	18.607	1.00	234.42
70	3284	CE1	PHE	B	31	48.909	51.828	19.854	1.00	234.42

	3285	CE2	PHE	B	31-	49.131	49.985	18.322	1.00	234.42
	3286	CZ	PHE	B	31	49.674	51.107	18.947	1.00	234.42
	3287	C	PHE	B	31	43.166	50.221	19.340	1.00	249.37
	3288	O	PHE	B	31	42.638	50.399	20.440	1.00	249.37
5	3289	N	PHE	B	32	42.579	49.581	18.332	1.00	162.47
	3290	CA	PHE	B	32	41.233	49.034	18.408	1.00	162.47
	3291	CB	PHE	B	32	40.337	49.732	17.386	1.00	249.69
	3292	CG	PHE	B	32	38.872	49.480	17.598	1.00	249.69
	3293	CD1	PHE	B	32	38.241	49.969	18.718	1.00	249.69
10	3294	CD2	PHE	B	32	38.130	48.733	16.690	1.00	249.69
	3295	CE1	PHE	B	32	36.894	49.721	18.931	1.00	249.69
	3296	CE2	PHE	B	32	36.772	48.482	16.901	1.00	249.69
	3297	CZ	PHE	B	32	36.170	48.988	18.039	1.00	249.69
	3298	C	PHE	B	32	41.243	47.533	18.118	1.00	162.47
15	3299	O	PHE	B	32	42.275	46.987	17.714	1.00	162.47
	3300	N	GLU	B	33	40.097	46.869	18.298	1.00	249.28
	3301	CA	GLU	B	33	40.035	45.425	18.046	1.00	249.28
	3302	CB	GLU	B	33	39.767	44.643	19.298	1.00	249.25
	3303	CG	GLU	B	33	39.978	43.139	19.158	1.00	249.25
20	3304	CD	GLU	B	33	41.395	42.776	18.727	1.00	249.25
	3305	OE1	GLU	B	33	42.373	43.401	19.192	1.00	249.25
	3306	OE2	GLU	B	33	41.565	41.829	17.938	1.00	249.25
	3307	C	GLU	B	33	38.993	44.918	17.083	1.00	249.28
	3308	O	GLU	B	33	39.312	44.164	16.171	1.00	249.28
25	3309	N	VAL	B	34	37.732	45.243	17.348	1.00	234.23
	3310	CA	VAL	B	34	36.657	44.756	16.507	1.00	234.23
	3311	CB	VAL	B	34	35.301	45.388	16.902	1.00	191.69
	3312	CG1	VAL	B	34	34.197	44.865	15.998	1.00	191.69
	3313	CG2	VAL	B	34	34.978	45.059	18.343	1.00	191.69
30	3314	C	VAL	B	34	36.919	44.972	15.029	1.00	234.23
	3315	O	VAL	B	34	37.592	45.923	14.632	1.00	234.23
	3316	N	SER	B	35	36.395	44.052	14.229	1.00	249.39
	3317	CA	SER	B	35	36.536	44.110	12.789	1.00	249.39
35	3318	CB	SER	B	35	37.053	42.775	12.246	1.00	187.29
	3319	OG	SER	B	35	36.078	41.759	12.404	1.00	187.29
	3320	C	SER	B	35	35.161	44.414	12.202	1.00	249.39
	3321	O	SER	B	35	35.008	44.523	10.988	1.00	249.39
	3322	N	SER	B	36	34.160	44.541	13.074	1.00	236.03
40	3323	CA	SER	B	36	32.796	44.846	12.641	1.00	236.03
	3324	CB	SER	B	36	31.770	43.967	13.369	1.00	174.69
	3325	OG	SER	B	36	31.663	44.323	14.735	1.00	174.69
	3326	C	SER	B	36	32.488	46.310	12.911	1.00	236.03
	3327	O	SER	B	36	32.037	46.684	13.992	1.00	236.03
45	3328	N	THR	B	37	32.752	47.137	11.910	1.00	186.56
	3329	CA	THR	B	37	32.516	48.565	11.996	1.00	186.56
	3330	CB	THR	B	37	33.852	49.349	11.926	1.00	204.69
	3331	OG1	THR	B	37	34.720	48.919	12.983	1.00	204.69
	3332	CG2	THR	B	37	33.611	50.838	12.065	1.00	204.69
50	3333	C	THR	B	37	31.649	48.899	10.789	1.00	186.56
	3334	O	THR	B	37	31.837	48.338	9.708	1.00	186.56
	3335	N	LYS	B	38	30.692	49.800	10.972	1.00	233.53
	3336	CA	LYS	B	38	29.803	50.182	9.883	1.00	233.53
	3337	CB	LYS	B	38	28.358	50.059	10.341	1.00	159.29
55	3338	CG	LYS	B	38	28.005	48.688	10.851	1.00	159.29
	3339	CD	LYS	B	38	26.556	48.633	11.299	1.00	159.29
	3340	CE	LYS	B	38	26.179	47.229	11.738	1.00	159.29
	3341	NZ	LYS	B	38	24.755	47.156	12.158	1.00	159.29
	3342	C	LYS	B	38	30.055	51.604	9.402	1.00	233.53
	3343	O	LYS	B	38	30.349	52.490	10.203	1.00	233.53
60	3344	N	TRP	B	39	29.936	51.818	8.092	1.00	87.42
	3345	CA	TRP	B	39	30.140	53.149	7.521	1.00	87.42
	3346	CB	TRP	B	39	31.422	53.229	6.688	1.00	107.80
	3347	CG	TRP	B	39	32.678	53.035	7.471	1.00	107.80
65	3348	CD2	TRP	B	39	33.240	53.923	8.438	1.00	107.80
	3349	CE2	TRP	B	39	34.427	53.326	8.904	1.00	107.80
	3350	CE3	TRP	B	39	32.857	55.160	8.954	1.00	107.80
	3351	CD1	TRP	B	39	33.521	51.968	7.395	1.00	107.80
	3352	NE1	TRP	B	39	34.574	52.135	8.253	1.00	107.80
	3353	CZ2	TRP	B	39	35.236	53.930	9.860	1.00	107.80
70	3354	CZ3	TRP	B	39	33.659	55.755	9.899	1.00	107.80

	3355	CH2	TRP	B	39	34.839	55.141	10.346	1.00	107.80
	3356	C	TRP	B	39	28.973	53.500	6.637	1.00	87.42
	3357	O	TRP	B	39	28.580	52.712	5.799	1.00	87.42
	3358	N	PHE	B	40	28.429	54.694	6.818	1.00	127.18
5	3359	CA	PHE	B	40	27.289	55.111	6.025	1.00	127.18
	3360	CB	PHE	B	40	26.052	55.264	6.908	1.00	155.57
	3361	CG	PHE	B	40	25.605	54.032	7.687	1.00	155.57
	3362	CD1	PHE	B	40	26.374	53.715	8.858	1.00	155.57
	3363	CD2	PHE	B	40	24.666	53.200	7.261	1.00	155.57
10	3364	CE1	PHE	B	40	26.024	52.589	9.600	1.00	155.57
	3365	CE2	PHE	B	40	24.308	52.074	7.991	1.00	155.57
	3366	CZ	PHE	B	40	24.987	51.764	9.162	1.00	155.57
	3367	C	PHE	B	40	27.523	56.414	5.281	1.00	127.18
	3368	O	PHE	B	40	27.208	57.495	5.773	1.00	127.18
15	3369	N	HIS	B	41	28.078	56.306	4.084	1.00	72.05
	3370	CA	HIS	B	41	28.329	57.484	3.260	1.00	72.05
	3371	CB	HIS	B	41	29.355	57.132	2.173	1.00	83.13
	3372	CG	HIS	B	41	29.650	58.256	1.230	1.00	83.13
	3373	CD2	HIS	B	41	29.801	58.274	-0.114	1.00	83.13
20	3374	ND1	HIS	B	41	29.837	59.553	1.656	1.00	83.13
	3375	CE1	HIS	B	41	30.087	60.323	0.614	1.00	83.13
	3376	NE2	HIS	B	41	30.071	59.571	-0.472	1.00	83.13
	3377	C	HIS	B	41	27.010	57.961	2.633	1.00	72.05
	3378	O	HIS	B	41	26.458	57.298	1.761	1.00	72.05
25	3379	N	ASN	B	42	26.527	59.123	3.069	1.00	104.44
	3380	CA	ASN	B	42	25.256	59.683	2.600	1.00	104.44
	3381	CB	ASN	B	42	25.240	59.870	1.077	1.00	64.53
	3382	CG	ASN	B	42	26.091	61.039	0.625	1.00	64.53
	3383	OD1	ASN	B	42	27.195	61.213	1.144	1.00	64.53
30	3384	ND2	ASN	B	42	25.618	61.828	-0.348	1.00	64.53
	3385	C	ASN	B	42	24.114	58.751	2.999	1.00	104.44
	3386	O	ASN	B	42	23.089	58.706	2.334	1.00	104.44
	3387	N	GLY	B	43	24.293	58.003	4.083	1.00	163.92
	3388	CA	GLY	B	43	23.246	57.092	4.522	1.00	163.92
35	3389	C	GLY	B	43	23.405	55.677	3.991	1.00	163.92
	3390	O	GLY	B	43	23.159	54.701	4.702	1.00	163.92
	3391	N	SER	B	44	23.816	55.562	2.735	1.00	175.12
	3392	CA	SER	B	44	24.017	54.262	2.106	1.00	175.12
	3393	CB	SER	B	44	24.326	54.445	0.620	1.00	173.04
40	3394	OG	SER	B	44	23.344	55.253	-0.002	1.00	173.04
	3395	C	SER	B	44	25.178	53.524	2.772	1.00	175.12
	3396	O	SER	B	44	26.275	54.070	2.899	1.00	175.12
	3397	N	LEU	B	45	24.944	52.285	3.197	1.00	151.43
	3398	CA	LEU	B	45	25.991	51.495	3.846	1.00	151.43
45	3399	CB	LEU	B	45	25.458	50.101	4.198	1.00	163.91
	3400	CG	LEU	B	45	26.424	49.160	4.922	1.00	163.91
	3401	CD1	LEU	B	45	26.972	49.825	6.176	1.00	163.91
	3402	CD2	LEU	B	45	25.701	47.872	5.275	1.00	163.91
	3403	C	LEU	B	45	27.220	51.376	2.944	1.00	151.43
50	3404	O	LEU	B	45	27.089	51.318	1.722	1.00	151.43
	3405	N	SER	B	46	28.411	51.350	3.541	1.00	127.11
	3406	CA	SER	B	46	29.646	51.241	2.770	1.00	127.11
	3407	CB	SER	B	46	30.724	52.142	3.366	1.00	226.86
	3408	OG	SER	B	46	31.902	52.103	2.574	1.00	226.86
55	3409	C	SER	B	46	30.103	49.791	2.810	1.00	127.11
	3410	O	SER	B	46	29.622	49.009	3.626	1.00	127.11
	3411	N	GLU	B	47	31.030	49.425	1.927	1.00	149.05
	3412	CA	GLU	B	47	31.486	48.041	1.929	1.00	149.05
	3413	CB	GLU	B	47	31.711	47.509	0.484	1.00	195.89
60	3414	CG	GLU	B	47	30.777	48.077	-0.608	1.00	195.89
	3415	CD	GLU	B	47	31.343	47.934	-2.030	1.00	195.89
	3416	OE1	GLU	B	47	32.086	48.832	-2.508	1.00	195.89
	3417	OE2	GLU	B	47	31.042	46.909	-2.685	1.00	195.89
	3418	C	GLU	B	47	32.738	47.807	2.808	1.00	149.05
65	3419	O	GLU	B	47	33.224	46.684	2.891	1.00	149.05
	3420	N	GLU	B	48	33.291	48.851	3.436	1.00	101.79
	3421	CA	GLU	B	48	34.458	48.628	4.299	1.00	101.79
	3422	CB	GLU	B	48	35.331	49.904	4.457	1.00	223.78
	3423	CG	GLU	B	48	36.479	49.790	5.499	1.00	223.78
70	3424	CD	GLU	B	48	37.584	48.801	5.127	1.00	223.78

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	3425	OE1	GLU	B	48	38.340	49.074	4.170	1.00	223.78
	3426	OE2	GLU	B	48	37.703	47.751	5.799	1.00	223.78
	3427	C	GLU	B	48	33.949	48.158	5.661	1.00	101.79
	3428	O	GLU	B	48	32.788	48.397	6.021	1.00	101.79
5	3429	N	THR	B	49	34.812	47.476	6.410	1.00	169.38
	3430	CA	THR	B	49	34.445	46.976	7.728	1.00	169.38
	3431	CB	THR	B	49	34.268	45.441	7.707	1.00	162.45
	3432	OG1	THR	B	49	35.467	44.824	7.222	1.00	162.45
	3433	CG2	THR	B	49	33.110	45.061	6.797	1.00	162.45
10	3434	C	THR	B	49	35.501	47.369	8.762	1.00	169.38
	3435	O	THR	B	49	35.190	47.530	9.940	1.00	169.38
	3436	N	ASN	B	50	36.745	47.531	8.319	1.00	110.90
	3437	CA	ASN	B	50	37.830	47.919	9.213	1.00	110.90
	3438	CB	ASN	B	50	39.130	48.104	8.418	1.00	249.40
15	3439	CG	ASN	B	50	40.355	48.183	9.311	1.00	249.40
	3440	OD1	ASN	B	50	40.232	48.440	10.508	1.00	249.40
	3441	ND2	ASN	B	50	41.539	47.979	8.738	1.00	249.40
	3442	C	ASN	B	50	37.403	49.246	9.854	1.00	110.90
	3443	O	ASN	B	50	36.644	50.010	9.250	1.00	110.90
20	3444	N	SER	B	51	37.872	49.520	11.072	1.00	116.16
	3445	CA	SER	B	51	37.515	50.763	11.761	1.00	116.16
	3446	CB	SER	B	51	38.004	50.728	13.210	1.00	152.88
	3447	OG	SER	B	51	39.421	50.782	13.277	1.00	152.88
25	3443	C	SER	B	51	38.084	52.007	11.066	1.00	116.16
	3449	O	SER	B	51	37.632	53.121	11.313	1.00	116.16
	3450	N	SER	B	52	39.080	51.819	10.206	1.00	154.44
	3451	CA	SER	B	52	39.684	52.939	9.501	1.00	154.44
	3452	CB	SER	B	52	41.210	52.899	9.637	1.00	81.31
30	3453	OG	SER	B	52	41.611	53.078	10.987	1.00	81.31
	3454	C	SER	B	52	39.294	52.908	8.036	1.00	154.44
	3455	O	SER	B	52	39.754	52.057	7.273	1.00	154.44
	3456	N	LEU	B	53	38.433	53.844	7.656	1.00	115.15
	3457	CA	LEU	B	53	37.961	53.963	6.280	1.00	115.15
35	3458	CB	LEU	B	53	36.477	54.348	6.281	1.00	65.06
	3459	CG	LEU	B	53	35.882	55.021	5.036	1.00	65.06
	3460	CD1	LEU	B	53	36.353	54.301	3.774	1.00	65.06
	3461	CD2	LEU	B	53	34.357	55.039	5.132	1.00	65.06
	3462	C	LEU	B	53	38.775	55.005	5.509	1.00	115.15
40	3463	O	LEU	B	53	38.547	56.209	5.659	1.00	115.15
	3464	N	ASN	B	54	39.712	54.549	4.676	1.00	78.33
	3465	CA	ASN	B	54	40.533	55.488	3.918	1.00	78.33
	3466	CB	ASN	B	54	41.826	54.832	3.460	1.00	116.91
	3467	CG	ASN	B	54	42.792	54.609	4.598	1.00	116.91
45	3468	OD1	ASN	B	54	43.166	55.545	5.307	1.00	116.91
	3469	ND2	ASN	B	54	43.204	53.364	4.782	1.00	116.91
	3470	C	ASN	B	54	39.834	56.084	2.716	1.00	78.33
	3471	O	ASN	B	54	38.853	55.548	2.226	1.00	78.33
	3472	N	ILE	B	55	40.333	57.227	2.269	1.00	83.98
50	3473	CA	ILE	B	55	39.800	57.906	1.100	1.00	83.98
	3474	CB	ILE	B	55	38.973	59.141	1.493	1.00	67.63
	3475	CG2	ILE	B	55	38.828	60.092	0.322	1.00	67.63
	3476	CG1	ILE	B	55	37.598	58.686	1.980	1.00	67.63
	3477	CD1	ILE	B	55	36.675	59.826	2.438	1.00	67.63
55	3478	C	ILE	B	55	41.015	58.329	0.298	1.00	83.98
	3479	O	ILE	B	55	41.882	59.043	0.805	1.00	83.98
	3480	N	VAL	B	56	41.099	57.866	-0.942	1.00	110.45
	3481	CA	VAL	B	56	42.231	58.216	-1.781	1.00	110.45
	3482	CB	VAL	B	56	42.737	56.993	-2.541	1.00	102.53
60	3483	CG1	VAL	B	56	44.131	57.246	-3.058	1.00	102.53
	3484	CG2	VAL	B	56	42.749	55.791	-1.618	1.00	102.53
	3485	C	VAL	B	56	41.796	59.306	-2.748	1.00	110.45
	3486	O	VAL	B	56	40.783	59.952	-2.515	1.00	110.45
	3487	N	ASN	B	57	42.556	59.515	-3.820	1.00	137.41
65	3488	CA	ASN	B	57	42.235	60.554	-4.794	1.00	137.41
	3489	CB	ASN	B	57	42.508	60.063	-6.216	1.00	211.36
	3490	CG	ASN	B	57	43.990	59.900	-6.493	1.00	211.36
	3491	OD1	ASN	B	57	44.776	60.825	-6.294	1.00	211.36
	3492	ND2	ASN	B	57	44.379	58.721	-6.959	1.00	211.36
	3493	C	ASN	B	57	40.795	61.032	-4.667	1.00	137.41
70	3494	O	ASN	B	57	39.885	60.501	-5.305	1.00	137.41

	3495	N	ALA	B	58	40.608	62.038	-3.818	1.00	74.20
	3496	CA	ALA	B	58	39.303	62.603	-3.561	1.00	74.20
	3497	CB	ALA	B	58	39.440	63.783	-2.609	1.00	169.14
5	3498	C	ALA	B	58	38.534	63.034	-4.817	1.00	74.20
	3499	O	ALA	B	58	38.983	63.895	-5.579	1.00	74.20
	3500	N	LYS	B	59	37.366	62.433	-5.015	1.00	107.95
	3501	CA	LYS	B	59	36.507	62.766	-6.137	1.00	107.95
	3502	CB	LYS	B	59	36.037	61.485	-6.837	1.00	214.35
	3503	CG	LYS	B	59	37.184	60.618	-7.354	1.00	214.35
10	3504	CD	LYS	B	59	36.703	59.292	-7.930	1.00	214.35
	3505	CE	LYS	B	59	37.872	58.451	-8.432	1.00	214.35
	3506	NZ	LYS	B	59	37.428	57.138	-8.972	1.00	214.35
	3507	C	LYS	B	59	35.330	63.514	-5.521	1.00	107.95
	3508	O	LYS	B	59	34.924	63.205	-4.397	1.00	107.95
15	3509	N	PHE	B	60	34.798	64.502	-6.234	1.00	88.51
	3510	CA	PHE	B	60	33.670	65.268	-5.716	1.00	88.51
	3511	CB	PHE	B	60	33.032	66.051	-6.845	1.00	104.07
	3512	CG	PHE	B	60	33.926	67.085	-7.419	1.00	104.07
	3513	CD1	PHE	B	60	33.803	67.477	-8.736	1.00	104.07
20	3514	CD2	PHE	B	60	34.893	67.682	-6.635	1.00	104.07
	3515	CE1	PHE	B	60	34.629	68.451	-9.266	1.00	104.07
	3516	CE2	PHE	B	60	35.725	68.654	-7.155	1.00	104.07
	3517	CZ	PHE	B	60	35.592	69.038	-8.473	1.00	104.07
	3518	C	PHE	B	60	32.616	64.397	-5.032	1.00	88.51
25	3519	O	PHE	B	60	31.988	64.816	-4.060	1.00	88.51
	3520	N	GLU	B	61	32.438	63.177	-5.536	1.00	122.82
	3521	CA	GLU	B	61	31.453	62.251	-4.988	1.00	122.82
	3522	CB	GLU	B	61	31.362	60.981	-5.838	1.00	242.03
	3523	CG	GLU	B	61	30.921	61.202	-7.268	1.00	242.03
30	3524	CD	GLU	B	61	31.866	62.107	-8.030	1.00	242.03
	3525	OE1	GLU	B	61	33.080	61.812	-8.056	1.00	242.03
	3526	OE2	GLU	B	61	31.395	63.111	-8.604	1.00	242.03
	3527	C	GLU	B	61	31.772	61.856	-3.563	1.00	122.82
	3528	O	GLU	B	61	30.884	61.426	-2.829	1.00	122.82
35	3529	N	ASP	B	62	33.038	61.982	-3.173	1.00	75.67
	3530	CA	ASP	B	62	33.435	61.622	-1.821	1.00	75.67
	3531	CB	ASP	B	62	34.954	61.524	-1.708	1.00	186.17
	3532	CG	ASP	B	62	35.544	60.572	-2.723	1.00	186.17
	3533	OD1	ASP	B	62	34.918	59.528	-2.996	1.00	186.17
40	3534	OD2	ASP	B	62	36.638	60.860	-3.242	1.00	186.17
	3535	C	ASP	B	62	32.889	62.643	-0.834	1.00	75.67
	3536	O	ASP	B	62	32.765	62.359	0.354	1.00	75.67
	3537	N	SER	B	63	32.553	63.832	-1.330	1.00	56.90
	3538	CA	SER	B	63	31.993	64.872	-0.471	1.00	56.90
45	3539	CB	SER	B	63	31.659	66.117	-1.286	1.00	80.16
	3540	OG	SER	B	63	32.823	66.739	-1.783	1.00	80.16
	3541	C	SER	B	63	30.710	64.291	0.102	1.00	56.90
	3542	O	SER	B	63	29.919	63.744	-0.643	1.00	56.90
	3543	N	GLY	B	64	30.482	64.385	1.407	1.00	91.31
50	3544	CA	GLY	B	64	29.254	63.819	1.941	1.00	91.31
	3545	C	GLY	B	64	29.177	63.712	3.447	1.00	91.31
	3546	O	GLY	B	64	30.012	64.259	4.164	1.00	91.31
	3547	N	GLU	B	65	28.154	63.014	3.922	1.00	66.19
	3548	CA	GLU	B	65	27.919	62.813	5.351	1.00	66.19
55	3549	CB	GLU	B	65	26.443	63.045	5.642	1.00	122.59
	3550	CG	GLU	B	65	25.981	62.639	7.018	1.00	122.59
	3551	CD	GLU	B	65	24.468	62.585	7.107	1.00	122.59
	3552	OE1	GLU	B	65	23.856	61.738	6.417	1.00	122.59
	3553	OE2	GLU	B	65	23.890	63.390	7.863	1.00	122.59
60	3554	C	GLU	B	65	28.311	61.374	5.711	1.00	66.19
	3555	O	GLU	B	65	27.826	60.434	5.088	1.00	66.19
	3556	N	TYR	B	66	29.183	61.182	6.697	1.00	58.72
	3557	CA	TYR	B	66	29.603	59.833	7.060	1.00	58.72
	3558	CB	TYR	B	66	31.093	59.680	6.855	1.00	55.88
65	3559	CG	TYR	B	66	31.576	59.790	5.452	1.00	55.88
	3560	CD1	TYR	B	66	31.703	61.020	4.825	1.00	55.88
	3561	CE1	TYR	B	66	32.243	61.109	3.548	1.00	55.88
	3562	CD2	TYR	B	66	31.986	58.657	4.772	1.00	55.88
	3563	CE2	TYR	B	66	32.521	58.726	3.505	1.00	55.88
70	3564	CZ	TYR	B	66	32.655	59.947	2.896	1.00	55.88

	3565	OH	TYR	B	66	33.230	59.979	1.643	1.00	55.88
	3566	C	TYR	B	66	29.320	59.544	8.522	1.00	58.72
	3567	O	TYR	B	66	29.111	60.482	9.311	1.00	58.72
	3568	N	LYS	B	67	29.347	58.257	8.884	1.00	128.26
5	3569	CA	LYS	B	67	29.129	57.823	10.269	1.00	128.26
	3570	CB	LYS	B	67	27.689	58.067	10.679	1.00	129.32
	3571	CG	LYS	B	67	26.702	57.535	9.689	1.00	129.32
	3572	CD	LYS	B	67	25.301	57.905	10.098	1.00	129.32
	3573	CE	LYS	B	67	24.314	57.545	9.007	1.00	129.32
10	3574	NZ	LYS	B	67	22.936	57.963	9.372	1.00	129.32
	3575	C	LYS	B	67	29.460	56.351	10.466	1.00	128.26
	3576	O	LYS	B	67	29.434	55.570	9.516	1.00	128.26
	3577	N	CYS	B	68	29.793	55.971	11.696	1.00	93.88
	3578	CA	CYS	B	68	30.107	54.581	11.964	1.00	93.88
15	3579	C	CYS	B	68	29.262	54.113	13.122	1.00	93.88
	3580	O	CYS	B	68	28.693	54.923	13.850	1.00	93.88
	3581	CB	CYS	B	68	31.609	54.381	12.247	1.00	200.62
	3582	SG	CYS	B	68	32.359	55.270	13.646	1.00	200.62
	3583	N	GLN	B	69	29.148	52.797	13.255	1.00	198.52
20	3584	CA	GLN	B	69	28.375	52.172	14.318	1.00	198.52
	3585	CB	GLN	B	69	26.897	52.107	13.926	1.00	207.53
	3586	CG	GLN	B	69	26.082	51.114	14.734	1.00	207.53
	3587	CD	GLN	B	69	24.654	50.983	14.233	1.00	207.53
	3588	OE1	GLN	B	69	24.419	50.759	13.044	1.00	207.53
25	3589	NE2	GLN	B	69	23.692	51.117	15.143	1.00	207.53
	3590	C	GLN	B	69	28.921	50.768	14.527	1.00	198.52
	3591	O	GLN	B	69	29.474	50.173	13.600	1.00	198.52
	3592	N	HIS	B	70	28.772	50.240	15.739	1.00	126.14
	3593	CA	HIS	B	70	29.266	48.903	16.020	1.00	126.14
30	3594	CB	HIS	B	70	30.134	48.915	17.265	1.00	193.31
	3595	CG	HIS	B	70	31.435	49.650	17.083	1.00	193.31
	3596	CD2	HIS	B	70	31.809	50.892	17.450	1.00	193.31
	3597	ND1	HIS	B	70	32.502	49.089	16.411	1.00	193.31
	3598	CE1	HIS	B	70	33.480	49.982	16.371	1.00	193.31
35	3599	NE2	HIS	B	70	33.095	51.074	16.992	1.00	193.31
	3600	C	HIS	B	70	28.144	47.890	16.193	1.00	126.14
	3601	O	HIS	B	70	26.974	48.180	15.915	1.00	126.14
	3602	N	GLN	B	71	28.511	46.697	16.639	1.00	181.78
	3603	CA	GLN	B	71	27.558	45.621	16.836	1.00	181.78
40	3604	CB	GLN	B	71	28.277	44.424	17.456	1.00	249.38
	3605	CG	GLN	B	71	27.687	43.082	17.057	1.00	249.38
	3606	CD	GLN	B	71	27.525	42.946	15.553	1.00	249.38
	3607	OE1	GLN	B	71	28.501	42.814	14.816	1.00	249.38
	3608	NE2	GLN	B	71	26.283	42.994	15.091	1.00	249.38
45	3609	C	GLN	B	71	26.374	46.062	17.711	1.00	181.78
	3610	O	GLN	B	71	25.214	45.948	17.300	1.00	181.78
	3611	N	GLN	B	72	26.666	46.582	18.902	1.00	249.48
	3612	CA	GLN	B	72	25.627	47.029	19.838	1.00	249.48
	3613	CB	GLN	B	72	25.631	46.132	21.084	1.00	225.39
50	3614	CG	GLN	B	72	24.511	46.421	22.083	1.00	225.39
	3615	CD	GLN	B	72	24.526	45.478	23.273	1.00	225.39
	3616	OE1	GLN	B	72	24.436	44.260	23.115	1.00	225.39
	3617	NE2	GLN	B	72	24.641	46.038	24.471	1.00	225.39
	3618	C	GLN	B	72	25.812	48.487	20.262	1.00	249.48
55	3619	O	GLN	B	72	25.935	48.787	21.455	1.00	249.48
	3620	N	VAL	B	73	25.821	49.395	19.288	1.00	181.22
	3621	CA	VAL	B	73	26.005	50.817	19.583	1.00	181.22
	3622	CB	VAL	B	73	27.465	51.205	19.481	1.00	249.28
	3623	CG1	VAL	B	73	27.738	52.552	20.109	1.00	249.28
60	3624	CG2	VAL	B	73	28.193	50.235	20.151	1.00	249.28
	3625	C	VAL	B	73	25.240	51.690	18.626	1.00	181.22
	3626	O	VAL	B	73	25.071	51.348	17.462	1.00	181.22
	3627	N	ASN	B	74	24.776	52.826	19.122	1.00	246.14
	3628	CA	ASN	B	74	24.042	53.744	18.278	1.00	246.14
65	3629	CB	ASN	B	74	23.201	54.681	19.141	1.00	197.13
	3630	CG	ASN	B	74	22.296	53.925	20.082	1.00	197.13
	3631	OD1	ASN	B	74	21.682	52.931	19.688	1.00	197.13
	3632	ND2	ASN	B	74	22.202	54.394	21.324	1.00	197.13
	3833	C	ASN	B	74	25.027	54.526	17.418	1.00	246.14
70	3634	O	ASN	B	74	26.004	55.081	17.922	1.00	246.14

	3635	N	GLU	B	75	24.761	54.542	16.114	1.00	146.48
	3636	CA	GLU	B	75	25.597	55.232	15.135	1.00	146.48
	3637	CB	GLU	B	75	24.848	55.331	13.807	1.00	234.88
	3638	CG	GLU	B	75	23.346	55.500	13.966	1.00	234.88
5	3639	CD	GLU	B	75	22.604	55.365	12.648	1.00	234.88
	3640	OE1	GLU	B	75	22.784	54.328	11.970	1.00	234.88
	3641	OE2	GLU	B	75	21.840	56.291	12.295	1.00	234.88
	3642	C	GLU	B	75	26.075	56.613	15.579	1.00	146.48
	3643	O	GLU	B	75	25.344	57.361	16.239	1.00	146.48
10	3644	N	SER	B	76	27.311	56.939	15.201	1.00	102.01
	3645	CA	SER	B	76	27.958	58.200	15.564	1.00	102.01
	3646	CB	SER	B	76	29.420	58.153	15.147	1.00	220.64
	3647	OG	SER	B	76	29.501	58.098	13.732	1.00	220.64
	3648	C	SER	B	76	27.336	59.426	14.930	1.00	102.01
15	3649	O	SER	B	76	26.652	59.332	13.921	1.00	102.01
	3650	N	GLU	B	77	27.604	60.583	15.522	1.00	133.62
	3651	CA	GLU	B	77	27.102	61.838	14.988	1.00	133.62
	3652	CB	GLU	B	77	27.429	62.993	15.941	1.00	240.61
	3653	CG	GLU	B	77	26.732	62.894	17.288	1.00	240.61
20	3654	CD	GLU	B	77	25.218	62.995	17.179	1.00	240.61
	3655	OE1	GLU	B	77	24.686	62.847	16.060	1.00	240.61
	3656	OE2	GLU	B	77	24.558	63.213	18.217	1.00	240.61
	3657	C	GLU	B	77	27.798	62.057	13.651	1.00	133.62
	3658	O	GLU	B	77	29.023	62.177	13.597	1.00	133.62
25	3659	N	PRO	B	78	27.030	62.096	12.549	1.00	89.52
	3660	CD	PRO	B	78	25.577	61.836	12.507	1.00	87.18
	3661	CA	PRO	B	78	27.543	62.294	11.196	1.00	89.52
	3662	CB	PRO	B	78	26.295	62.633	10.408	1.00	87.18
	3663	CG	PRO	B	78	25.313	61.698	11.009	1.00	87.18
30	3664	C	PRO	B	78	28.586	63.370	11.098	1.00	89.52
	3665	O	PRO	B	78	28.644	64.258	11.943	1.00	89.52
	3666	N	VAL	B	79	29.430	63.270	10.082	1.00	99.13
	3667	CA	VAL	B	79	30.475	64.256	9.872	1.00	99.13
	3668	CB	VAL	B	79	31.833	63.720	10.291	1.00	115.84
35	3669	CG1	VAL	B	79	32.929	64.618	9.749	1.00	115.84
	3670	CG2	VAL	B	79	31.908	63.671	11.798	1.00	115.84
	3871	C	VAL	B	79	30.512	64.571	8.401	1.00	99.13
	3672	O	VAL	B	79	30.573	63.654	7.592	1.00	99.13
	3673	N	TYR	B	80	30.480	65.853	8.044	1.00	70.58
40	3674	CA	TYR	B	80	30.490	66.213	6.637	1.00	70.58
	3675	CB	TYR	B	80	29.622	67.426	6.352	1.00	173.93
	3676	CG	TYR	B	80	29.319	67.524	4.884	1.00	173.93
	3677	CD1	TYR	B	80	28.546	66.550	4.261	1.00	173.93
	3678	CE1	TYR	B	80	28.266	66.604	2.913	1.00	173.93
45	3679	CD2	TYR	B	80	29.824	68.559	4.106	1.00	173.93
	3680	CE2	TYR	B	80	29.561	68.613	2.729	1.00	173.93
	3681	CZ	TYR	B	80	28.769	67.630	2.148	1.00	173.93
	3682	OH	TYR	B	80	28.432	67.702	0.811	1.00	173.93
	3683	C	TYR	B	80	31.858	66.511	6.103	1.00	70.58
50	3684	O	TYR	B	80	32.657	67.183	6.739	1.00	70.58
	3685	N	LEU	B	81	32.109	66.033	4.902	1.00	86.81
	3686	CA	LEU	B	81	33.375	66.256	4.254	1.00	86.81
	3687	CB	LEU	B	81	34.030	64.899	3.970	1.00	52.23
	3688	CG	LEU	B	81	35.301	65.038	3.148	1.00	52.23
55	3689	CD1	LEU	B	81	36.303	65.810	3.970	1.00	52.23
	3690	CD2	LEU	B	81	35.843	63.724	2.783	1.00	52.23
	3691	C	LEU	B	81	33.090	66.999	2.944	1.00	86.81
	3692	O	LEU	B	81	32.240	66.576	2.171	1.00	86.81
	3693	N	GLU	B	82	33.777	68.104	2.682	1.00	81.52
60	3694	CA	GLU	B	82	33.537	68.808	1.430	1.00	81.52
	3695	CB	GLU	B	82	33.000	70.212	1.700	1.00	166.15
	3696	CG	GLU	B	82	32.168	70.757	0.552	1.00	166.15
	3697	CD	GLU	B	82	31.619	72.139	0.827	1.00	166.15
	3698	OE1	GLU	B	82	31.239	72.409	1.988	1.00	166.15
65	3699	OE2	GLU	B	82	31.557	72.953	-0.118	1.00	166.15
	3700	C	GLU	B	82	34.800	68.898	0.584	1.00	81.52
	3701	O	GLU	B	82	35.856	69.283	1.072	1.00	81.52
	3702	N	VAL	B	83	34.691	68.555	-0.692	1.00	81.14
	3703	CA	VAL	B	83	35.842	68.595	-1.584	1.00	81.14
70	3704	CB	VAL	B	83	35.910	67.346	-2.417	1.00	54.13

	3705	CG1	VAL	B	83	37.014	67.472	-3.433	1.00	54.13
	3706	CG2	VAL	B	83	36.159	66.136	-1.512	1.00	54.13
	3707	C	VAL	B	83	35.848	69.781	-2.535	1.00	81.14
	3708	O	VAL	B	83	34.831	70.075	-3.168	1.00	81.14
5	3709	N	PHE	B	84	37.000	70.441	-2.667	1.00	61.79
	3710	CA	PHE	B	84	37.084	71.612	-3.530	1.00	61.79
	3711	CB	PHE	B	84	37.407	72.864	-2.729	1.00	77.82
	3712	CG	PHE	B	84	36.432	73.162	-1.660	1.00	77.82
	3713	CD1	PHE	B	84	36.408	72.410	-0.500	1.00	77.82
10	3714	CD2	PHE	B	84	35.555	74.223	-1.790	1.00	77.82
	3715	CE1	PHE	B	84	35.513	72.699	0.522	1.00	77.82
	3716	CE2	PHE	B	84	34.650	74.529	-0.779	1.00	77.82
	3717	CZ	PHE	B	84	34.634	73.766	0.384	1.00	77.82
	3718	C	PHE	B	84	38.081	71.568	-4.654	1.00	61.79
15	3719	O	PHE	B	84	38.978	70.728	-4.701	1.00	61.79
	3720	N	SER	B	85	37.893	72.538	-5.543	1.00	129.28
	3721	CA	SER	B	85	38.736	72.777	-6.696	1.00	129.28
	3722	CB	SER	B	85	38.066	72.284	-7.980	1.00	132.41
	3723	OG	SER	B	85	38.879	72.526	-9.116	1.00	132.41
20	3724	C	SER	B	85	38.840	74.296	-6.713	1.00	129.28
	3725	O	SER	B	85	37.845	74.988	-6.967	1.00	129.28
	3726	N	ASP	B	86	40.026	74.811	-6.395	1.00	77.53
	3727	CA	ASP	B	86	40.255	76.257	-6.385	1.00	77.53
	3728	CB	ASP	B	86	39.348	76.933	-5.354	1.00	206.86
25	3729	CG	ASP	B	86	38.874	78.300	-5.809	1.00	206.86
	3730	OD1	ASP	B	86	39.733	79.139	-6.163	1.00	206.86
	3731	OD2	ASP	B	86	37.644	78.535	-5.812	1.00	206.86
	3732	C	ASP	B	86	41.719	76.537	-6.065	1.00	77.53
	3733	O	ASP	B	86	42.423	75.643	-5.601	1.00	77.53
30	3734	N	TRP	B	87	42.186	77.759	-6.313	1.00	63.09
	3735	CA	TRP	B	87	43.589	78.072	-6.048	1.00	63.09
	3736	CB	TRP	B	87	43.934	79.488	-6.505	1.00	213.86
	3737	CG	TRP	B	87	44.332	79.502	-7.919	1.00	213.86
	3738	CD2	TRP	B	87	43.467	79.711	-9.031	1.00	213.86
35	3739	CE2	TRP	B	87	44.225	79.492	-10.196	1.00	213.86
	3740	CE3	TRP	B	87	42.115	80.053	-9.157	1.00	213.86
	3741	CD1	TRP	B	87	45.561	79.186	-8.435	1.00	213.86
	3742	NE1	TRP	B	87	45.500	79.175	-9.807	1.00	213.86
	3743	CZ2	TRP	B	87	43.674	79.604	-11.468	1.00	213.86
40	3744	CZ3	TRP	B	87	41.570	80.162	-10.423	1.00	213.86
	3745	CH2	TRP	B	87	42.347	79.943	-11.559	1.00	213.86
	3746	C	TRP	B	87	43.913	77.935	-4.589	1.00	63.09
	3747	O	TRP	B	87	44.856	77.221	-4.208	1.00	63.09
	3748	N	LEU	B	88	43.110	78.622	-3.783	1.00	95.94
45	3749	CA	LEU	B	88	43.280	78.617	-2.349	1.00	95.94
	3750	CB	LEU	B	88	43.600	80.021	-1.861	1.00	93.07
	3751	CG	LEU	B	88	44.931	80.558	-2.325	1.00	93.07
	3752	CD1	LEU	B	88	45.167	81.882	-1.668	1.00	93.07
	3753	CD2	LEU	B	88	46.019	79.559	-1.955	1.00	93.07
50	3754	C	LEU	B	88	42.050	78.126	-1.621	1.00	95.94
	3755	O	LEU	B	88	40.927	78.425	-2.004	1.00	95.94
	3756	N	LEU	B	89	42.276	77.380	-0.550	1.00	57.56
	3757	CA	LEU	B	89	41.191	76.863	0.265	1.00	57.56
	3758	CB	LEU	B	89	41.063	75.370	0.059	1.00	98.29
55	3759	CG	LEU	B	89	39.972	74.802	0.940	1.00	98.29
	3760	CD1	LEU	B	89	38.700	75.640	0.767	1.00	98.29
	3761	CD2	LEU	B	89	39.741	73.357	0.564	1.00	98.29
	3762	C	LEU	B	89	41.488	77.138	1.724	1.00	57.56
	3763	O	LEU	B	89	42.566	76.832	2.192	1.00	57.56
60	3764	N	LEU	B	90	40.553	77.737	2.444	1.00	82.03
	3765	CA	LEU	B	90	40.787	78.008	3.857	1.00	82.03
	3766	CB	LEU	B	90	40.005	79.244	4.303	1.00	51.54
	3767	CG	LEU	B	90	40.073	79.537	5.807	1.00	51.54
	3768	CD1	LEU	B	90	41.486	79.805	6.154	1.00	51.54
65	3769	CD2	LEU	B	90	39.203	80.720	6.203	1.00	51.54
	3770	C	LEU	B	90	40.347	76.808	4.674	1.00	82.03
	3771	O	LEU	B	90	39.173	76.431	4.667	1.00	82.03
	3772	N	GLN	B	91	41.274	76.199	5.391	1.00	55.00
	3773	CA	GLN	B	91	40.904	75.024	6.182	1.00	55.00
70	3774	CB	GLN	B	91	41.909	73.900	5.955	1.00	79.62

	3775	CG	GLN	B	91	42.017	73.500	4.501	1.00	79.62
	3776	CD	GLN	B	91	42.871	72.287	4.316	1.00	79.62
	3777	OE1	GLN	B	91	44.072	72.334	4.524	1.00	79.62
	3778	NE2	GLN	B	91	42.253	71.180	3.942	1.00	79.62
5	3779	C	GLN	B	91	40.793	75.316	7.670	1.00	55.00
	3780	O	GLN	B	91	41.552	76.118	8.212	1.00	55.00
	3781	N	ALA	B	92	39.846	74.680	8.344	1.00	72.63
	3782	CA	ALA	B	92	39.692	74.939	9.760	1.00	72.63
	3783	CB	ALA	B	92	38.406	75.678	10.004	1.00	131.49
10	3784	C	ALA	B	92	39.691	73.632	10.519	1.00	72.63
	3785	O	ALA	B	92	39.122	72.634	10.050	1.00	72.63
	3786	N	SER	B	93	40.338	73.624	11.685	1.00	73.84
	3787	CA	SER	B	93	40.381	72.421	12.512	1.00	73.84
	3788	CB	SER	B	93	41.018	72.709	13.873	1.00	152.84
15	3789	OG	SER	B	93	40.445	73.845	14.491	1.00	152.84
	3790	C	SER	B	93	38.934	72.013	12.691	1.00	73.84
	3791	O	SER	B	93	38.515	70.973	12.179	1.00	73.84
	3792	N	ALA	B	94	38.167	72.859	13.378	1.00	105.05
	3793	CA	ALA	B	94	36.743	72.624	13.619	1.00	105.05
20	3794	CB	ALA	B	94	36.517	72.246	15.061	1.00	185.57
	3795	C	ALA	B	94	35.978	73.898	13.280	1.00	105.05
	3796	O	ALA	B	94	36.478	74.988	13.524	1.00	105.05
	3797	N	GLU	B	95	34.776	73.763	12.724	1.00	101.72
	3798	CA	GLU	B	95	34.005	74.936	12.340	1.00	101.72
25	3799	CB	GLU	B	95	33.081	74.601	11.175	1.00	160.65
	3800	CG	GLU	B	95	33.822	74.120	9.941	1.00	160.65
	3801	CD	GLU	B	95	32.955	74.120	8.692	1.00	160.65
	3802	OE1	GLU	B	95	33.455	73.705	7.625	1.00	160.65
	3803	OE2	GLU	B	95	31.779	74.538	8.771	1.00	160.65
30	3804	C	GLU	B	95	33.205	75.550	13.473	1.00	101.72
	3805	O	GLU	B	95	32.732	76.677	13.354	1.00	101.72
	3806	N	VAL	B	96	33.050	74.807	14.565	1.00	87.11
	3807	CA	VAL	B	96	32.322	75.296	15.730	1.00	87.11
	3808	CB	VAL	B	96	30.947	74.746	15.781	1.00	166.75
35	3809	CG1	VAL	B	96	30.147	75.595	16.714	1.00	166.75
	3810	CG2	VAL	B	96	30.349	74.728	14.367	1.00	166.75
	3811	C	VAL	B	96	33.096	74.866	16.955	1.00	87.11
	3812	O	VAL	B	96	33.528	73.724	17.052	1.00	87.11
	3813	N	VAL	B	97	33.260	75.781	17.900	1.00	103.60
40	3814	CA	VAL	B	97	34.080	75.505	19.067	1.00	103.60
	3815	CB	VAL	B	97	35.444	76.140	18.858	1.00	67.08
	3816	CG1	VAL	B	97	36.415	75.622	19.857	1.00	67.08
	3817	CG2	VAL	B	97	35.924	75.882	17.456	1.00	67.08
	3818	C	VAL	B	97	33.591	76.003	20.417	1.00	103.60
45	3819	O	VAL	B	97	33.142	77.136	20.533	1.00	103.60
	3820	N	MET	B	98	33.730	75.168	21.441	1.00	173.13
	3821	CA	MET	B	98	33.341	75.542	22.798	1.00	173.13
	3822	CB	MET	B	98	33.361	74.306	23.696	1.00	240.86
	3823	CG	MET	B	98	32.369	73.237	23.290	1.00	240.86
50	3824	SD	MET	B	98	30.722	73.639	23.866	1.00	240.86
	3825	CE	MET	B	98	30.921	73.267	25.612	1.00	240.86
	3826	C	MET	B	98	34.341	76.573	23.323	1.00	173.13
	3827	O	MET	B	98	35.547	76.380	23.185	1.00	173.13
	3828	N	GLU	B	99	33.849	77.658	23.918	1.00	116.59
55	3829	CA	GLU	B	99	34.731	78.695	24.451	1.00	116.59
	3830	CB	GLU	B	99	33.954	79.631	25.376	1.00	249.41
	3831	CG	GLU	B	99	34.810	80.985	25.567	1.00	249.41
	3832	CD	GLU	B	99	34.016	81.763	26.727	1.00	249.41
	3833	OE1	GLU	B	99	32.782	81.690	26.920	1.00	249.41
60	3834	OE2	GLU	B	99	34.781	82.455	27.435	1.00	249.41
	3835	C	GLU	B	99	35.853	78.023	25.247	1.00	116.59
	3836	O	GLU	B	99	35.582	77.203	26.127	1.00	116.59
	3837	N	GLY	B	100	37.106	78.351	24.935	1.00	84.75
65	3838	CA	GLY	B	100	38.221	77.751	25.651	1.00	84.75
	3839	C	GLY	B	100	39.031	76.722	24.883	1.00	84.75
	3840	O	GLY	B	100	40.171	76.451	25.243	1.00	84.75
	3841	N	GLN	B	101	38.464	76.151	23.824	1.00	108.09
	3842	CA	GLN	B	101	39.167	75.134	23.033	1.00	108.09
	3843	CB	GLN	B	101	38.151	74.231	22.324	1.00	249.17
70	3844	CG	GLN	B	101	37.313	73.397	23.267	1.00	249.17

	3845	CD	GLN	B	101	38.163	72.685	24.297	1.00	249.17
	3846	OE1	GLN	B	101	38.643	73.292	25.255	1.00	249.17
	3847	NE2	GLN	B	101	38.370	71.395	24.094	1.00	249.17
5	3848	C	GLN	B	101	40.159	75.687	22.000	1.00	108.09
	3849	O	GLN	B	101	40.186	76.880	21.723	1.00	108.09
	3850	N	PRO	B	102	40.996	74.815	21.422	1.00	84.30
	3851	CD	PRO	B	102	41.175	73.371	21.665	1.00	171.21
	3852	CA	PRO	B	102	41.948	75.301	20.429	1.00	84.30
10	3853	CB	PRO	B	102	43.006	74.212	20.431	1.00	171.21
	3854	CG	PRO	B	102	42.177	72.979	20.592	1.00	171.21
	3855	C	PRO	B	102	41.270	75.466	19.051	1.00	84.30
	3856	O	PRO	B	102	40.260	74.799	18.745	1.00	84.30
	3857	N	LEU	B	103	41.828	76.351	18.228	1.00	75.78
15	3858	CA	LEU	B	103	41.299	76.588	16.900	1.00	75.78
	3859	CB	LEU	B	103	40.437	77.830	16.910	1.00	79.40
	3860	CG	LEU	B	103	39.866	78.063	15.515	1.00	79.40
	3861	CD1	LEU	B	103	38.942	76.897	15.142	1.00	79.40
	3862	CD2	LEU	B	103	39.117	79.391	15.483	1.00	79.40
20	3863	C	LEU	B	103	42.411	76.793	15.892	1.00	75.78
	3864	O	LEU	B	103	43.216	77.686	16.078	1.00	75.78
	3865	N	PHE	B	104	42.470	75.993	14.828	1.00	73.92
	3866	CA	PHE	B	104	43.524	76.182	13.838	1.00	73.92
25	3867	CB	PHE	B	104	44.441	74.953	13.752	1.00	179.34
	3868	CG	PHE	B	104	45.088	74.577	15.054	1.00	179.34
	3869	CD1	PHE	B	104	44.366	73.908	16.035	1.00	179.34
	3870	CD2	PHE	B	104	46.423	74.880	15.299	1.00	179.34
	3871	CE1	PHE	B	104	44.960	73.550	17.248	1.00	179.34
30	3872	CE2	PHE	B	104	47.028	74.527	16.512	1.00	179.34
	3873	CZ	PHE	B	104	46.295	73.857	17.485	1.00	179.34
	3874	C	PHE	B	104	42.958	76.472	12.448	1.00	73.92
	3875	O	PHE	B	104	42.121	75.717	11.947	1.00	73.92
	3876	N	LEU	B	105	43.387	77.581	11.838	1.00	49.92
35	3877	CA	LEU	B	105	42.985	77.920	10.468	1.00	49.92
	3878	CB	LEU	B	105	42.503	79.354	10.385	1.00	78.62
	3879	CG	LEU	B	105	41.409	79.667	11.381	1.00	78.62
	3880	CD1	LEU	B	105	40.828	81.064	11.137	1.00	78.62
	3881	CD2	LEU	B	105	40.368	78.612	11.223	1.00	78.62
40	3882	C	LEU	B	105	44.224	77.773	9.580	1.00	49.92
	3883	O	LEU	B	105	45.327	78.095	9.991	1.00	49.92
	3884	N	ARG	B	106	44.051	77.317	8.355	1.00	79.70
	3885	CA	ARG	B	106	45.195	77.131	7.494	1.00	79.70
	3886	CB	ARG	B	106	45.537	75.649	7.475	1.00	126.47
45	3887	CG	ARG	B	106	46.633	75.284	6.526	1.00	126.47
	3888	CD	ARG	B	106	46.738	73.775	6.383	1.00	126.47
	3889	NE	ARG	B	106	47.760	73.414	5.412	1.00	126.47
	3890	CZ	ARG	B	106	47.802	72.255	4.773	1.00	126.47
	3891	NH1	ARG	B	106	46.869	71.343	5.006	1.00	126.47
50	3892	NH2	ARG	B	106	48.768	72.018	3.891	1.00	126.47
	3893	C	ARG	B	106	44.800	77.615	6.083	1.00	79.70
	3894	O	ARG	B	106	43.899	77.192	5.483	1.00	79.70
	3895	N	CYS	B	107	45.730	78.518	5.553	1.00	64.58
	3896	CA	CYS	B	107	45.507	78.971	4.177	1.00	64.58
55	3897	C	CYS	B	107	46.217	77.938	3.331	1.00	64.58
	3898	O	CYS	B	107	47.442	77.869	3.318	1.00	64.58
	3899	CB	CYS	B	107	46.087	80.353	3.919	1.00	64.58
	3900	SG	CYS	B	107	45.402	81.142	2.422	1.00	107.35
	3901	N	HIS	B	108	45.435	77.124	2.639	1.00	107.35
60	3902	CA	HIS	B	108	45.970	76.037	1.845	1.00	77.57
	3903	CB	HIS	B	108	45.151	74.790	2.131	1.00	77.57
	3904	OG	HIS	B	108	45.702	73.548	1.513	1.00	100.22
	3905	CD2	HIS	B	108	45.138	72.631	0.691	1.00	100.22
	3906	ND1	HIS	B	108	46.977	73.098	1.776	1.00	100.22
65	3907	CE1	HIS	B	108	47.170	71.951	1.149	1.00	100.22
	3908	NE2	HIS	B	108	46.070	71.645	0.483	1.00	100.22
	3909	C	HIS	B	108	46.002	76.296	0.352	1.00	77.57
	3910	O	HIS	B	108	44.981	76.659	-0.262	1.00	77.57
	3911	N	GLY	B	109	47.180	76.079	-0.231	1.00	82.92
70	3912	CA	GLY	B	109	47.338	76.303	-1.652	1.00	82.92
	3913	C	GLY	B	109	47.018	75.057	-2.430	1.00	82.92
	3914	O	GLY	B	109	47.115	73.962	-1.886	1.00	82.92

	3915	N	TRP	B	110	46.628	75.221	-3.692	1.00	89.13
	3916	CA	TRP	B	110	46.294	74.086	-4.536	1.00	89.13
	3917	CB	TRP	B	110	45.749	74.564	-5.874	1.00	136.31
	3918	CG	TRP	B	110	45.538	73.457	-6.838	1.00	136.31
5	3919	CD2	TRP	B	110	44.323	72.730	-7.054	1.00	136.31
	3920	CE2	TRP	B	110	44.590	71.748	-8.028	1.00	136.31
	3921	CE3	TRP	B	110	43.025	72.815	-6.517	1.00	136.31
	3922	CD1	TRP	B	110	46.464	72.907	-7.659	1.00	136.31
	3923	NE1	TRP	B	110	45.908	71.879	-8.380	1.00	136.31
10	3924	CZ2	TRP	B	110	43.615	70.853	-8.484	1.00	136.31
	3925	CZ3	TRP	B	110	42.052	71.923	-6.969	1.00	136.31
	3926	CH2	TRP	B	110	42.356	70.954	-7.943	1.00	136.31
	3927	C	TRP	B	110	47.525	73.218	-4.759	1.00	89.13
	3928	O	TRP	B	110	48.662	73.698	-4.730	1.00	89.13
15	3929	N	ARG	B	111	47.294	71.927	-4.960	1.00	107.42
	3930	CA	ARG	B	111	48.376	70.980	-5.192	1.00	107.42
	3931	CB	ARG	B	111	48.900	71.128	-6.598	1.00	249.40
	3932	CG	ARG	B	111	48.148	70.283	-7.546	1.00	249.40
	3933	CD	ARG	B	111	48.856	70.281	-8.825	1.00	249.40
20	3934	NE	ARG	B	111	48.857	68.940	-9.379	1.00	249.40
	3935	CZ	ARG	B	111	49.507	67.898	-8.862	1.00	249.40
	3936	NH1	ARG	B	111	50.222	68.039	-7.753	1.00	249.40
	3937	NH2	ARG	B	111	49.435	66.714	-9.465	1.00	249.40
	3938	C	ARG	B	111	49.528	71.110	-4.237	1.00	107.42
25	3939	O	ARG	B	111	50.645	70.724	-4.550	1.00	107.42
	3940	N	ASN	B	112	49.249	71.676	-3.075	1.00	103.89
	3941	CA	ASN	B	112	50.250	71.869	-2.050	1.00	103.89
	3942	CB	ASN	B	112	50.805	70.525	-1.599	1.00	101.72
	3943	CG	ASN	B	112	51.387	70.592	-0.214	1.00	101.72
30	3944	OD1	ASN	B	112	51.759	71.673	0.261	1.00	101.72
	3945	ND2	ASN	B	112	51.479	69.442	0.449	1.00	101.72
	3946	C	ASN	B	112	51.405	72.778	-2.470	1.00	103.89
	3947	O	ASN	B	112	52.504	72.698	-1.905	1.00	103.89
	3948	N	TRP	B	113	51.177	73.636	-3.460	1.00	84.24
35	3949	CA	TRP	B	113	52.232	74.553	-3.854	1.00	84.24
	3950	CB	TRP	B	113	51.806	75.411	-5.031	1.00	165.30
	3951	CG	TRP	B	113	51.859	74.694	-6.297	1.00	165.30
	3952	CD2	TRP	B	113	50.952	74.827	-7.383	1.00	165.30
	3953	CE2	TRP	B	113	51.420	73.995	-8.423	1.00	165.30
40	3954	CE3	TRP	B	113	49.785	75.580	-7.589	1.00	165.30
	3955	CD1	TRP	B	113	52.816	73.805	-6.695	1.00	165.30
	3956	NE1	TRP	B	113	52.561	73.380	-7.973	1.00	165.30
	3957	CZ2	TRP	B	113	50.763	73.890	-9.652	1.00	165.30
	3958	CZ3	TRP	B	113	49.128	75.478	-8.808	1.00	165.30
45	3959	CH2	TRP	B	113	43.619	74.634	-9.826	1.00	165.30
	3960	C	TRP	B	113	52.597	75.473	-2.697	1.00	84.24
	3961	O	TRP	B	113	52.201	75.258	-1.543	1.00	84.24
	3962	N	ASP	B	114	53.370	76.501	-3.013	1.00	127.07
	3963	CA	ASP	B	114	53.773	77.459	-2.006	1.00	127.07
50	3964	CB	ASP	B	114	55.289	77.629	-2.007	1.00	190.00
	3965	CG	ASP	B	114	55.992	76.535	-1.236	1.00	190.00
	3966	OD1	ASP	B	114	55.702	76.387	-0.030	1.00	190.00
	3967	OD2	ASP	B	114	56.831	75.825	-1.829	1.00	190.00
	3968	C	ASP	B	114	53.098	78.794	-2.255	1.00	127.07
55	3969	O	ASP	B	114	52.985	79.253	-3.402	1.00	127.07
	3970	N	VAL	B	115	52.641	79.406	-1.165	1.00	97.38
	3971	CA	VAL	B	115	51.969	80.696	-1.229	1.00	97.38
	3972	CB	VAL	B	115	50.571	80.635	-0.623	1.00	112.10
	3973	CG1	VAL	B	115	49.833	81.905	-0.946	1.00	112.10
60	3974	CG2	VAL	B	115	49.830	79.436	-1.155	1.00	112.10
	3975	C	VAL	B	115	52.767	81.723	-0.451	1.00	97.38
	3976	O	VAL	B	115	53.333	81.428	0.613	1.00	97.38
	3977	N	TYR	B	116	52.804	82.940	-0.985	1.00	76.30
	3978	CA	TYR	B	116	53.547	84.019	-0.335	1.00	76.30
65	3979	CB	TYR	B	116	54.745	84.433	-1.206	1.00	116.08
	3980	CG	TYR	B	116	55.758	83.328	-1.431	1.00	116.08
	3981	CD1	TYR	B	116	55.720	82.529	-2.581	1.00	116.08
	3982	CE1	TYR	B	116	56.634	81.486	-2.770	1.00	116.08
	3983	CD2	TYR	B	116	56.736	83.061	-0.476	1.00	116.08
70	3984	CE2	TYR	B	116	57.657	82.024	-0.650	1.00	116.08

	3985	CZ	TYR	B	116	57.602	81.238	-1.798	1.00	116.08
	3986	OH	TYR	B	116	58.498	80.201	-1.964	1.00	116.08
	3987	C	TYR	B	116	52.654	85.227	-0.059	1.00	76.30
5	3988	O	TYR	B	116	51.502	85.276	-0.514	1.00	76.30
	3989	N	LYS	B	117	53.193	86.190	0.692	1.00	87.81
	3990	CA	LYS	B	117	52.463	87.411	1.036	1.00	87.81
	3991	CB	LYS	B	117	52.371	88.354	-0.171	1.00	224.81
	3992	CG	LYS	B	117	53.560	89.283	-0.373	1.00	224.81
	3993	CD	LYS	B	117	53.183	90.436	-1.295	1.00	224.81
10	3994	CE	LYS	B	117	52.028	91.248	-0.711	1.00	224.81
	3995	NZ	LYS	B	117	51.604	92.373	-1.593	1.00	224.81
	3996	C	LYS	B	117	51.059	87.049	1.489	1.00	87.81
	3997	O	LYS	B	117	50.060	87.542	0.946	1.00	87.81
	3998	N	VAL	B	118	50.983	86.194	2.498	1.00	60.09
15	3999	CA	VAL	B	118	49.696	85.737	2.994	1.00	60.09
	4000	CB	VAL	B	118	49.815	84.344	3.577	1.00	85.68
	4001	CG1	VAL	B	118	48.782	84.141	4.647	1.00	85.68
	4002	CG2	VAL	B	118	49.604	83.325	2.485	1.00	85.68
	4003	C	VAL	B	118	49.066	86.622	4.034	1.00	60.09
20	4004	O	VAL	B	118	49.752	87.066	4.963	1.00	60.09
	4005	N	ILE	B	119	47.753	86.837	3.901	1.00	64.26
	4006	CA	ILE	B	119	47.003	87.686	4.830	1.00	64.26
	4007	CB	ILE	B	119	46.704	89.027	4.196	1.00	68.56
	4008	CG2	ILE	B	119	46.039	89.920	5.184	1.00	68.56
25	4009	CG1	ILE	B	119	47.998	89.654	3.705	1.00	68.56
	4010	CD1	ILE	B	119	47.766	90.828	2.843	1.00	68.56
	4011	C	ILE	B	119	45.672	87.052	5.173	1.00	64.26
	4012	O	ILE	B	119	44.890	86.771	4.259	1.00	64.26
	4013	N	TYR	B	120	45.402	86.803	6.458	1.00	74.17
30	4014	CA	TYR	B	120	44.110	86.216	6.816	1.00	74.17
	4015	CB	TYR	B	120	44.176	85.345	8.066	1.00	67.28
	4016	CG	TYR	B	120	44.901	84.067	7.887	1.00	67.28
	4017	CD1	TYR	B	120	46.269	84.024	8.002	1.00	67.28
	4018	CE1	TYR	B	120	46.975	82.840	7.818	1.00	67.28
35	4019	CD2	TYR	B	120	44.225	82.896	7.582	1.00	67.28
	4020	CE2	TYR	B	120	44.909	81.695	7.390	1.00	67.28
	4021	CZ	TYR	B	120	46.286	81.680	7.511	1.00	67.28
	4022	OH	TYR	B	120	46.966	80.507	7.340	1.00	67.28
	4023	C	TYR	B	120	43.185	87.348	7.125	1.00	74.17
40	4024	O	TYR	B	120	43.613	88.351	7.669	1.00	74.17
	4025	N	TYR	B	121	41.916	87.180	6.799	1.00	60.66
	4026	CA	TYR	B	121	40.938	88.213	7.080	1.00	60.66
	4027	CB	TYR	B	121	40.355	88.760	5.776	1.00	108.81
	4028	CG	TYR	B	121	41.299	89.557	4.908	1.00	108.81
45	4029	CD1	TYR	B	121	42.398	88.961	4.308	1.00	108.81
	4030	CE1	TYR	B	121	43.239	89.678	3.449	1.00	108.81
	4031	CD2	TYR	B	121	41.058	90.900	4.640	1.00	108.81
	4032	CE2	TYR	B	121	41.890	91.629	3.788	1.00	108.81
	4033	CZ	TYR	B	121	42.976	91.009	3.195	1.00	108.81
50	4034	OH	TYR	B	121	43.794	91.710	2.340	1.00	108.81
	4035	C	TYR	B	121	39.781	87.692	7.936	1.00	60.66
	4036	O	TYR	B	121	39.301	86.560	7.736	1.00	60.66
	4037	N	LYS	B	122	39.332	88.510	8.885	1.00	76.13
	4038	CA	LYS	B	122	38.194	88.138	9.715	1.00	76.13
55	4039	CB	LYS	B	122	38.594	87.874	11.168	1.00	102.31
	4040	CG	LYS	B	122	37.410	87.462	12.032	1.00	102.31
	4041	CD	LYS	B	122	37.738	87.523	13.489	1.00	102.31
	4042	CE	LYS	B	122	36.509	87.285	14.327	1.00	102.31
	4043	NZ	LYS	B	122	36.834	87.504	15.762	1.00	102.31
60	4044	C	LYS	B	122	37.200	89.289	9.679	1.00	76.13
	4045	O	LYS	B	122	37.507	90.390	10.145	1.00	76.13
	4046	N	ASP	B	123	36.013	89.034	9.131	1.00	98.55
	4047	CA	ASP	B	123	34.968	90.049	9.023	1.00	98.55
	4048	CB	ASP	B	123	34.492	90.473	10.414	1.00	136.85
65	4049	CG	ASP	B	123	33.604	89.429	11.059	1.00	136.85
	4050	OD1	ASP	B	123	32.692	88.925	10.363	1.00	136.85
	4051	OD2	ASP	B	123	33.810	89.122	12.256	1.00	136.85
	4052	C	ASP	B	123	35.420	91.268	8.217	1.00	98.55
	4053	O	ASP	B	123	35.168	92.418	8.597	1.00	98.55
70	4054	N	GLY	B	124	36.094	90.997	7.099	1.00	109.74

	4055	CA	GLY	B	124	36.578	92.050	6.224	1.00	109.74
	4056	C	GLY	B	124	37.817	92.800	6.688	1.00	109.74
	4057	O	GLY	B	124	38.371	93.600	5.938	1.00	109.74
	4058	N	GLU	B	125	38.269	92.542	7.911	1.00	80.11
5	4059	CA	GLU	B	125	39.438	93.230	8.468	1.00	80.11
	4060	CB	GLU	B	125	39.276	93.432	9.990	1.00	173.35
	4061	CG	GLU	B	125	38.192	94.412	10.446	1.00	173.35
	4062	CD	GLU	B	125	38.621	95.865	10.344	1.00	173.35
	4063	OE1	GLU	B	125	39.591	96.256	11.030	1.00	173.35
10	4064	OE2	GLU	B	125	37.982	96.615	9.577	1.00	173.35
	4065	C	GLU	B	125	40.723	92.462	8.243	1.00	80.11
	4066	O	GLU	B	125	40.728	91.235	8.308	1.00	80.11
	4067	N	ALA	B	126	41.817	93.171	7.986	1.00	116.19
	4068	CA	ALA	B	126	43.101	92.501	7.826	1.00	116.19
15	4069	CB	ALA	B	126	44.165	93.513	7.450	1.00	157.65
	4070	C	ALA	B	126	43.385	91.901	9.216	1.00	116.19
	4071	O	ALA	B	126	43.051	92.516	10.227	1.00	116.19
	4072	N	LEU	B	127	43.985	90.715	9.286	1.00	101.69
	4073	CA	LEU	B	127	44.246	90.109	10.586	1.00	101.69
20	4074	CB	LEU	B	127	43.383	88.875	10.761	1.00	85.89
	4075	CG	LEU	B	127	43.207	88.660	12.259	1.00	85.89
	4076	CD1	LEU	B	127	42.594	89.929	12.853	1.00	85.89
	4077	CD2	LEU	B	127	42.337	87.450	12.551	1.00	85.89
	4078	C	LEU	B	127	45.696	89.750	10.902	1.00	101.69
25	4079	O	LEU	B	127	46.240	90.197	11.910	1.00	101.69
	4080	N	LYS	B	128	46.306	88.916	10.070	1.00	84.42
	4081	CA	LYS	B	128	47.701	88.530	10.256	1.00	84.42
	4082	CB	LYS	B	128	47.794	87.118	10.847	1.00	200.20
	4083	CG	LYS	B	128	47.160	86.955	12.220	1.00	200.20
30	4084	CD	LYS	B	128	47.968	87.634	13.317	1.00	200.20
	4085	CE	LYS	B	128	47.352	87.350	14.684	1.00	200.20
	4086	NZ	LYS	B	128	48.172	87.864	15.817	1.00	200.20
	4087	C	LYS	B	128	48.360	88.558	8.877	1.00	84.42
	4088	O	LYS	B	128	47.675	88.404	7.853	1.00	84.42
35	4089	N	TYR	B	129	49.675	88.750	8.839	1.00	107.40
	4090	CA	TYR	B	129	50.387	88.773	7.566	1.00	107.40
	4091	CB	TYR	B	129	50.519	90.208	7.067	1.00	112.63
	4092	CG	TYR	B	129	51.618	90.368	6.043	1.00	112.63
	4093	CD1	TYR	B	129	51.417	90.021	4.712	1.00	112.63
40	4094	CE1	TYR	B	129	52.442	90.116	3.781	1.00	112.63
	4095	CD2	TYR	B	129	52.879	90.814	6.422	1.00	112.63
	4096	CE2	TYR	B	129	53.915	90.911	5.502	1.00	112.63
	4097	CZ	TYR	B	129	53.693	90.562	4.183	1.00	112.63
	4098	OH	TYR	B	129	54.719	90.665	3.260	1.00	112.63
45	4099	C	TYR	B	129	51.779	88.146	7.621	1.00	107.40
	4100	O	TYR	B	129	52.518	88.373	8.575	1.00	107.40
	4101	N	TRP	B	130	52.138	87.376	6.587	1.00	87.42
	4102	CA	TRP	B	130	53.454	86.735	6.524	1.00	87.42
	4103	CB	TRP	B	130	53.400	85.311	7.090	1.00	190.57
50	4104	CG	TRP	B	130	52.744	85.171	8.423	1.00	190.57
	4105	CD2	TRP	B	130	53.401	84.954	9.674	1.00	190.57
	4106	CE2	TRP	B	130	52.392	84.829	10.656	1.00	190.57
	4107	CE3	TRP	B	130	54.746	84.861	10.062	1.00	190.57
	4108	CD1	TRP	B	130	51.406	85.166	8.687	1.00	190.57
55	4109	NE1	TRP	B	130	51.185	84.959	10.025	1.00	190.57
	4110	CZ2	TRP	B	130	52.686	84.607	12.010	1.00	190.57
	4111	CZ3	TRP	B	130	55.041	84.641	11.412	1.00	190.57
	4112	CH2	TRP	B	130	54.011	84.510	12.366	1.00	190.57
	4113	C	TRP	B	130	53.968	86.652	5.085	1.00	87.42
60	4114	O	TRP	B	130	53.209	86.847	4.127	1.00	87.42
	4115	N	TYR	B	131	55.259	86.362	4.940	1.00	97.57
	4116	CA	TYR	B	131	55.848	86.212	3.621	1.00	97.57
	4117	CB	TYR	B	131	57.339	86.504	3.647	1.00	249.42
	4118	CG	TYR	B	131	57.881	86.590	2.250	1.00	249.42
65	4119	CD1	TYR	B	131	57.611	87.707	1.453	1.00	249.42
	4120	CE1	TYR	B	131	57.982	87.746	0.133	1.00	249.42
	4121	CD2	TYR	B	131	58.554	85.514	1.676	1.00	249.42
	4122	CE2	TYR	B	131	58.929	85.544	0.355	1.00	249.42
	4123	CZ	TYR	B	131	58.628	86.660	-0.404	1.00	249.42
70	4124	OH	TYR	B	131	58.902	86.675	-1.726	1.00	249.42

	4125	C	TYR	B	131	55.619	84.751	3.231	1.00	97.57
	4126	O	TYR	B	131	54.661	84.439	2.509	1.00	97.57
	4127	N	GLU	B	132	56.517	83.862	3.669	1.00	249.33
	4128	CA	GLU	B	132	56.333	82.428	3.432	1.00	249.33
5	4129	CB	GLU	B	132	57.528	81.602	3.941	1.00	249.46
	4130	CG	GLU	B	132	58.788	81.623	3.066	1.00	249.46
	4131	CD	GLU	B	132	59.162	80.239	2.532	1.00	249.46
	4132	OE1	GLU	B	132	58.693	79.231	3.102	1.00	249.46
	4133	OE2	GLU	B	132	59.935	80.161	1.551	1.00	249.46
10	4134	C	GLU	B	132	55.158	82.276	4.384	1.00	249.33
	4135	O	GLU	B	132	55.259	82.685	5.543	1.00	249.33
	4136	N	ASN	B	133	54.047	81.711	3.924	1.00	134.43
	4137	CA	ASN	B	133	52.884	81.642	4.798	1.00	134.43
	4138	CB	ASN	B	133	51.649	81.176	4.033	1.00	135.42
15	4139	CG	ASN	B	133	51.534	79.690	3.981	1.00	135.42
	4140	OD1	ASN	B	133	52.489	78.995	3.617	1.00	135.42
	4141	ND2	ASN	B	133	50.358	79.176	4.337	1.00	135.42
	4142	C	ASN	B	133	53.019	80.848	6.080	1.00	134.43
	4143	O	ASN	B	133	54.026	80.185	6.338	1.00	134.43
20	4144	N	HIS	B	134	51.962	80.932	6.875	1.00	135.01
	4145	CA	HIS	B	134	51.905	80.302	8.174	1.00	135.01
	4146	CB	HIS	B	134	52.150	81.381	9.224	1.00	225.09
	4147	CG	HIS	B	134	52.262	80.865	10.622	1.00	225.09
	4148	CD2	HIS	B	134	51.493	81.086	11.714	1.00	225.09
25	4149	ND1	HIS	B	134	53.283	80.038	11.032	1.00	225.09
	4150	CE1	HIS	B	134	53.140	79.772	12.320	1.00	225.09
	4151	NE2	HIS	B	134	52.063	80.396	12.756	1.00	225.09
	4152	C	HIS	B	134	50.531	79.673	8.355	1.00	135.01
	4153	O	HIS	B	134	49.789	79.494	7.385	1.00	135.01
30	4154	N	ASN	B	135	50.197	79.346	9.601	1.00	105.44
	4155	CA	ASN	B	135	48.928	78.730	9.922	1.00	105.44
	4156	CB	ASN	B	135	49.090	77.209	10.001	1.00	235.21
	4157	CG	ASN	B	135	49.415	76.600	8.653	1.00	235.21
35	4158	OD1	ASN	B	135	48.779	76.948	7.657	1.00	235.21
	4159	ND2	ASN	B	135	50.383	75.689	8.604	1.00	235.21
	4160	C	ASN	B	135	48.399	79.280	11.223	1.00	105.44
	4161	O	ASN	B	135	48.611	78.700	12.279	1.00	105.44
	4162	N	ILE	B	136	47.718	80.417	11.134	1.00	66.02
	4163	CA	ILE	B	136	47.123	81.076	12.304	1.00	66.02
40	4164	CB	ILE	B	136	46.015	82.066	11.860	1.00	141.15
	4165	CG2	ILE	B	136	45.045	81.385	10.926	1.00	141.15
	4166	CG1	ILE	B	136	45.283	82.620	13.068	1.00	141.15
	4167	CD1	ILE	B	136	44.290	83.673	12.695	1.00	141.15
	4168	C	ILE	B	136	46.555	80.069	13.307	1.00	66.02
45	4169	O	ILE	B	136	45.602	79.339	13.022	1.00	66.02
	4170	N	SER	B	137	47.160	80.045	14.486	1.00	95.21
	4171	CA	SER	B	137	46.768	79.114	15.538	1.00	95.21
	4172	CB	SER	B	137	47.968	78.233	15.897	1.00	97.51
	4173	OG	SER	B	137	47.742	77.531	17.105	1.00	97.51
50	4174	C	SER	B	137	46.218	79.776	16.807	1.00	95.21
	4175	O	SER	B	137	46.625	80.869	17.185	1.00	95.21
	4176	N	ILE	B	138	45.298	79.095	17.472	1.00	236.44
	4177	CA	ILE	B	138	44.698	79.625	18.688	1.00	236.44
	4178	CB	ILE	B	138	43.295	80.153	18.420	1.00	113.67
55	4179	CG2	ILE	B	138	42.601	80.445	19.737	1.00	113.67
	4180	CG1	ILE	B	138	43.363	81.397	17.533	1.00	113.67
	4181	CD1	ILE	B	138	42.021	81.787	16.948	1.00	113.67
	4182	C	ILE	B	138	44.580	78.558	19.761	1.00	236.44
	4183	O	ILE	B	138	43.936	77.531	19.555	1.00	236.44
60	4184	N	THR	B	139	45.180	78.816	20.915	1.00	117.60
	4185	CA	THR	B	139	45.131	77.865	22.018	1.00	117.60
	4186	CB	THR	B	139	46.259	78.143	23.020	1.00	212.12
	4187	OG1	THR	B	139	46.227	79.521	23.406	1.00	212.12
	4188	CG2	THR	B	139	47.609	77.830	22.390	1.00	212.12
65	4189	C	THR	B	139	43.780	77.942	22.733	1.00	117.60
	4190	O	THR	B	139	42.898	77.092	22.541	1.00	117.60
	4191	N	ASN	B	140	43.633	78.960	23.573	1.00	147.27
	4192	CA	ASN	B	140	42.396	79.189	24.308	1.00	147.27
	4193	CB	ASN	B	140	42.685	79.890	25.631	1.00	247.00
70	4194	CG	ASN	B	140	41.426	80.263	26.369	1.00	247.00

	4195	OD1	ASN	B	140	40.498	80.833	25.789	1.00	247.00
	4196	ND2	ASN	B	140	41.395	79.951	27.658	1.00	247.00
	4197	C	ASN	B	140	41.572	80.103	23.421	1.00	147.27
	4198	O	ASN	B	140	42.004	81.206	23.092	1.00	147.27
5	4199	N	ALA	B	141	40.383	79.652	23.048	1.00	102.95
	4200	CA	ALA	B	141	39.537	80.432	22.163	1.00	102.95
	4201	CB	ALA	B	141	38.862	79.519	21.162	1.00	101.29
	4202	C	ALA	B	141	38.493	81.273	22.850	1.00	102.95
	4203	O	ALA	B	141	37.722	80.782	23.680	1.00	102.95
10	4204	N	THR	B	142	38.458	82.546	22.474	1.00	139.44
	4205	CA	THR	B	142	37.495	83.478	23.021	1.00	139.44
	4206	CB	THR	B	142	38.055	84.903	22.959	1.00	140.37
	4207	OG1	THR	B	142	39.366	84.918	23.544	1.00	140.37
	4208	CG2	THR	B	142	37.166	85.858	23.725	1.00	140.37
15	4209	C	THR	B	142	36.220	83.361	22.184	1.00	139.44
	4210	O	THR	B	142	36.216	82.675	21.160	1.00	139.44
	4211	N	VAL	B	143	35.132	83.988	22.623	1.00	168.09
	4212	CA	VAL	B	143	33.884	83.922	21.866	1.00	168.09
	4213	CB	VAL	B	143	32.633	84.134	22.755	1.00	243.26
20	4214	CG1	VAL	B	143	32.616	85.552	23.305	1.00	243.26
	4215	CG2	VAL	B	143	31.366	83.867	21.946	1.00	243.26
	4216	C	VAL	B	143	33.925	85.029	20.834	1.00	168.09
	4217	O	VAL	B	143	33.150	85.035	19.878	1.00	168.09
	4218	N	GLU	B	144	34.839	85.971	21.035	1.00	126.58
25	4219	CA	GLU	B	144	34.975	87.081	20.108	1.00	126.58
	4220	CB	GLU	B	144	35.750	88.229	20.751	1.00	249.26
	4221	CG	GLU	B	144	35.040	88.850	21.840	1.00	249.26
	4222	CD	GLU	B	144	35.771	88.603	23.243	1.00	249.26
	4223	OE1	GLU	B	144	36.942	89.024	23.353	1.00	249.26
30	4224	OE2	GLU	B	144	35.181	87.989	24.157	1.00	249.26
	4225	C	GLU	B	144	35.673	86.623	18.840	1.00	126.58
	4226	O	GLU	B	144	35.633	87.305	17.826	1.00	126.58
	4227	N	ASP	B	145	36.307	85.457	18.903	1.00	80.30
	4228	CA	ASP	B	145	36.997	84.893	17.752	1.00	80.30
35	4229	CB	ASP	B	145	37.911	83.753	18.189	1.00	204.44
	4230	CG	ASP	B	145	39.132	84.250	18.918	1.00	204.44
	4231	OD1	ASP	B	145	39.896	85.030	18.310	1.00	204.44
	4232	OD2	ASP	B	145	39.326	83.869	20.092	1.00	204.44
	4233	C	ASP	B	145	36.026	84.395	16.699	1.00	80.30
40	4234	O	ASP	B	145	36.421	84.133	15.569	1.00	80.30
	4235	N	SER	B	146	34.755	84.263	17.062	1.00	110.67
	4236	CA	SER	B	146	33.761	83.800	16.108	1.00	110.67
	4237	CB	SER	B	146	32.421	83.569	16.815	1.00	166.23
	4238	OG	SER	B	146	32.547	82.573	17.814	1.00	166.23
45	4239	C	SER	B	146	33.646	84.870	15.022	1.00	110.67
	4240	O	SER	B	146	33.736	86.063	15.302	1.00	110.67
	4241	N	GLY	B	147	33.487	84.436	13.778	1.00	85.62
	4242	CA	GLY	B	147	33.375	85.365	12.670	1.00	85.62
	4243	C	GLY	B	147	33.473	84.635	11.353	1.00	85.62
50	4244	O	GLY	B	147	33.311	83.417	11.301	1.00	85.62
	4245	N	THR	B	148	33.737	85.372	10.279	1.00	63.43
	4246	CA	THR	B	148	33.851	84.756	8.952	1.00	63.43
	4247	CB	THR	B	148	32.729	85.244	7.841	1.00	111.42
	4248	OG1	THR	B	148	33.253	86.223	7.103	1.00	111.42
55	4249	CG2	THR	B	148	31.609	85.879	8.767	1.00	111.42
	4250	C	THR	B	148	35.227	85.092	8.397	1.00	63.43
	4251	O	THR	B	148	35.568	86.244	8.176	1.00	63.43
	4252	N	TYR	B	149	36.024	84.069	8.183	1.00	61.50
	4253	CA	TYR	B	149	37.366	84.273	7.705	1.00	61.50
60	4254	CB	TYR	B	149	38.298	83.380	8.514	1.00	61.70
	4255	CG	TYR	B	149	38.353	83.629	10.007	1.00	61.70
	4256	CD1	TYR	B	149	37.273	83.361	10.839	1.00	61.70
	4257	CE1	TYR	B	149	37.373	83.572	12.217	1.00	61.70
	4258	CD2	TYR	B	149	39.514	84.106	10.587	1.00	61.70
65	4259	CE2	TYR	B	149	39.626	84.317	11.939	1.00	61.70
	4260	CZ	TYR	B	149	38.571	84.060	12.757	1.00	61.70
	4261	OH	TYR	B	149	38.744	84.327	14.104	1.00	61.70
	4262	C	TYR	B	149	37.540	83.934	6.223	1.00	61.50
	4263	O	TYR	B	149	36.666	83.307	5.605	1.00	61.50
70	4264	N	TYR	B	150	38.674	84.372	5.669	1.00	57.66

	4265	CA	TYR	B	150	39.090	84.071	4.302	1.00	57.66
	4266	CB	TYR	B	150	38.189	84.760	3.264	1.00	101.41
	4267	CG	TYR	B	150	38.386	86.234	3.018	1.00	101.41
	4268	CD1	TYR	B	150	39.493	86.704	2.338	1.00	101.41
5	4269	CE1	TYR	B	150	39.653	88.065	2.074	1.00	101.41
	4270	CD2	TYR	B	150	37.435	87.160	3.428	1.00	101.41
	4271	CE2	TYR	B	150	37.582	88.520	3.163	1.00	101.41
	4272	CZ	TYR	B	150	38.693	88.967	2.489	1.00	101.41
	4273	OH	TYR	B	150	38.855	90.316	2.245	1.00	101.41
10	4274	C	TYR	B	150	40.539	84.536	4.251	1.00	57.66
	4275	O	TYR	B	150	40.952	85.331	5.109	1.00	57.66
	4276	N	CYS	B	151	41.340	84.020	3.318	1.00	78.79
	4277	CA	CYS	B	151	42.736	84.458	3.227	1.00	78.79
	4278	C	CYS	B	151	43.124	84.856	1.804	1.00	78.79
15	4279	O	CYS	B	151	42.464	84.461	0.849	1.00	78.79
	4280	CB	CYS	B	151	43.680	83.369	3.736	1.00	103.97
	4281	SG	CYS	B	151	43.510	81.730	2.951	1.00	103.97
	4282	N	THR	B	152	44.174	85.668	1.673	1.00	109.05
	4283	CA	THR	B	152	44.663	86.107	0.370	1.00	109.05
20	4284	CB	THR	B	152	44.524	87.630	0.206	1.00	169.15
	4285	OG1	THR	B	152	45.394	88.296	1.133	1.00	169.15
	4286	CG2	THR	B	152	43.097	88.056	0.475	1.00	169.15
	4287	C	THR	B	152	46.139	85.728	0.297	1.00	109.05
	4288	O	THR	B	152	46.839	85.740	1.317	1.00	109.05
25	4289	N	GLY	B	153	46.611	85.381	-0.898	1.00	135.93
	4290	CA	GLY	B	153	48.007	85.000	-1.054	1.00	135.93
	4291	C	GLY	B	153	48.447	85.023	-2.501	1.00	135.93
	4292	O	GLY	B	153	47.618	85.025	-3.404	1.00	135.93
	4293	N	LYS	B	154	49.751	85.038	-2.734	1.00	88.42
30	4294	CA	LYS	B	154	50.252	85.068	-4.096	1.00	88.42
	4295	CB	LYS	B	154	51.392	86.090	-4.216	1.00	187.09
	4296	CG	LYS	B	154	51.920	86.317	-5.630	1.00	187.09
	4297	CD	LYS	B	154	53.003	87.393	-5.619	1.00	187.09
	4298	CE	LYS	B	154	53.634	87.579	-6.975	1.00	187.09
35	4299	NZ	LYS	B	154	54.766	88.490	-6.839	1.00	187.09
	4300	C	LYS	B	154	50.744	83.673	-4.404	1.00	88.42
	4301	O	LYS	B	154	51.450	83.057	-3.592	1.00	88.42
	4302	N	VAL	B	155	50.332	83.166	-5.561	1.00	135.91
	4303	CA	VAL	B	155	50.742	81.845	-6.018	1.00	135.91
40	4304	CB	VAL	B	155	49.550	80.923	-6.254	1.00	118.28
	4305	CG1	VAL	B	155	50.030	79.574	-6.748	1.00	118.28
	4306	CG2	VAL	B	155	48.773	80.767	-4.968	1.00	118.28
	4307	C	VAL	B	155	51.459	82.067	-7.332	1.00	135.91
	4308	O	VAL	B	155	50.938	82.731	-8.237	1.00	135.91
45	4309	N	TRP	B	156	52.655	81.505	-7.433	1.00	121.66
	4310	CA	TRP	B	156	53.453	81.702	-8.624	1.00	121.66
	4311	CB	TRP	B	156	52.679	81.359	-9.884	1.00	200.98
	4312	CG	TRP	B	156	52.385	79.963	-9.953	1.00	200.98
	4313	CD2	TRP	B	156	53.333	78.905	-9.901	1.00	200.98
50	4314	CE2	TRP	B	156	52.609	77.699	-9.839	1.00	200.98
	4315	CE3	TRP	B	156	54.730	78.860	-9.823	1.00	200.98
	4316	CD1	TRP	B	156	51.160	79.393	-10.027	1.00	200.98
	4317	NE1	TRP	B	156	51.283	78.024	-10.013	1.00	200.98
	4318	CZ2	TRP	B	156	53.232	76.454	-9.905	1.00	200.98
55	4319	CZ3	TRP	B	156	55.352	77.622	-9.790	1.00	200.98
	4320	CH2	TRP	B	156	54.59b	76.432	-9.834	1.00	200.98
	4321	C	TRP	B	156	53.739	83.168	-8.671	1.00	121.66
	4322	O	TRP	B	156	54.677	83.647	-8.029	1.00	121.66
	4323	N	GLN	B	157	52.883	83.878	-9.403	1.00	111.84
60	4324	CA	GLN	B	157	53.057	85.297	-9.568	1.00	111.84
	4325	CB	GLN	B	157	53.912	85.525	-10.808	1.00	249.48
	4326	CG	GLN	B	157	55.364	85.155	-10.531	1.00	249.48
	4327	CD	GLN	B	157	55.818	85.806	-9.260	1.00	249.48
	4328	OE1	GLN	B	157	55.599	86.983	-9.081	1.00	249.48
65	4329	NE2	GLN	B	157	56.437	85.047	-8.360	1.00	249.48
	4330	C	GLN	B	157	51.781	86.092	-9.614	1.00	111.84
	4331	O	GLN	B	157	51.785	87.265	-9.988	1.00	111.84
	4332	N	LEU	B	158	50.688	85.447	-9.217	1.00	140.68
	4333	CA	LEU	B	158	49.392	86.104	-9.195	1.00	140.68
70	4334	CB	LEU	B	158	48.463	85.512	-10.253	1.00	225.85

	4335	CG	LEU	B	158	48.673	85.926	-11.710	1.00	225.85
	4336	CD1	LEU	B	158	47.296	86.093	-12.325	1.00	225.85
	4337	CD2	LEU	B	158	49.447	87.239	-11.827	1.00	225.85
5	4338	C	LEU	B	158	48.724	86.035	-7.829	1.00	140.68
	4339	O	LEU	B	158	48.980	85.125	-7.039	1.00	140.68
	4340	N	ASP	B	159	47.870	87.017	-7.560	1.00	142.12
	4341	CA	ASP	B	159	47.162	87.101	-6.291	1.00	142.12
	4342	CB	ASP	B	159	46.879	88.574	-5.943	1.00	249.27
	4343	CG	ASP	B	159	48.138	89.443	-5.949	1.00	249.27
10	4344	OD1	ASP	B	159	49.066	89.181	-5.152	1.00	249.27
	4345	OD2	ASP	B	159	48.194	90.399	-6.754	1.00	249.27
	4346	C	ASP	B	159	45.846	86.325	-6.363	1.00	142.12
	4347	O	ASP	B	159	45.204	86.280	-7.414	1.00	142.12
	4348	N	TYR	B	160	45.456	85.711	-5.244	1.00	173.61
15	4349	CA	TYR	B	160	44.209	84.946	-5.164	1.00	173.61
	4350	CB	TYR	B	160	44.442	83.463	-5.430	1.00	249.32
	4351	CG	TYR	B	160	45.173	83.176	-6.709	1.00	249.32
	4352	CD1	TYR	B	160	46.561	83.098	-6.731	1.00	249.32
	4353	CE1	TYR	B	160	47.246	82.846	-7.908	1.00	249.32
20	4354	CD2	TYR	B	160	44.481	82.995	-7.903	1.00	249.32
	4355	CE2	TYR	B	160	45.155	82.744	-9.091	1.00	249.32
	4356	CZ	TYR	B	160	46.540	82.671	-9.085	1.00	249.32
	4357	OH	TYR	B	160	47.221	82.428	-10.254	1.00	249.32
	4358	C	TYR	B	160	43.517	85.072	-3.818	1.00	173.61
25	4359	O	TYR	B	160	44.155	85.185	-2.768	1.00	173.61
	4360	N	GLU	B	161	42.194	85.014	-3.871	1.00	90.61
	4361	CA	GLU	B	161	41.341	85.130	-2.695	1.00	90.61
	4362	CB	GLU	B	161	40.333	86.257	-2.926	1.00	219.32
	4363	CG	GLU	B	161	39.312	86.469	-1.834	1.00	219.32
30	4364	CD	GLU	B	161	38.626	87.808	-1.980	1.00	219.32
	4365	OE1	GLU	B	161	37.530	87.986	-1.409	1.00	219.32
	4366	OE2	GLU	B	161	39.197	88.688	-2.663	1.00	219.32
	4367	C	GLU	B	161	40.634	83.792	-2.513	1.00	90.61
	4368	O	GLU	B	161	40.215	83.179	-3.486	1.00	90.61
35	4369	N	SER	B	162	40.522	83.335	-1.270	1.00	91.35
	4370	CA	SER	B	162	39.884	82.057	-0.957	1.00	91.35
	4371	CB	SER	B	162	40.575	81.414	0.251	1.00	56.32
	4372	OG	SER	B	162	40.507	82.266	1.391	1.00	58.32
	4373	C	SER	B	162	38.401	82.220	-0.664	1.00	91.35
40	4374	O	SER	B	162	37.909	83.344	-0.522	1.00	91.35
	4375	N	GLU	B	163	37.690	81.097	-0.574	1.00	79.84
	4376	CA	GLU	B	163	36.253	81.114	-0.287	1.00	79.84
	4377	CB	GLU	B	163	35.639	79.737	-0.529	1.00	200.03
	4378	CG	GLU	B	163	35.475	79.360	-1.993	1.00	200.03
45	4379	CD	GLU	B	163	34.355	80.127	-2.674	1.00	200.03
	4380	OE1	GLU	B	163	33.206	80.054	-2.187	1.00	200.03
	4381	OE2	GLU	B	163	34.621	80.795	-3.698	1.00	200.03
	4382	C	GLU	B	163	36.094	81.500	1.169	1.00	79.84
	4383	O	GLU	B	163	36.886	81.075	1.996	1.00	79.84
50	4384	N	PRO	B	164	35.068	82.315	1.508	1.00	60.77
	4385	CD	PRO	B	164	34.003	82.898	0.682	1.00	73.97
	4386	CA	PRO	B	164	34.904	82.700	2.920	1.00	60.77
	4387	CB	PRO	B	164	33.877	83.829	2.847	1.00	73.97
	4388	CG	PRO	B	164	33.008	83.388	1.730	1.00	73.97
55	4389	C	PRO	B	164	34.431	81.530	3.744	1.00	60.77
	4390	O	PRO	B	164	33.842	80.588	3.223	1.00	60.77
	4391	N	LEU	B	165	34.700	81.568	5.035	1.00	63.41
	4392	CA	LEU	B	165	34.288	80.472	5.889	1.00	63.41
	4393	CB	LEU	B	165	35.440	79.499	6.070	1.00	68.59
60	4394	CG	LEU	B	165	35.185	78.450	7.138	1.00	68.59
	4395	CD1	LEU	B	165	33.824	77.858	6.851	1.00	68.59
	4396	CD2	LEU	B	165	36.264	77.380	7.140	1.00	68.59
	4397	C	LEU	B	165	33.847	80.963	7.250	1.00	63.41
	4398	O	LEU	B	165	34.613	81.635	7.953	1.00	63.41
65	4399	N	ASN	B	166	32.623	80.613	7.628	1.00	64.97
	4400	CA	ASN	B	166	32.078	81.041	8.911	1.00	64.97
	4401	CB	ASN	B	166	30.556	81.011	8.900	1.00	96.05
	4402	CG	ASN	B	166	29.945	82.338	8.491	1.00	96.05
	4403	OD1	ASN	B	166	30.504	83.403	8.737	1.00	96.05
70	4404	ND2	ASN	B	166	28.773	82.270	7.884	1.00	96.05

	4405	C	ASN	B	166	32.556	80.174	10.040	1.00	64.97
	4406	O	ASN	B	166	32.754	78.988	9.860	1.00	64.97
	4407	N	ILE	B	167	32.720	80.766	11.213	1.00	77.41
	4408	CA	ILE	B	167	33.183	80.034	12.375	1.00	77.41
5	4409	CB	ILE	B	167	34.653	80.263	12.591	1.00	59.98
	4410	CG2	ILE	B	167	35.050	79.859	13.985	1.00	59.98
	4411	CG1	ILE	B	167	35.434	79.484	11.546	1.00	59.98
	4412	CD1	ILE	B	167	36.942	79.537	11.784	1.00	59.98
	4413	C	ILE	B	167	32.467	80.488	13.622	1.00	77.41
10	4414	O	ILE	B	167	32.375	81.676	13.896	1.00	77.41
	4415	N	THR	B	168	31.972	79.548	14.405	1.00	104.04
	4416	CA	THR	B	168	31.283	79.938	15.610	1.00	104.04
	4417	CB	THR	B	168	29.817	79.572	15.536	1.00	107.45
	4418	OG1	THR	B	168	29.239	80.179	14.374	1.00	107.45
15	4419	CG2	THR	B	168	29.096	80.067	16.766	1.00	107.45
	4420	C	THR	B	168	31.888	79.326	16.850	1.00	104.04
	4421	O	THR	B	168	32.254	78.155	16.886	1.00	104.04
	4422	N	VAL	B	169	32.012	80.155	17.867	1.00	108.46
	4423	CA	VAL	B	169	32.544	79.737	19.146	1.00	108.46
20	4424	CB	VAL	B	169	33.748	80.618	19.563	1.00	68.82
	4425	CG1	VAL	B	169	33.974	80.539	21.049	1.00	68.82
	4426	CG2	VAL	B	169	34.981	80.174	18.834	1.00	68.82
	4427	C	VAL	B	169	31.394	79.942	20.129	1.00	108.46
	4428	O	VAL	B	169	31.047	81.082	20.455	1.00	108.46
25	4429	N	ILE	B	170	30.790	78.844	20.579	1.00	128.18
	4430	CA	ILE	B	170	29.679	78.917	21.525	1.00	128.18
	4431	CB	ILE	B	170	28.680	77.760	21.285	1.00	141.23
	4432	CG2	ILE	B	170	28.276	77.749	19.833	1.00	141.23
	4433	CG1	ILE	B	170	29.321	76.414	21.631	1.00	141.23
30	4434	CD1	ILE	B	170	28.423	75.218	21.463	1.00	141.23
	4435	C	ILE	B	170	30.228	78.854	22.946	1.00	128.18
	4436	O	ILE	B	170	31.426	78.679	23.142	1.00	128.18
	4437	N	LYS	B	171	29.365	79.005	23.941	1.00	164.76
	4438	CA	LYS	B	171	29.816	78.956	25.328	1.00	164.76
35	4439	CB	LYS	B	171	29.779	80.358	25.929	1.00	211.84
	4440	CG	LYS	B	171	28.416	81.020	25.858	1.00	211.84
	4441	CD	LYS	B	171	28.536	82.537	25.911	1.00	211.84
	4442	CE	LYS	B	171	29.207	83.011	27.190	1.00	211.84
	4443	NZ	LYS	B	171	29.341	84.494	27.217	1.00	211.84
40	4444	C	LYS	B	171	28.987	77.998	26.180	1.00	164.76
	4445	O	LYS	B	171	29.329	77.724	27.330	1.00	164.76
	4446	C1	NAG	B	221	47.345	59.956	-1.693	1.00	249.77
	4447	C2	NAG	B	221	48.521	60.923	-1.796	1.00	249.77
	4448	N2	NAG	B	221	48.022	62.275	-1.936	1.00	249.77
45	4449	C7	NAG	B	221	48.763	63.299	-1.535	1.00	249.77
	4450	O7	NAG	B	221	49.873	63.160	-1.022	1.00	249.77
	4451	C8	NAG	B	221	48.181	64.690	-1.724	1.00	249.77
	4452	C3	NAG	B	221	49.387	60.591	-3.002	1.00	249.77
	4453	O3	NAG	B	221	50.560	61.387	-2.974	1.00	249.77
50	4454	C4	NAG	B	221	49.783	59.115	-3.044	1.00	249.77
	4455	O4	NAG	B	221	50.388	58.867	-4.330	1.00	249.77
	4456	C5	NAG	B	221	48.535	58.221	-2.850	1.00	249.77
	4457	O5	NAG	B	221	47.825	58.605	-1.651	1.00	249.77
	4458	C6	NAG	B	221	48.869	56.745	-2.696	1.00	249.77
55	4459	O6	NAG	B	221	49.689	56.518	-1.557	1.00	249.77
	4460	C1	NAG	B	222	51.148	57.718	-4.505	1.00	249.77
	4461	C2	NAG	B	222	52.440	58.058	-5.267	1.00	249.77
	4462	N2	NAG	B	222	53.222	59.027	-4.521	1.00	249.77
	4463	C7	NAG	B	222	54.445	58.717	-4.103	1.00	249.77
60	4464	O7	NAG	B	222	54.970	57.622	-4.314	1.00	249.77
	4465	C8	NAG	B	222	55.199	59.786	-3.332	1.00	249.77
	4466	C3	NAG	B	222	52.103	58.614	-6.661	1.00	249.77
	4467	O3	NAG	B	222	53.301	58.775	-7.409	1.00	249.77
	4468	C4	NAG	B	222	51.148	57.668	-7.412	1.00	249.77
65	4469	O4	NAG	B	222	50.712	58.282	-8.619	1.00	249.77
	4470	C5	NAG	B	222	49.930	57.333	-6.541	1.00	249.77
	4471	O5	NAG	B	222	50.362	56.787	-5.270	1.00	249.77
	4472	C6	NAG	B	222	49.003	56.316	-7.180	1.00	249.77
	4473	O6	NAG	B	222	47.646	56.720	-7.068	1.00	249.77
70	4474	C1	NAG	B	242	26.466	62.870	-0.923	1.00	89.47

4475	C2	NAG	B	242	26.972	62.476	-2.293	1.00	89.47
4476	N2	NAG	B	242	27.712	61.243	-2.203	1.00	89.47
4477	C7	NAG	B	242	27.358	60.216	-2.956	1.00	89.47
4478	O7	NAG	B	242	26.416	60.270	-3.732	1.00	89.47
4479	C8	NAG	B	242	28.159	58.938	-2.829	1.00	89.47
4480	C3	NAG	B	242	27.882	63.561	-2.855	1.00	89.47
4481	O3	NAG	B	242	28.253	63.234	-4.180	1.00	89.47
4482	C4	NAG	B	242	27.180	64.901	-2.854	1.00	89.47
4483	O4	NAG	B	242	28.116	65.947	-3.186	1.00	89.47
4484	C5	NAG	B	242	26.567	65.197	-1.493	1.00	89.47
4485	O5	NAG	B	242	25.753	64.083	-1.046	1.00	89.47
4486	C6	NAG	B	242	25.657	66.413	-1.634	1.00	89.47
4487	O6	NAG	B	242	25.965	67.439	-0.691	1.00	89.47
4488	C1	NAG	B	243	27.860	66.616	-0.363	1.00	124.06
4489	C2	NAG	B	243	28.444	68.031	-4.311	1.00	124.06
4490	N2	NAG	B	243	27.812	68.814	-3.263	1.00	124.06
4491	C7	NAG	B	243	28.560	69.543	-2.441	1.00	124.06
4492	O7	NAG	B	243	29.786	69.568	-2.502	1.00	124.06
4493	C8	NAG	B	243	27.853	70.353	-1.378	1.00	124.06
4494	C3	NAG	B	243	28.214	68.724	-5.658	1.00	124.06
4495	O3	NAG	B	243	28.825	70.012	-5.653	1.00	124.06
4496	C4	NAG	B	243	28.765	67.860	-6.816	1.00	124.06
4497	O4	NAG	B	243	28.392	68.459	-8.089	1.00	124.06
4498	C5	NAG	B	243	28.162	66.455	-6.717	1.00	124.06
4499	O5	NAG	B	243	28.449	65.870	-5.432	1.00	124.06
4500	C6	NAG	B	243	28.638	65.499	-7.762	1.00	124.06
4501	O6	NAG	B	243	30.003	65.214	-7.571	1.00	124.06
4502	C1	MAN	B	244	29.308	68.650	-9.080	1.00	182.20
4503	C2	MAN	B	244	30.527	69.553	-8.800	1.00	182.20
4504	O2	MAN	B	244	31.636	68.751	-8.489	1.00	182.20
4505	C3	MAN	B	244	30.736	70.260	-10.177	1.00	182.20
4506	O3	MAN	B	244	31.834	71.153	-10.165	1.00	182.20
4507	C4	MAN	B	244	30.850	69.264	-11.367	1.00	182.20
4508	O4	MAN	B	244	31.059	69.973	-12.588	1.00	182.20
4509	C5	MAN	B	244	29.519	68.480	-11.433	1.00	182.20
4510	O5	MAN	B	244	29.290	67.732	-10.210	1.00	182.20
4511	C6	MAN	B	244	29.376	67.561	-12.650	1.00	182.20
4512	O6	MAN	B	244	30.030	66.327	-12.454	1.00	182.20
4513	C1	NAG	B	250	42.367	49.115	8.367	1.00	249.70
4514	C2	NAG	B	250	43.729	49.074	9.087	1.00	249.70
4515	N2	NAG	B	250	43.544	49.049	10.526	1.00	249.70
4516	C7	NAG	B	250	43.853	47.960	11.227	1.00	249.70
4517	O7	NAG	B	250	44.295	46.930	10.709	1.00	249.70
4518	C8	NAG	B	250	43.632	48.021	12.734	1.00	249.70
4519	C3	NAG	B	250	44.545	50.311	8.692	1.00	249.70
4520	O3	NAG	B	250	45.842	50.245	9.269	1.00	249.70
4521	C4	NAG	B	250	44.660	50.407	7.167	1.00	249.70
4522	O4	NAG	B	250	45.304	51.625	6.813	1.00	249.70
4523	C5	NAG	B	250	43.262	50.349	6.521	1.00	249.70
4524	O5	NAG	B	250	42.562	49.158	6.946	1.00	249.70
4525	C6	NAG	B	250	43.315	50.314	5.003	1.00	249.70
4526	O6	NAG	B	250	42.060	49.940	4.449	1.00	249.70
4527	C1	NAG	B	274	20.954	54.260	22.053	1.00	246.89
4528	C2	NAG	B	274	20.822	55.380	23.099	1.00	246.89
4529	N2	NAG	B	274	21.918	55.314	24.050	1.00	246.89
4530	C7	NAG	B	274	22.298	56.407	24.706	1.00	246.89
4531	O7	NAG	B	274	21.767	57.506	24.541	1.00	246.89
4532	C8	NAG	B	274	23.446	56.263	25.690	1.00	246.89
4533	C3	NAG	B	274	19.484	55.246	23.844	1.00	246.89
4534	O3	NAG	B	274	19.302	56.360	24.707	1.00	246.89
4535	C4	NAG	B	274	18.314	55.163	22.856	1.00	246.89
4536	O4	NAG	B	274	17.111	54.887	23.563	1.00	246.89
4537	C5	NAG	B	274	18.576	54.059	21.820	1.00	246.89
4538	O5	NAG	B	274	19.837	54.291	21.151	1.00	246.89
4539	C6	NAG	B	274	17.507	53.987	20.743	1.00	246.89
4540	O6	NAG	B	274	17.896	53.120	19.688	1.00	246.89
4541	C1	NAG	B	335	50.085	74.386	8.041	1.00	247.49
4542	C2	NAG	B	335	50.430	73.230	9.006	1.00	247.49
4543	N2	NAG	B	335	50.451	73.760	10.357	1.00	247.49
4544	C7	NAG	B	335	49.583	73.330	11.267	1.00	247.49

	4545	O7	NAG	B	335	48.734	72.471	11.036	1.00	247.49
	4546	C8	NAG	B	335	49.680	73.947	12.649	1.00	247.49
	4547	C3	NAG	B	335	51.781	72.552	8.725	1.00	247.49
	4548	O3	NAG	B	335	51.808	71.282	9.359	1.00	247.49
5	4549	C4	NAG	B	335	52.016	72.369	7.231	1.00	247.49
	4550	O4	NAG	B	335	53.304	71.813	7.004	1.00	247.49
	4551	C5	NAG	B	335	51.906	73.729	6.561	1.00	247.49
	4552	O5	NAG	B	335	50.550	74.212	6.679	1.00	247.49
	4553	C6	NAG	B	335	52.229	73.654	5.078	1.00	247.49
10	4554	O6	NAG	B	335	53.343	74.471	4.748	1.00	247.49
	4555	C1	NAG	B	340	41.414	81.009	28.648	1.00	249.67
	4556	C2	NAG	B	340	40.114	80.981	29.434	1.00	249.67
	4557	N2	NAG	B	340	38.971	81.033	28.539	1.00	249.67
	4558	C7	NAG	B	340	37.997	80.133	28.666	1.00	249.67
15	4559	O7	NAG	B	340	38.012	79.245	29.526	1.00	249.67
	4560	C8	NAG	B	340	36.831	80.226	27.702	1.00	249.67
	4561	C3	NAG	B	340	40.092	82.143	30.420	1.00	249.67
	4562	O3	NAG	B	340	38.904	82.071	31.207	1.00	249.67
	4563	C4	NAG	B	340	41.329	82.067	31.330	1.00	249.67
20	4564	O4	NAG	B	340	41.393	83.255	32.105	1.00	249.67
	4565	C5	NAG	B	340	42.643	81.894	30.520	1.00	249.67
	4566	O5	NAG	B	340	42.519	80.841	29.539	1.00	249.67
	4567	C6	NAG	B	340	43.832	81.515	31.388	1.00	249.67
	4568	O6	NAG	B	340	44.745	80.677	30.696	1.00	249.67
25	4569	C1	NAG	B	366	28.147	83.475	7.400	1.00	133.05
	4570	C2	NAG	B	366	27.352	83.132	6.154	1.00	133.05
	4571	N2	NAG	B	366	28.247	82.591	5.149	1.00	133.05
	4572	C7	NAG	B	366	28.452	81.278	5.075	1.00	133.05
	4573	O7	NAG	B	366	27.909	80.467	5.829	1.00	133.05
30	4574	C8	NAG	B	366	29.408	80.789	3.998	1.00	133.05
	4575	C3	NAG	B	366	26.651	84.373	5.618	1.00	133.05
	4576	O3	NAG	B	366	25.783	84.003	4.553	1.00	133.05
	4577	C4	NAG	B	366	25.842	85.068	6.713	1.00	133.05
	4578	O4	NAG	B	366	25.403	86.347	6.211	1.00	133.05
35	4579	C5	NAG	B	366	26.688	85.270	7.986	1.00	133.05
	4580	O5	NAG	B	366	27.291	84.029	8.400	1.00	133.05
	4581	C6	NAG	B	366	25.864	85.757	9.163	1.00	133.05
	4582	O6	NAG	B	366	26.677	85.957	10.310	1.00	133.05
	4583	C1	NAG	B	367	24.042	86.610	6.284	1.00	230.72
40	4584	C2	NAG	B	367	23.806	88.121	6.264	1.00	230.72
	4585	N2	NAG	B	367	24.497	88.757	7.369	1.00	230.72
	4586	C7	NAG	B	367	25.574	89.501	7.133	1.00	230.72
	4587	O7	NAG	B	367	26.030	89.681	6.002	1.00	230.72
	4588	C8	NAG	B	367	26.251	90.141	8.334	1.00	230.72
45	4589	C3	NAG	B	367	22.301	88.392	6.337	1.00	230.72
	4590	O3	NAG	B	367	22.054	89.791	6.274	1.00	230.72
	4591	C4	NAG	B	367	21.604	87.688	5.169	1.00	230.72
	4592	O4	NAG	B	367	20.197	87.854	5.276	1.00	230.72
	4593	C5	NAG	B	367	21.956	86.193	5.170	1.00	230.72
50	4594	O5	NAG	B	367	23.395	86.007	5.152	1.00	230.72
	4595	C6	NAG	B	367	21.396	85.477	3.959	1.00	230.72
	4596	O6	NAG	B	367	22.431	85.064	3.078	1.00	230.72
	4597	CB	LYS	D	4	55.111	67.727	55.236	1.00	220.56
	4598	CG	LYS	D	4	54.671	66.297	54.972	1.00	220.56
55	4599	CD	LYS	D	4	54.274	65.601	56.262	1.00	220.56
	4600	CE	LYS	D	4	53.817	64.172	56.007	1.00	220.56
	4601	NZ	LYS	D	4	53.427	63.496	57.274	1.00	220.56
	4602	C	LYS	D	4	54.245	68.471	53.028	1.00	175.22
	4603	O	LYS	D	4	53.112	68.293	53.459	1.00	175.22
60	4604	N	LYS	D	4	55.813	69.908	54.320	1.00	175.22
	4605	CA	LYS	D	4	55.442	68.509	53.968	1.00	175.22
	4606	N	PRO	D	5	54.485	68.654	51.722	1.00	119.81
	4607	CD	PRO	D	5	55.727	69.166	51.125	1.00	90.67
	4608	CA	PRO	D	5	53.397	68.631	50.737	1.00	119.81
65	4609	CB	PRO	D	5	53.950	69.490	49.602	1.00	90.67
	4610	CG	PRO	D	5	55.400	69.182	49.643	1.00	90.67
	4611	C	PRO	D	5	53.035	67.215	50.281	1.00	119.81
	4612	O	PRO	D	5	53.836	66.281	50.412	1.00	119.81
	4613	N	LYS	D	6	51.824	67.054	49.752	1.00	86.52
70	4614	CA	LYS	D	6	51.373	65.747	49.285	1.00	96.52

	4615	CB	LYS	D	6	50.549	65.060	50.379	1.00	171.50
	4616	CG	LYS	D	6	50.141	63.639	50.041	1.00	171.50
	4617	CD	LYS	D	6	49.490	62.929	51.225	1.00	171.50
	4618	CE	LYS	D	6	49.128	61.483	50.860	1.00	171.50
5	4619	NZ	LYS	D	6	48.560	60.707	52.003	1.00	171.50
	4620	C	LYS	D	6	50.557	65.881	47.994	1.00	96.52
	4621	O	LYS	D	6	49.495	66.491	47.981	1.00	96.52
	4622	N	VAL	D	7	51.072	65.306	46.911	1.00	68.94
	4623	CA	VAL	D	7	50.422	65.353	45.604	1.00	68.94
10	4624	CB	VAL	D	7	51.321	64.793	44.498	1.00	87.54
	4625	CG1	VAL	D	7	50.661	65.026	43.147	1.00	87.54
	4626	CG2	VAL	D	7	52.693	65.408	44.566	1.00	87.54
	4627	C	VAL	D	7	49.159	64.529	45.521	1.00	68.94
	4628	O	VAL	D	7	49.213	63.311	45.658	1.00	68.94
15	4629	N	SER	D	8	48.033	65.178	45.263	1.00	67.77
	4630	CA	SER	D	8	46.766	64.465	45.138	1.00	67.77
	4631	CB	SER	D	8	45.651	65.209	45.877	1.00	176.15
	4632	OG	SER	D	8	45.554	66.551	45.438	1.00	176.15
	4633	C	SER	D	8	46.434	64.349	43.651	1.00	67.77
20	4634	O	SER	D	8	47.041	65.043	42.834	1.00	67.77
	4635	N	LEU	D	9	45.500	63.459	43.304	1.00	116.14
	4636	CA	LEU	D	9	45.098	63.252	41.912	1.00	116.14
	4637	CB	LEU	D	9	45.531	61.883	41.396	1.00	98.23
	4638	CG	LEU	D	9	47.001	61.491	41.352	1.00	98.23
25	4639	CD1	LEU	D	9	47.193	60.359	40.372	1.00	98.23
	4640	CD2	LEU	D	9	47.818	62.671	40.913	1.00	98.23
	4641	C	LEU	D	9	43.596	63.326	41.770	1.00	116.14
	4642	O	LEU	D	9	42.865	63.094	42.732	1.00	116.14
	4643	N	ASN	D	10	43.135	63.630	40.560	1.00	87.18
30	4644	CA	ASN	D	10	41.699	63.718	40.284	1.00	87.18
	4645	CB	ASN	D	10	41.130	65.052	40.768	1.00	123.83
	4646	CG	ASN	D	10	39.625	65.064	40.746	1.00	123.83
	4647	OD1	ASN	D	10	38.973	64.342	41.505	1.00	123.83
	4648	ND2	ASN	D	10	39.058	65.867	39.857	1.00	123.83
35	4649	C	ASN	D	10	41.419	63.561	38.797	1.00	87.18
	4650	O	ASN	D	10	41.732	64.453	38.000	1.00	87.18
	4651	N	PRO	D	11	40.804	62.432	38.402	1.00	137.25
	4652	CD	PRO	D	11	40.609	62.151	36.972	1.00	119.64
	4653	CA	PRO	D	11	40.349	61.301	39.221	1.00	137.25
40	4654	CB	PRO	D	11	39.877	60.298	38.167	1.00	119.64
	4655	CG	PRO	D	11	39.503	61.164	37.007	1.00	119.64
	4656	C	PRO	D	11	41.422	60.689	40.148	1.00	137.25
	4657	O	PRO	D	11	42.614	60.926	39.952	1.00	137.25
	4658	N	PRO	D	12	41.017	59.899	41.164	1.00	96.57
45	4659	CD	PRO	D	12	39.630	59.557	41.534	1.00	83.9
	4660	CA	PRO	D	12	41.951	59.269	42.104	1.00	96.57
	4661	CB	PRO	D	12	41.041	58.629	43.151	1.00	83.91
	4662	CG	PRO	D	12	39.761	59.344	43.011	1.00	83.91
	4663	C	PRO	D	12	42.774	58.205	41.374	1.00	96.57
50	4664	O	PRO	D	12	43.874	57.834	41.802	1.00	96.57
	4665	N	TRP	D	13	42.222	57.717	40.268	1.00	86.01
	4666	CA	TRP	D	13	42.869	56.675	39.486	1.00	86.01
	4667	CB	TRP	D	13	42.032	56.366	38.247	1.00	97.24
	4668	CG	TRP	D	13	40.601	56.191	38.568	1.00	97.24
55	4669	CD2	TRP	D	13	40.049	55.556	39.724	1.00	97.2
	4670	CE2	TRP	D	13	38.651	55.664	39.631	1.00	97.24
	4671	CE3	TRP	D	13	40.604	54.902	40.836	1.00	97.24
	4672	CD1	TRP	D	13	39.546	56.637	37.836	1.00	97.24
	4673	NE1	TRP	D	13	38.370	56.330	38.469	1.00	97.24
60	4674	CZ2	TRP	D	13	37.795	55.147	40.609	1.00	97.24
	4675	CZ3	TRP	D	13	39.753	54.387	41.804	1.00	97.24
	4676	CH2	TRP	D	13	38.364	54.515	41.686	1.00	97.24
	4677	C	TRP	D	13	44.278	57.041	39.075	1.00	86.01
	4678	O	TRP	D	13	44.493	58.036	38.401	1.00	86.01
65	4679	N	ASN	D	14	45.244	56.231	39.488	1.00	79.52
	4680	CA	ASN	D	14	46.627	56.488	39.122	1.00	79.52
	4681	CB	ASN	D	14	47.534	56.449	40.358	1.00	103.31
	4682	CG	ASN	D	14	47.664	55.067	40.958	1.00	103.31
	4683	OD1	ASN	D	14	46.671	54.415	41.283	1.00	103.31
70	4684	ND2	ASN	D	14	48.895	54.618	41.124	1.00	103.31

	4685	C	ASN	D	14	47.153	55.545	38.031	1.00	79.52
	4686	O	ASN	D	14	48.358	55.444	37.825	1.00	79.52
	4687	N	ARG	D	15	46.248	54.842	37.351	1.00	58.96
	4688	CA	ARG	D	15	46.609	53.977	36.231	1.00	58.96
5	4689	CB	ARG	D	15	46.413	52.517	36.552	1.00	70.76
	4690	CG	ARG	D	15	46.829	52.131	37.918	1.00	70.76
	4691	CD	ARG	D	15	46.633	50.641	38.077	1.00	70.76
	4692	NE	ARG	D	15	47.557	49.869	37.263	1.00	70.76
	4693	CZ	ARG	D	15	47.280	48.660	36.802	1.00	70.76
10	4694	NH1	ARG	D	15	46.108	48.121	37.078	1.00	70.76
	4695	NH2	ARG	D	15	48.170	47.981	36.079	1.00	70.76
	4696	C	ARG	D	15	45.573	54.375	35.202	1.00	58.96
	4697	O	ARG	D	15	44.384	54.102	35.367	1.00	58.96
	4698	N	ILE	D	16	46.006	55.037	34.144	1.00	65.25
15	4699	CA	ILE	D	16	45.052	55.457	33.146	1.00	65.25
	4700	CB	ILE	D	16	44.928	56.967	33.117	1.00	107.28
	4701	CG2	ILE	D	16	44.319	57.455	34.414	1.00	107.28
	4702	CG1	ILE	D	16	46.303	57.587	32.876	1.00	107.28
	4703	CD1	ILE	D	16	46.295	59.099	32.854	1.00	107.28
20	4704	C	ILE	D	16	45.380	54.992	31.754	1.00	65.25
	4705	O	ILE	D	16	46.492	54.553	31.461	1.00	65.25
	4706	N	PHE	D	17	44.373	55.117	30.905	1.00	82.89
	4707	CA	PHE	D	17	44.429	54.750	29.509	1.00	82.89
	4708	CB	PHE	D	17	43.011	54.508	29.030	1.00	73.74
25	4709	CG	PHE	D	17	42.550	53.099	29.186	1.00	73.74
	4710	CD1	PHE	D	17	41.245	52.822	29.578	1.00	73.74
	4711	CD2	PHE	D	17	43.379	52.052	28.825	1.00	73.74
	4712	CE1	PHE	D	17	40.779	51.529	29.625	1.00	73.74
	4713	CE2	PHE	D	17	42.918	50.741	28.866	1.00	73.74
30	4714	CZ	PHE	D	17	41.609	50.484	29.258	1.00	73.74
	4715	C	PHE	D	17	45.066	55.863	28.677	1.00	82.89
	4716	O	PHE	D	17	45.154	57.009	29.117	1.00	82.89
	4717	N	LYS	D	18	45.502	55.531	27.469	1.00	90.77
	4718	CA	LYS	D	18	46.117	56.516	26.588	1.00	90.77
35	4719	CB	LYS	D	18	46.681	55.810	25.357	1.00	139.85
	4720	CG	LYS	D	18	47.467	56.691	24.410	1.00	139.85
	4721	CD	LYS	D	18	48.254	55.822	23.441	1.00	139.85
	4722	CE	LYS	D	18	49.094	56.637	22.472	1.00	139.85
	4723	NZ	LYS	D	18	48.256	57.533	21.630	1.00	139.85
40	4724	C	LYS	D	18	45.079	57.556	26.156	1.00	90.77
	4725	O	LYS	D	18	43.975	57.212	25.731	1.00	90.77
	4726	N	GLY	D	19	45.420	58.832	26.284	1.00	135.30
	4727	CA	GLY	D	19	44.501	59.869	25.859	1.00	135.30
	4728	C	GLY	D	19	43.585	60.458	26.909	1.00	135.30
45	4729	O	GLY	D	19	42.914	61.451	26.641	1.00	135.30
	4730	N	GLU	D	20	43.539	59.863	28.096	1.00	90.73
	4731	CA	GLU	D	20	42.679	60.387	29.158	1.00	90.73
	4732	CB	GLU	D	20	42.370	59.283	30.165	1.00	145.66
	4733	CG	GLU	D	20	41.858	58.007	29.497	1.00	145.66
50	4734	CD	GLU	D	20	41.421	56.945	30.491	1.00	145.66
	4735	OE1	GLU	D	20	42.233	56.567	31.363	1.00	145.66
	4736	OE2	GLU	D	20	40.265	56.483	30.393	1.00	145.66
	4737	C	GLU	D	20	43.339	61.593	29.844	1.00	90.73
	4738	O	GLU	D	20	44.510	61.887	29.590	1.00	90.73
55	4739	N	ASN	D	21	42.592	62.311	30.682	1.00	106.51
	4740	CA	ASN	D	21	43.163	63.469	31.364	1.00	106.51
	4741	CB	ASN	D	21	42.409	64.761	31.030	1.00	191.80
	4742	CG	ASN	D	21	42.014	64.865	29.580	1.00	191.80
	4743	OD1	ASN	D	21	42.781	64.543	28.677	1.00	191.80
60	4744	ND2	ASN	D	21	40.797	65.346	29.365	1.00	191.80
	4745	C	ASN	D	21	43.127	63.300	32.872	1.00	106.51
	4746	O	ASN	D	21	42.165	62.756	33.424	1.00	106.51
	4747	N	VAL	D	22	44.170	63.792	33.533	1.00	83.07
	4748	CA	VAL	D	22	44.267	63.727	34.984	1.00	83.07
65	4749	CB	VAL	D	22	45.143	62.571	35.425	1.00	85.11
	4750	CG1	VAL	D	22	46.555	62.774	34.923	1.00	85.11
	4751	CG2	VAL	D	22	45.134	62.475	36.937	1.00	85.11
	4752	C	VAL	D	22	44.885	65.015	35.514	1.00	83.07
	4753	O	VAL	D	22	45.701	65.643	34.833	1.00	83.07
70	4754	N	THR	D	23	44.517	65.401	36.731	1.00	66.58

	4755	CA	THR	D	23	45.024	66.635	37.318	1.00	66.58
	4756	CB	THR	D	23	43.848	67.553	37.646	1.00	160.89
	4757	OG1	THR	D	23	43.036	67.717	36.477	1.00	160.89
5	4758	CG2	THR	D	23	44.344	68.902	38.121	1.00	160.89
	4759	C	THR	D	23	45.820	66.391	38.598	1.00	66.58
	4760	O	THR	D	23	45.330	65.718	39.498	1.00	66.58
	4761	N	LEU	D	24	47.035	66.923	38.705	1.00	91.98
	4762	CA	LEU	D	24	47.810	66.708	39.933	1.00	91.98
	4763	CB	LEU	D	24	49.235	66.263	39.632	1.00	82.54
10	4764	CG	LEU	D	24	49.491	65.315	38.471	1.00	82.54
	4765	CD1	LEU	D	24	50.891	64.750	38.587	1.00	82.54
	4766	CD2	LEU	D	24	48.509	64.210	38.476	1.00	82.54
	4767	C	LEU	D	24	47.882	67.967	40.785	1.00	91.98
	4768	O	LEU	D	24	48.622	68.895	40.479	1.00	91.98
15	4769	N	THR	D	25	47.131	67.992	41.873	1.00	89.48
	4770	CA	THR	D	25	47.122	69.153	42.732	1.00	89.48
	4771	CB	THR	D	25	45.754	69.300	43.385	1.00	145.87
	4772	OG1	THR	D	25	44.757	69.342	42.357	1.00	145.87
	4773	CG2	THR	D	25	45.686	70.568	44.198	1.00	145.87
20	4774	C	THR	D	25	48.199	69.028	43.794	1.00	89.48
	4775	O	THR	D	25	48.404	67.956	44.359	1.00	89.48
	4776	N	CYS	D	26	48.909	70.117	44.050	1.00	125.74
	4777	CA	CYS	D	26	49.942	70.082	45.070	1.00	125.74
	4778	C	CYS	D	26	49.298	70.358	46.407	1.00	125.74
25	4779	O	CYS	D	26	48.415	71.196	46.512	1.00	125.74
	4780	CB	CYS	D	26	51.034	71.118	44.810	1.00	105.78
	4781	SG	CYS	D	26	52.476	70.930	45.922	1.00	105.78
	4782	N	ASN	D	27	49.751	69.628	47.416	1.00	184.56
	4783	CA	ASN	D	27	49.263	69.743	48.776	1.00	184.56
30	4784	CB	ASN	D	27	50.450	69.894	49.698	1.00	249.08
	4785	CG	ASN	D	27	50.107	69.554	51.100	1.00	249.08
	4786	OD1	ASN	D	27	49.328	68.630	51.334	1.00	249.08
	4787	ND2	ASN	D	27	50.683	70.281	52.054	1.00	249.08
	4788	C	ASN	D	27	48.283	70.880	49.023	1.00	184.56
35	4789	O	ASN	D	27	48.686	71.988	49.365	1.00	184.56
	4790	N	GLY	D	28	46.995	70.600	48.844	1.00	249.39
	4791	CA	GLY	D	28	45.972	71.612	49.043	1.00	249.39
	4792	C	GLY	D	28	44.644	71.030	48.616	1.00	249.39
	4793	O	GLY	D	28	44.494	70.609	47.470	1.00	249.39
40	4794	N	ASN	D	29	43.674	71.006	49.524	1.00	249.47
	4795	CA	ASN	D	29	42.377	70.429	49.206	1.00	249.47
	4796	CB	ASN	D	29	41.619	70.112	50.497	1.00	246.79
	4797	CG	ASN	D	29	40.397	69.249	50.256	1.00	246.79
	4798	OD1	ASN	D	29	40.234	68.672	49.182	1.00	246.79
45	4799	ND2	ASN	D	29	39.536	69.146	51.262	1.00	246.79
	4800	C	ASN	D	29	41.494	71.261	48.274	1.00	249.47
	4801	O	ASN	D	29	41.005	70.746	47.265	1.00	249.47
	4802	N	ASN	D	30	41.294	72.538	48.594	1.00	206.51
	4803	CA	ASN	D	30	40.437	73.386	47.766	1.00	206.51
50	4804	CB	ASN	D	30	39.137	73.705	48.518	1.00	210.57
	4805	CG	ASN	D	30	38.302	72.469	48.794	1.00	210.57
	4806	OD1	ASN	D	30	37.878	72.232	49.926	1.00	210.57
	4807	ND2	ASN	D	30	38.054	71.678	47.757	1.00	210.57
	4808	C	ASN	D	30	41.073	74.685	47.297	1.00	206.51
55	4809	O	ASN	D	30	41.381	74.848	46.115	1.00	206.51
	4810	N	PHE	D	31	41.266	75.614	48.224	1.00	230.41
	4811	CA	PHE	D	31	41.829	76.899	47.860	1.00	230.41
	4812	CB	PHE	D	31	40.891	78.020	48.330	1.00	249.56
	4813	CG	PHE	D	31	39.472	77.878	47.828	1.00	249.56
60	4814	CD1	PHE	D	31	38.588	76.991	48.440	1.00	249.56
	4815	CD2	PHE	D	31	39.030	78.608	46.725	1.00	249.56
	4816	CE1	PHE	D	31	37.283	76.839	47.969	1.00	249.56
	4817	CE2	PHE	D	31	37.727	78.463	46.245	1.00	249.56
	4818	CZ	PHE	D	31	36.853	77.574	46.866	1.00	249.56
65	4819	C	PHE	D	31	43.249	77.132	48.360	1.00	230.41
	4820	O	PHE	D	31	43.542	76.994	49.552	1.00	230.41
	4821	N	PHE	D	32	44.122	77.486	47.416	1.00	186.13
	4822	CA	PHE	D	32	45.531	77.753	47.683	1.00	186.13
70	4823	CB	PHE	D	32	46.392	78.753	46.925	1.00	237.35
	4824	CG	PHE	D	32	47.810	76.726	47.381	1.00	237.35

	4825	CD1	PHE D	32	48.121	76.283	48.659	1.00	237.35
	4826	CD2	PHE D	32	48.835	77.167	46.552	1.00	237.35
	4827	CE1	PHE D	32	49.434	76.277	49.112	1.00	237.35
	4828	CE2	PHE D	32	50.156	77.166	46.998	1.00	237.35
5	4829	CZ	PHE D	32	50.454	76.719	48.286	1.00	237.35
	4830	C	PHE D	32	45.909	79.173	47.251	1.00	186.13
	4831	O	PHE D	32	45.122	79.856	46.601	1.00	186.13
	4832	N	GLU D	33	47.117	79.617	47.595	1.00	249.49
	4833	CA	GLU D	33	47.539	80.969	47.225	1.00	249.49
10	4834	CB	GLU D	33	47.683	81.860	48.457	1.00	249.38
	4835	CG	GLU D	33	47.919	83.321	48.090	1.00	249.38
	4836	CD	GLU D	33	46.730	83.912	47.362	1.00	249.38
	4837	OE1	GLU D	33	45.593	83.561	47.740	1.00	249.38
	4838	OE2	GLU D	33	46.914	84.731	46.433	1.00	249.38
15	4839	C	GLU D	33	48.822	81.120	46.422	1.00	249.49
	4840	O	GLU D	33	48.826	81.765	45.372	1.00	249.49
	4841	N	VAL D	34	49.918	80.566	46.929	1.00	207.78
	4842	CA	VAL D	34	51.194	80.698	46.247	1.00	207.78
	4843	CB	VAL D	34	52.284	79.859	46.944	1.00	207.37
20	4844	CG1	VAL D	34	53.608	80.005	46.212	1.00	207.37
	4845	CG2	VAL D	34	52.437	80.316	48.384	1.00	207.37
	4846	C	VAL D	34	51.130	80.333	44.770	1.00	207.78
	4847	O	VAL D	34	50.333	79.492	44.343	1.00	207.78
	4848	N	SER D	35	51.966	81.007	43.992	1.00	228.15
25	4849	CA	SER D	35	52.043	80.778	42.563	1.00	228.15
	4850	CB	SER D	35	51.944	82.104	41.810	1.00	249.21
	4851	OG	SER D	35	53.093	82.901	42.038	1.00	249.21
	4852	C	SER D	35	53.386	80.116	42.275	1.00	228.15
	4853	O	SER D	35	53.703	79.813	41.126	1.00	228.15
30	4854	N	SER D	36	54.177	79.906	43.326	1.00	238.59
	4855	CA	SER D	36	55.481	79.265	43.185	1.00	238.59
	4856	CB	SER D	36	56.552	80.002	43.997	1.00	200.88
	4857	OG	SER D	36	56.368	79.808	45.389	1.00	200.88
	4858	C	SER D	36	55.395	77.821	43.653	1.00	238.59
35	4859	O	SER D	36	55.568	77.519	44.835	1.00	238.59
	4860	N	THR D	37	55.115	76.935	42.706	1.00	119.38
	4861	CA	THR D	37	55.004	75.514	42.974	1.00	119.38
	4862	CB	THR D	37	53.561	75.034	42.738	1.00	138.47
	4863	OG1	THR D	37	52.664	75.794	43.557	1.00	138.47
40	4864	CG2	THR D	37	53.426	73.568	43.078	1.00	138.47
	4865	C	THR D	37	55.950	74.838	41.992	1.00	119.38
	4866	O	THR D	37	56.054	75.258	40.841	1.00	119.38
	4867	N	LYS D	38	56.653	73.808	42.446	1.00	140.44
	4868	CA	LYS D	38	57.594	73.098	41.585	1.00	140.44
45	4869	CB	LYS D	38	58.938	72.982	42.288	1.00	200.36
	4870	CG	LYS D	38	59.508	74.309	42.714	1.00	200.36
	4871	CD	LYS D	38	60.837	74.125	43.415	1.00	200.36
	4872	CE	LYS D	38	61.449	75.465	43.766	1.00	200.36
	4873	NZ	LYS D	38	62.770	75.308	44.427	1.00	200.36
50	4874	C	LYS D	38	57.100	71.701	41.218	1.00	140.44
	4875	O	LYS D	38	56.507	71.013	42.045	1.00	140.44
	4876	N	TRP D	39	57.341	71.284	39.976	1.00	125.62
	4877	CA	TRP D	39	56.934	69.953	39.520	1.00	125.62
	4878	CB	TRP D	39	55.830	70.028	38.470	1.00	111.13
55	4879	CG	TRP D	39	54.540	70.582	38.973	1.00	111.13
	4880	CD2	TRP D	39	53.645	69.978	39.915	1.00	111.13
	4881	CE2	TRP D	39	52.567	70.867	40.090	1.00	111.13
	4882	CE3	TRP D	39	53.651	68.776	40.628	1.00	111.13
	4883	CD1	TRP D	39	53.984	71.774	38.628	1.00	111.13
60	4884	NE1	TRP D	39	52.798	71.953	39.295	1.00	111.13
	4885	CZ2	TRP D	39	51.503	70.588	40.948	1.00	111.13
	4886	CZ3	TRP D	39	52.589	68.503	41.482	1.00	111.13
	4887	CH2	TRP D	39	51.531	69.405	41.633	1.00	111.13
	4888	C	TRP D	39	58.115	69.240	38.913	1.00	125.62
65	4889	O	TRP D	39	58.809	69.797	38.077	1.00	125.62
	4890	N	PHE D	40	58.331	68.000	39.318	1.00	94.48
	4891	CA	PHE D	40	59.458	67.260	38.800	1.00	94.48
	4892	CB	PHE D	40	60.475	66.976	39.910	1.00	162.61
	4893	CG	PHE D	40	60.977	68.203	40.607	1.00	162.61
70	4894	CD1	PHE D	40	60.217	68.816	41.594	1.00	162.61

	4895	CD2	PHE	D	40 ·	62.222	68.734	40.292	1.00	162.61
	4896	CE1	PHE	D	40	60.687	69.941	42.264	1.00	162.61
	4897	CE2	PHE	D	40	62.705	69.859	40.953	1.00	162.61
	4898	CZ	PHE	D	40	61.934	70.465	41.945	1.00	162.61
5	4899	C	PHE	D	40	59.063	65.951	38.152	1.00	94.48
	4900	O	PHE	D	40	59.061	64.906	38.803	1.00	94.48
	4901	N	HIS	D	41	58.727	66.006	36.869	1.00	72.94
	4902	CA	HIS	D	41	58.368	64.797	36.133	1.00	·72.94
	4903	CB	HIS	D	41	57.649	65.192	34.848	1.00	108.26
10	4904	CG	HIS	D	41	57.262	64.034	33.991	1.00	108.26
	4905	CD2	HIS	D	41	57.305	63.866	32.649	1.00	108.26
	4906	ND1	HIS	D	41	56.717	62.879	34.507	1.00	108.26
	·:907	CE1	HIS	D	41	56.441	62.049	33.519	1.00	108.26
	⸌908	NE2	HIS	D	41	56.788	62.625	32.381	1.00	108.26
15	4909	C	HIS	D	41	59.642	63.973	35.816	1.00	72.94
	4910	O	HIS	D	41	60.482	64.384	35.014	1.00	72.94
	4911	N	ASN	D	42	59.770	62.805	36.445	1.00	79.39
	4912	CA	ASN	D	42	60.939	61.934	36.277	1.00	79.39
	4913	CB	ASN	D	42	61.153	61.⸱⸱⸱⸥	34.808	1.00	100.05
20	4914	CG	ASN	D	42	60.141	60.504	34.327	·.00	100.05
	4915	OD1	ASN	D	42	58.962	60.635	34.637	1.00	100.05
	4916	ND2	ASN	D	42	60.578	59.502	33.560	1.00	100.05
	4917	C	ASN	D	42	62.190	62.653	36.783	1.00	79.39
	4918	O	ASN	D	42	63.298	62.386	36.318	1.00	79.39
25	4919	N	GLY	D	43	62.013	63.562	37.739	1.00	194.33
	4920	CA	GLY	D	43	63.147	64.294	38.279	1.00	194.33
	4921	C	GLY	D	43	63.397	65.624	37.584	1.00	194.33
	4922	O	GLY	D	43	63.744	66.616	38.226	1.00	194.33
	4923	N	SER	D	44	63.221	65.644	36.267	1.00	226.19
30	4924	CA	SER	D	44	63.422	66.852	35.476	1.00	226.19
	4925	CB	SER	D	44	63.315	66.520	33.987	1.00	149.84
	4926	OG	SER	D	44	64.180	65.450	˙33.639	1.00	149.84
	4927	C	SER	D	44	62.376	67.899	35.837	1.00	226.19
	4928	O	SER	D	44	61.179	67.617	35.812	1.00	226.19
35	4929	N	LEU	D	45	62.824	69.107	36.172	1.00	151.08
	4930	CA	LEU	D	45	61.897	70.180	36.531	1.00	151.08
	4931	CB	LEU	D	45	62.673	71.473	36.830	1.00	168.08
	4932	CG	LEU	D	45	61.854	72.699	37.259	1.00	168.08
	4933	CD1	LEU	D	45	60.980	72.345	38.451	1.00	168.08
40	4934	CD2	LEU	D	45	62.788	73.853	37.607	1.00	168.08
	4935	C	LEU	D	45	60.885	70.422	35.398	1.00	151.08
	4936	O	LEU	D	45	61.215	70.281	34.219	1.00	151.08
	4937	N	SER	D	46	59.650	70.772	35.755	1.00	118.65
	4938	CA	SER	D	46	58.614	71.032	34.762	1.00	118.65
45	4939	CB	SER	D	46	57.279	70.467	35.236	1.00	145.92
	4940	OG	SER	D	46	56.288	70.641	34.240	1.00	145.92
	4941	C	SER	D	46	58.499	72.537	34.569	1.00	118.65
	4942	O	SER	D	46	59.012	73.306	35.378	1.00	118.65
	4943	N	GLU	D	47	57.828	72.965	33.505	1.00	181.92
50	4944	CA	GLU	D	47	57.679	74.395	33.255	1.00	181.92
	4945	CB	GLU	D	47	57.725	74.692	31.746	1.00	232.55
	4946	CG	GLU	D	47	58.747	73.882	30.951	1.00	232.55
	4947	CD	GLU	D	47	58.494	73.918	29.437	1.00	232.55
	4948	OE1	GLU	D	47	57.657	73.130	28.947	1.00	232.55
55	4949	OE2	GLU	D	47	59.123	74.749	28.747	1.00	232.55
	4950	C	GLU	D	47	56.398	74.999	33.858	1.00	181.92
	4951	O	GLU	D	47	56.185	76.203	33.732	1.00	181.92
	4952	N	GLU	D	48	55.538	74.196	34.492	1.00	100.90
	4953	CA	GLU	D	48	54.330	74.777	35.104	1.00	100.90
60	4954	CB	GLU	D	48	53.184	73.753	35.227	1.00	175.62
	4955	CG	GLU	D	48	51.945	74.246	36.025	1.00	175.62
	4956	CD	GLU	D	48	51.173	75.384	35.355	1.00	175.62
	4957	OE1	GLU	D	48	50.544	75.147	34.300	1.00	175.62
	4958	OE2	GLU	D	48	51.193	76.517	35.887	1.00	175.62
65	4959	C	GLU	D	48	54.698	75.309	36.490	1.00	100.90
	4960	O	GLU	D	48	55.679	74.868	37.096	1.00	100.90
	4961	N	THR	D	49	53.927	76.275	36.977	1.00	145.22
	4962	CA	THR	D	49	54.186	76.860	38.287	1.00	145.22
	4963	CB	THR	D	49	54.710	78.308	38.155	1.00	156.90
70	4964	OG1	THR	D	49	53.774	79.094	37.405	1.00	156.90

	4965	CG2	THR	D	49	56.059	78.319	37.442	1.00	156.90
	4966	C	THR	D	49	52.921	76.841	39.150	1.00	145.22
	4967	O	THR	D	49	53.002	76.780	40.384	1.00	145.22
	4968	N	ASN	D	50	51.757	76.881	38.500	1.00	138.33
5	4969	CA	ASN	D	50	50.486	76.844	39.213	1.00	138.33
	4970	CB	ASN	D	50	49.323	76.826	38.220	1.00	234.43
	4971	CG	ASN	D	50	47.991	77.129	38.880	1.00	234.43
	4972	OD1	ASN	D	50	47.868	77.026	40.100	1.00	234.43
	4973	ND2	ASN	D	50	46.989	77.490	38.081	1.00	234.43
10	4974	C	ASN	D	50	50.480	75.564	40.054	1.00	138.33
	4975	O	ASN	D	50	51.104	74.574	39.683	1.00	138.33
	4976	N	SER	D	51	49.782	75.578	41.183	1.00	192.24
	4977	CA	SER	D	51	49.733	74.400	42.046	1.00	192.24
	4978	CB	SER	D	51	49.042	74.734	43.376	1.00	111.18
15	4979	OG	SER	D	51	47.655	74.994	43.211	1.00	111.18
	4980	C	SER	D	51	49.023	73.213	41.399	1.00	192.24
	4981	O	SER	D	51	49.166	72.078	41.848	1.00	192.24
	4982	N	SER	D	52	48.252	73.470	40.351	1.00	99.05
	4983	CA	SER	D	52	47.526	72.400	39.677	1.00	99.05
20	4984	CB	SER	D	52	46.041	72.765	39.522	1.00	120.15
	4985	OG	SER	D	52	45.402	72.880	40.781	1.00	120.15
	4986	C	SER	D	52	48.147	72.145	38.314	1.00	99.05
	4987	O	SER	D	52	48.052	72.970	37.410	1.00	99.05
	4988	N	LEU	D	53	48.797	70.997	38.183	1.00	107.39
25	4989	CA	LEU	D	53	49.443	70.602	36.938	1.00	107.39
	4990	CB	LEU	D	53	50.774	69.910	37.246	1.00	80.33
	4991	CG	LEU	D	53	51.398	68.972	36.203	1.00	80.33
	4992	CD1	LEU	D	53	51.298	69.580	34.817	1.00	80.33
	4993	CD2	LEU	D	53	52.856	68.675	36.589	1.00	80.33
30	4994	C	LEU	D	53	48.548	69.654	36.158	1.00	107.39
	4995	O	LEU	D	53	48.472	68.474	36.476	1.00	107.39
	4996	N	ASN	D	54	47.876	70.159	35.130	1.00	103.21
	4997	CA	ASN	D	54	46.989	69.314	34.339	1.00	103.21
	4998	CB	ASN	D	54	45.977	70.162	33.573	1.00	126.61
35	4999	CG	ASN	D	54	44.932	70.755	34.475	1.00	126.61
	5000	OD1	ASN	D	54	44.260	70.038	35.217	1.00	126.61
	5001	ND2	ASN	D	54	44.781	72.072	34.420	1.00	126.61
	5002	C	ASN	D	54	47.732	68.434	33.362	1.00	103.21
	5003	O	ASN	D	54	48.882	68.690	33.026	1.00	103.21
40	5004	N	ILE	D	55	47.056	67.381	32.921	1.00	179.18
	5005	CA	ILE	D	55	47.601	66.449	31.947	1.00	179.18
	5006	CB	ILE	D	55	48.061	65.127	32.606	1.00	94.31
	5007	CG2	ILE	D	55	48.187	64.027	31.558	1.00	94.31
	5008	CG1	ILE	D	55	49.393	65.356	33.324	1.00	94.31
45	5009	CD1	ILE	D	55	49.946	64.146	34.029	1.00	94.31
	5010	C	ILE	D	55	46.473	66.173	30.975	1.00	179.18
	5011	O	ILE	D	55	45.402	65.719	31.373	1.00	179.18
	5012	N	VAL	D	56	46.701	66.476	29.704	1.00	148.36
	5013	CA	VAL	D	56	45.674	66.254	28.704	1.00	148.36
50	5014	CB	VAL	D	56	45.589	67.433	27.737	1.00	191.19
	5015	CG1	VAL	D	56	44.260	67.393	26.992	1.00	191.19
	5016	CG2	VAL	D	56	45.729	68.734	28.509	1.00	191.19
	5017	C	VAL	D	56	45.998	64.975	27.956	1.00	148.36
	5018	O	VAL	D	56	46.797	64.180	28.445	1.00	148.36
55	5019	N	ASN	D	57	45.386	64.774	26.789	1.00	142.96
	5020	CA	ASN	D	57	45.604	63.560	25.999	1.00	142.96
	5021	CB	ASN	D	57	45.673	63.895	24.509	1.00	249.24
	5022	CG	ASN	D	57	44.331	64.323	23.952	1.00	249.24
	5023	OD1	ASN	D	57	43.331	63.617	24.101	1.00	249.24
60	5024	ND2	ASN	D	57	44.298	65.482	23.307	1.00	249.24
	5025	C	ASN	D	57	46.861	62.815	26.436	1.00	142.96
	5026	O	ASN	D	57	47.956	63.052	25.919	1.00	142.96
	5027	N	ALA	D	58	46.683	61.917	27.403	1.00	155.81
	5028	CA	ALA	D	58	47.775	61.140	27.966	1.00	155.81
65	5029	CB	ALA	D	58	47.245	60.191	29.002	1.00	45.44
	5030	C	ALA	D	58	48.595	60.375	26.939	1.00	155.81
	5031	O	ALA	D	58	48.086	59.524	26.214	1.00	155.81
	5032	N	LYS	D	59	49.881	60.690	26.890	1.00	75.94
	5033	CA	LYS	D	59	50.807	60.036	25.979	1.00	75.94
70	5034	CB	LYS	D	59	51.654	61.085	25.248	1.00	205.66

	5035	CG	LYS	D	59	50.830	62.088	24.439	1.00	205.66
	5036	CD	LYS	D	59	51.689	63.187	23.829	1.00	205.66
	5037	CE	LYS	D	59	50.838	64.174	23.036	1.00	205.66
5	5038	NZ	LYS	D	59	51.652	65.278	22.452	1.00	205.66
	5039	C	LYS	D	59	51.673	59.164	26.886	1.00	75.94
	5040	O	LYS	D	59	51.945	59.548	28.028	1.00	75.94
	5041	N	PHE	D	60	52.082	57.991	26.398	1.00	73.11
	5042	CA	PHE	D	60	52.916	57.070	27.183	1.00	73.11
	5043	CB	PHE	D	60	53.521	56.025	26.277	1.00	111.86
10	5044	CG	PHE	D	60	52.512	55.131	25.662	1.00	111.86
	5045	CD1	PHE	D	60	52.745	54.540	24.431	1.00	111.86
	5046	CD2	PHE	D	60	51.323	54.863	26.314	1.00	111.86
	5047	CE1	PHE	D	60	51.810	53.690	23.853	1.00	111.86
	5048	CE2	PHE	D	60	50.379	54.018	25.750	1.00	111.86
15	5049	CZ	PHE	D	60	50.622	53.429	24.517	1.00	111.86
	5050	C	PHE	D	60	54.026	57.782	27.946	1.00	73.11
	5051	O	PHE	D	60	54.401	57.368	29.037	1.00	73.11
	5052	N	GLU	D	61	54.544	58.863	27.369	1.00	133.04
	5053	CA	GLU	D	61	55.611	59.639	27.993	1.00	133.04
20	5054	CB	GLU	D	61	56.112	60.736	27.046	1.00	249.40
	5055	CG	GLU	D	61	56.707	60.232	25.750	1.00	249.40
	5056	CD	GLU	D	61	55.711	59.447	24.926	1.00	249.40
	5057	OE1	GLU	D	61	54.616	59.981	24.643	1.00	249.40
	5058	OE2	GLU	D	61	56.023	58.296	24.561	1.00	249.40
25	5059	C	GLU	D	61	55.162	60.298	29.289	1.00	133.04
	5060	O	GLU	D	61	55.995	60.638	30.124	1.00	133.04
	5061	N	ASP	D	62	53.854	60.493	29.452	1.00	85.82
	5062	CA	ASP	D	62	53.344	61.130	30.659	1.00	85.82
	5063	CB	ASP	D	62	51.887	61.546	30.471	1.00	150.56
30	5064	CG	ASP	D	62	51.694	62.436	29.258	1.00	150.56
	5065	OD1	ASP	D	62	52.584	63.274	28.983	1.00	150.56
	5066	OD2	ASP	D	62	50.650	62.302	28.585	1.00	150.56
	5067	C	ASP	D	62	53.484	60.179	31.838	1.00	85.82
	5068	O	ASP	D	62	53.464	60.605	32.999	1.00	85.82
35	5069	N	SER	D	63	53.636	58.888	31.532	1.00	75.53
	5070	CA	SER	D	63	53.798	57.858	32.566	1.00	75.53
	5071	CB	SER	D	63	53.958	56.471	31.933	1.00	120.69
	5072	OG	SER	D	63	52.776	56.060	31.271	1.00	120.69
	5073	C	SER	D	63	55.064	58.219	33.303	1.00	75.53
40	5074	O	SER	D	63	56.071	58.440	32.671	1.00	75.53
	5075	N	GLY	D	64	55.038	58.291	34.624	1.00	67.79
	5076	CA	GLY	D	64	56.262	58.644	35.318	1.00	67.79
	5077	C	GLY	D	64	56.113	58.959	36.798	1.00	67.79
	5078	O	GLY	D	64	55.060	58.708	37.391	1.00	67.79
45	5079	N	GLU	D	65	57.173	59.500	37.396	1.00	63.91
	5080	CA	GLU	D	65	57.212	59.843	38.817	1.00	63.91
	5081	CB	GLU	D	65	58.542	59.353	39.392	1.00	198.27
	5082	CG	GLU	D	65	58.869	59.830	40.778	1.00	198.27
	5083	CD	GLU	D	65	60.319	59.576	41.129	1.00	198.27
50	5084	OE1	GLU	D	65	61.203	60.162	40.465	1.00	198.27
	5085	OE2	GLU	D	65	60.576	58.786	42.061	1.00	198.27
	5086	C	GLU	D	65	57.098	61.355	38.943	1.00	63.91
	5087	O	GLU	D	65	57.862	62.078	38.322	1.00	63.91
	5088	N	TYR	D	66	56.151	61.849	39.727	1.00	104.89
55	5089	CA	TYR	D	66	55.995	63.295	39.869	1.00	104.89
	5090	CB	TYR	D	66	54.621	63.739	39.384	1.00	61.05
	5091	CG	TYR	D	66	54.348	63.543	37.922	1.00	61.05
	5092	CD1	TYR	D	66	54.057	62.291	37.403	1.00	61.05
	5093	CE1	TYR	D	66	53.721	62.142	36.065	1.00	61.05
60	5094	CD2	TYR	D	66	54.307	64.633	37.065	1.00	61.05
	5095	CE2	TYR	D	66	53.972	64.489	35.737	1.00	61.05
	5096	CZ	TYR	D	66	53.679	63.253	35.239	1.00	61.05
	5097	OH	TYR	D	66	53.338	63.149	33.911	1.00	61.05
	5098	C	TYR	D	66	56.119	63.743	41.314	1.00	104.89
65	5099	O	TYR	D	66	55.990	62.923	42.228	1.00	104.89
	5100	N	LYS	D	67	56.343	65.046	41.518	1.00	107.31
	5101	CA	LYS	D	67	56.437	65.618	42.867	1.00	107.31
	5102	CB	LYS	D	67	57.700	65.134	43.562	1.00	121.51
	5103	CG	LYS	D	67	58.926	65.307	42.721	1.00	121.51
70	5104	CD	LYS	D	67	60.124	64.712	43.416	1.00	121.51

	5105	CE	LYS	D	67	61.319	64.708	42.461	1.00	121.51
	5106	NZ	LYS	D	67	62.482	64.056	43.140	1.00	121.51
	5107	C	LYS	D	67	56.419	67.137	42.839	1.00	107.31
5	5108	O	LYS	D	67	56.758	67.744	41.836	1.00	107.31
	5109	N	CYS	D	68	55.994	67.747	43.937	1.00	110.81
	5110	CA	CYS	D	68	55.962	69.190	44.011	1.00	110.81
	5111	C	CYS	D	68	56.694	69.634	45.260	1.00	110.81
	5112	O	CYS	D	68	56.922	68.842	46.170	1.00	110.81
	5113	CB	CYS	D	68	54.518	69.727	43.988	1.00	140.31
10	5114	SG	CYS	D	68	53.384	69.216	45.310	1.00	140.31
	5115	N	GLN	D	69	57.093	70.900	45.274	1.00	126.93
	5116	CA	GLN	D	69	57.804	71.490	46.396	1.00	126.93
	5117	CB	GLN	D	69	59.300	71.191	46.281	1.00	112.91
	5118	CG	GLN	D	69	60.185	72.102	47.115	1.00	112.91
15	5119	CD	GLN	D	69	61.665	71.867	46.875	1.00	112.91
	5120	OE1	GLN	D	69	62.131	71.871	45.730	1.00	112.91
	5121	NE2	GLN	D	69	62.416	71.667	47.959	1.00	112.91
	5122	C	GLN	D	69	57.566	72.990	46.341	1.00	126.93
	5123	O	GLN	D	69	57.314	73.542	45.269	1.00	126.93
20	5124	N	HIS	D	70	57.642	73.652	47.488	1.00	191.71
	5125	CA	HIS	D	70	57.429	75.090	47.528	1.00	191.71
	5126	CB	HIS	D	70	56.372	75.434	48.577	1.00	178.35
	5127	CG	HIS	D	70	54.997	74.961	48.219	1.00	178.35
	5128	CD2	HIS	D	70	54.315	73.848	48.585	1.00	178.35
25	5129	ND1	HIS	D	70	54.173	75.648	47.353	1.00	178.35
	5130	CE1	HIS	D	70	53.041	74.981	47.202	1.00	178.35
	5131	NE2	HIS	D	70	53.101	73.886	47.940	1.00	178.35
	5132	C	HIS	D	70	58.711	75.856	47.808	1.00	191.71
	5133	O	HIS	D	70	59.813	75.299	47.784	1.00	191.71
30	5134	N	GLN	D	71	58.553	77.145	48.068	1.00	249.37
	5135	CA	GLN	D	71	59.681	78.018	48.338	1.00	249.37
	5136	CB	GLN	D	71	59.161	79.419	48.681	1.00	212.46
	5137	CG	GLN	D	71	60.101	80.540	48.260	1.00	212.46
	5138	CD	GLN	D	71	60.527	80.432	46.806	1.00	212.46
35	5139	OE1	GLN	D	71	59.736	80.661	45.894	1.00	212.46
	5140	NE2	GLN	D	71	61.786	80.066	46.587	1.00	212.46
	5141	C	GLN	D	71	60.570	77.474	49.462	1.00	249.37
	5142	O	GLN	D	71	61.775	77.297	49.269	1.00	249.37
	5143	N	GLN	D	72	59.974	77.195	50.622	1.00	156.64
40	5144	CA	GLN	D	72	60.728	76.683	51.771	1.00	156.64
	5145	CB	GLN	D	72	60.738	77.728	52.895	1.00	249.31
	5146	CG	GLN	D	72	61.596	77.360	54.104	1.00	249.31
	5147	CD	GLN	D	72	61.612	78.445	55.168	1.00	249.31
	5148	OE1	GLN	D	72	62.001	79.584	54.904	1.00	249.31
45	5149	NE2	GLN	D	72	61.187	78.096	56.378	1.00	249.31
	5150	C	GLN	D	72	60.149	75.374	52.302	1.00	156.64
	5151	O	GLN	D	72	59.772	75.277	53.472	1.00	156.64
	5152	N	VAL	D	73	60.084	74.362	51.446	1.00	234.28
	5153	CA	VAL	D	--	59.530	73.078	51.852	1.00	234.28
50	5154	CB	VAL	D	73	58.026	73.002	51.529	1.00	131.77
	5155	CG1	VAL	D	73	57.398	71.832	52.244	1.00	131.77
	5156	CG2	VAL	D	73	57.350	74.292	51.910	1.00	131.77
	5157	C	VAL	D	73	60.224	71.930	51.141	1.00	234.28
	5158	O	VAL	D	73	60.652	72.060	49.995	1.00	234.28
55	5159	N	ASN	D	74	60.337	70.802	51.824	1.00	160.29
	5160	CA	ASN	D	74	60.971	69.646	51.228	1.00	160.29
	5161	CB	ASN	D	74	61.437	68.687	52.321	1.00	140.71
	5162	CG	ASN	D	74	62.337	69.366	53.332	1.00	140.71
	5163	OD1	ASN	D	74	63.216	70.152	52.957	1.00	140.71
60	5164	ND2	ASN	D	74	62.130	69.065	54.613	1.00	140.71
	5165	C	ASN	D	74	59.985	68.964	50.286	1.00	160.29
	5166	O	ASN	D	74	58.839	68.692	50.653	1.00	160.29
	5167	N	GLU	D	75	60.446	68.711	49.064	1.00	155.73
	5168	CA	GLU	D	75	59.644	68.074	48.028	1.00	155.73
65	5169	CB	GLU	D	75	60.555	67.631	46.881	1.00	134.99
	5170	CG	GLU	D	75	61.940	67.190	47.322	1.00	134.99
	5171	CD	GLU	D	75	62.884	66.978	46.149	1.00	134.99
	5172	OE1	GLU	D	75	63.056	67.916	45.340	1.00	134.99
	5173	OE2	GLU	D	75	63.460	65.875	46.038	1.00	134.99
70	5174	C	GLU	D	75	58.794	66.907	48.520	1.00	155.73

	5175	O	GLU	D	75	59.207	66.137	49.385	1.00	155.73
	5176	N	SER	D	76	57.601	66.792	47.946	1.00	91.19
	5177	CA	SER	D	76	56.635	65.760	48.302	1.00	91.19
	5178	CB	SER	D	76	55.314	66.052	47.619	1.00	86.66
5	5179	OG	SER	D	76	55.477	65.917	46.224	1.00	86.66
	5180	C	SER	D	76	57.050	64.349	47.909	1.00	91.19
	5181	O	SER	D	76	57.892	64.165	47.020	1.00	91.19
	5182	N	GLU	D	77	56.431	63.362	48.562	1.00	100.72
	5183	CA	GLU	D	77	56.701	61.959	48.272	1.00	100.72
10	5184	CB	GLU	D	77	55.971	61.046	49.259	1.00	188.13
	5185	CG	GLU	D	77	56.457	61.191	50.694	1.00	188.13
	5186	CD	GLU	D	77	57.912	60.781	50.876	1.00	188.13
	5187	OE1	GLU	D	77	58.637	60.666	49.867	1.00	188.13
	5188	OE2	GLU	D	77	58.343	60.589	52.036	1.00	188.13
15	5189	C	GLU	D	77	56.203	61.715	46.857	1.00	100.72
	5190	O	GLU	D	77	55.012	61.851	46.588	1.00	100.72
	5191	N	PRO	D	78	57.108	61.380	45.928	1.00	89.58
	5192	CD	PRO	D	78	58.577	61.416	46.096	1.00	142.24
	5193	CA	PRO	D	78	56.752	61.125	44.532	1.00	89.58
20	5194	CB	PRO	D	78	58.018	60.508	43.955	1.00	142.24
	5195	CG	PRO	D	78	59.097	61.270	44.669	1.00	142.24
	5196	C	PRO	D	78	55.529	60.249	44.351	1.00	89.58
	5197	O	PRO	D	78	55.169	59.471	45.234	1.00	89.58
	5198	N	VAL	D	79	54.889	60.397	43.201	1.00	92.62
25	5199	CA	VAL	D	79	53.713	59.620	42.893	1.00	92.62
	5200	CB	VAL	D	79	52.466	60.484	42.999	1.00	66.56
	5201	CG1	VAL	D	79	51.284	59.785	42.333	1.00	66.56
	5202	CG2	VAL	D	79	52.177	60.763	44.458	1.00	66.56
	5203	C	VAL	D	79	53.834	59.092	41.483	1.00	92.62
30	5204	O	VAL	D	79	54.122	59.880	40.566	1.00	92.62
	5205	N	TYR	D	80	53.625	57.782	41.295	1.00	61.19
	5206	CA	TYR	D	80	53.757	57.256	39.952	1.00	61.19
	5207	CB	TYR	D	80	54.372	55.878	39.936	1.00	249.26
	5208	CG	TYR	D	80	54.869	55.534	38.557	1.00	249.26
35	5209	CD1	TYR	D	80	55.895	56.275	37.979	1.00	249.26
	5210	CE1	TYR	D	80	56.370	55.971	36.708	1.00	249.26
	5211	CD2	TYR	D	80	54.335	54.491	37.816	1.00	249.26
	5212	CE2	TYR	D	80	54.829	54.208	36.532	1.00	249.26
	5213	CZ	TYR	D	80	55.822	54.920	35.993	1.00	249.26
40	5214	OH	TYR	D	80	56.359	54.647	34.755	1.00	249.26
	5215	C	TYR	D	80	52.471	57.184	39.194	1.00	61.19
	5216	O	TYR	D	80	51.448	56.804	39.737	1.00	61.19
	5217	N	LEU	D	81	52.529	57.540	37.924	1.00	59.82
	5218	CA	LEU	D	81	51.354	57.492	37.090	1.00	59.82
45	5219	CB	LEU	D	81	51.089	58.875	36.535	1.00	66.30
	5220	CG	LEU	D	81	49.972	58.868	35.515	1.00	66.30
	5221	CD1	LEU	D	81	48.705	58.435	36.202	1.00	66.30
	5222	CD2	LEU	D	81	49.808	60.240	34.932	1.00	66.30
	5223	C	LEU	D	81	51.664	56.531	35.945	1.00	59.82
50	5224	O	LEU	D	81	52.715	56.663	35.333	1.00	59.82
	5225	N	GLU	D	82	50.795	55.561	35.658	1.00	81.20
	5226	CA	GLU	D	82	51.069	54.640	34.557	1.00	81.20
	5227	CB	GLU	D	82	51.229	53.211	35.072	1.00	125.93
	5228	CG	GLU	D	82	52.081	52.353	34.149	1.00	125.93
55	5229	CD	GLU	D	82	52.264	50.938	34.661	1.00	125.93
	5230	OE1	GLU	D	82	52.389	50.771	35.897	1.00	125.93
	5231	OE2	GLU	D	82	52.299	50.001	33.829	1.00	125.93
	5232	C	GLU	D	82	49.959	54.695	33.498	1.00	81.20
	5233	O	GLU	D	82	48.765	54.633	33.821	1.00	81.20
60	5234	N	VAL	D	83	50.348	54.809	32.230	1.00	74.09
	5235	CA	VAL	D	83	49.379	54.891	31.140	1.00	74.09
	5236	CB	VAL	D	83	49.747	56.013	30.177	1.00	86.03
	5237	CG1	VAL	D	83	48.810	55.997	28.998	1.00	86.03
	5238	CG2	VAL	D	83	49.675	57.340	30.895	1.00	86.03
65	5239	C	VAL	D	83	49.250	53.603	30.340	1.00	74.09
	5240	O	VAL	D	83	50.237	53.000	29.949	1.00	74.09
	5241	N	PHE	D	84	48.023	53.191	30.067	1.00	81.44
	5242	CA	PHE	D	84	47.811	51.957	29.331	1.00	81.44
	5243	CB	PHE	D	84	47.087	50.944	30.191	1.00	68.59
70	5244	CG	PHE	D	84	47.803	50.598	31.437	1.00	68.59

	5245	CD1	PHE	D	84	47.835	51.485	32.486	1.00	68.59
	5246	CD2	PHE	D	84	48.418	49.359	31.583	1.00	68.59
	5247	CE1	PHE	D	84	48.470	51.153	33.667	1.00	68.59
	5248	CE2	PHE	D	84	49.058	49.016	32.765	1.00	68.59
5	5249	CZ	PHE	D	84	49.078	49.917	33.809	1.00	68.59
	5250	C	PHE	D	84	47.029	52.029	28.041	1.00	81.44
	5251	O	PHE	D	84	46.324	52.998	27.746	1.00	81.44
	5252	N	SER	D	85	47.149	50.938	27.301	1.00	99.54
	5253	CA	SER	D	85	46.462	50.731	26.049	1.00	99.54
10	5254	CB	SER	D	85	47.414	50.901	24.866	1.00	104.48
	5255	OG	SER	D	85	46.741	50.652	23.644	1.00	104.48
	5256	C	SER	D	85	46.015	49.277	26.155	1.00	99.54
	5257	O	SER	D	85	46.843	48.362	26.130	1.00	99.54
	5258	N	ASP	D	86	44.713	49.067	26.315	1.00	64.12
15	5259	CA	ASP	D	86	44.166	47.724	26.426	1.00	64.12
	5260	CB	ASP	D	86	44.715	47.030	27.676	1.00	91.49
	5261	CG	ASP	D	86	44.939	45.556	27.454	1.00	91.49
	5262	OD1	ASP	D	86	43.981	44.874	27.027	1.00	91.49
	5263	OD2	ASP	D	86	46.065	¨ 077	27.697	1.00	91.49
20	5264	C	ASP	D	86	42.631	47.816	26.481	1.00	64.12
	5265	O	ASP	D	86	42.085	48.907	26.673	1.00	64.12
	5266	N	TRP	D	87	41.937	46.686	26.293	1.00	76.92
	5267	CA	TRP	D	87	40.470	46.689	26.321	1.00	76.92
25	5268	CB	TRP	D	87	39.893	45.330	25.950	1.00	235.26
	5269	CG	TRP	D	87	39.745	45.196	24.519	1.00	235.26
	5270	CD2	TRP	D	87	40.716	44.672	23.629	1.00	235.26
	5271	CE2	TRP	D	87	40.219	44.865	22.334	1.00	235.26
	5272	CE3	TRP	D	87	41.945	44.025	23.805	1.00	235.26
	5273	CD1	TRP	D	87	38.730	45.693	23.748	1.00	235.26
30	5274	NE1	TRP	D	87	39.014	45.491	22.409	1.00	235.26
	5275	CZ2	TRP	D	87	40.942	44.480	21.244	1.00	235.26
	5276	CZ3	TRP	D	87	42.651	43.619	22.683	1.00	235.26
	5277	CH2	TRP	D	87	42.147	43.865	21.422	1.00	235.26
	5278	C	TRP	D	87	39.956	47.074	27.680	1.00	76.92
35	5279	O	TRP	D	87	39.124	47.968	27.818	1.00	76.92
	5280	N	LEU	D	88	40.465	46.386	28.690	1.00	86.84
	5281	CA	LEU	D	88	40.070	46.643	30.064	1.00	86.84
	5282	CB	LEU	D	88	39.344	45.435	30.635	1.00	73.66
	5283	CG	LEU	D	88	38.028	45.109	29.953	1.00	73.66
40	5284	CD1	LEU	D	88	37.368	43.952	30.664	1.00	73.66
	5285	CD2	LEU	D	88	37.156	46.335	29.991	1.00	73.66
	5286	C	LEU	D	88	41.248	46.962	30.953	1.00	86.84
	5287	O	LEU	D	88	42.330	46.396	30.820	1.00	86.84
	5288	N	LEU	D	89	41.022	47.870	31.883	1.00	45.19
45	5289	CA	LEU	D	89	42.067	48.266	32.809	1.00	45.19
	5290	CB	LEU	D	89	42.573	49.655	32.473	1.00	158.38
	5291	CG	LEU	D	89	43.628	50.105	33.471	1.00	158.38
	5292	CD1	LEU	D	89	44.671	49.002	33.642	1.00	158.38
	5293	CD2	LEU	D	89	44.255	51.392	32.982	1.00	158.38
50	5294	C	LEU	D	89	41.502	48.263	34.219	1.00	45.19
	5295	O	LEU	D	89	40.455	48.848	34.463	1.00	45.19
	5296	N	LEU	D	90	42.164	47.592	35.153	1.00	80.53
	5297	CA	LEU	D	90	41.666	47.579	36.523	1.00	80.53
	5298	CB	LEU	D	90	42.086	46.305	37.234	1.00	38.85
55	5299	CG	LEU	D	90	41.710	46.256	38.724	1.00	38.85
	5300	CD1	LEU	D	90	40.189	46.295	38.793	1.00	38.85
	5301	CD2	LEU	D	90	42.228	45.002	39.432	1.00	38.85
	5302	C	LEU	D	90	42.245	48.766	37.280	1.00	80.53
	5303	O	LEU	D	90	43.445	48.858	37.467	1.00	80.53
60	5304	N	GLN	D	91	41.400	49.670	37.742	1.00	44.32
	5305	CA	GLN	D	91	41.899	50.833	38.464	1.00	44.32
	5306	CB	GLN	D	91	41.209	52.089	37.953	1.00	57.44
	5307	CG	GLN	D	91	41.391	52.283	36.487	1.00	57.44
	5308	CD	GLN	D	91	40.897	53.611	36.016	1.00	57.44
65	5309	OE1	GLN	D	91	39.700	53.857	35.979	1.00	57.44
	5310	NE2	GLN	D	91	41.816	54.489	35.664	1.00	57.44
	5311	C	GLN	D	91	41.685	50.714	39.963	1.00	44.32
	5312	O	GLN	D	91	40.691	50.176	40.435	1.00	44.32
	5313	N	ALA	D	92	42.613	51.230	40.737	1.00	48.50
70	5314	CA	ALA	D	92	42.451	51.152	42.169	1.00	48.50

	5315	CB	ALA	D	92	43.463	50.189	42.739	1.00	52.70
	5316	C	ALA	D	92	42.636	52.538	42.787	1.00	48.50
	5317	O	ALA	D	92	43.475	53.347	42.341	1.00	48.50
	5318	N	SER	D	93	41.846	52.825	43.811	1.00	53.99
5	5319	CA	SER	D	93	41.960	54.102	44.481	1.00	53.99
	5320	CB	SER	D	93	41.048	54.158	45.713	1.00	83.49
	5321	OG	SER	D	93	41.207	53.030	46.543	1.00	83.49
	5322	C	SER	D	93	43.412	54.212	44.877	1.00	53.99
	5323	O	SER	D	93	44.134	55.046	44.361	1.00	53.99
10	5324	N	ALA	D	94	43.850	53.338	45.764	1.00	62.76
	5325	CA	ALA	D	94	45.232	53.342	46.220	1.00	62.76
	5326	CB	ALA	D	94	45.301	53.851	47.636	1.00	112.27
	5327	C	ALA	D	94	45.723	51.909	46.150	1.00	62.76
	5328	O	ALA	D	94	44.942	50.990	46.361	1.00	62.76
15	5329	N	GLU	D	95	47.006	51.704	45.854	1.00	73.31
	5330	CA	GLU	D	95	47.535	50.339	45.746	1.00	73.31
	5331	CB	GLU	D	95	48.677	50.301	44.746	1.00	116.96
	5332	CG	GLU	D	95	48.262	50.756	43.364	1.00	116.96
	5333	CL	GLU	D	95	49.287	50.405	42.301	1.00	116.96
20	5334	OE1	GLU	D	95	49.057	50.758	41.121	1.00	116.96
	5335	OE2	GLU	D	95	50.320	49.776	42.643	1.00	116.96
	5336	C	GLU	D	95	47.987	49.724	47.063	1.00	73.31
	5337	O	GLU	D	95	48.194	48.517	47.143	1.00	73.31
	5338	N	VAL	D	96	48.139	50.563	48.089	1.00	71.30
25	5339	CA	VAL	D	96	48.557	50.126	49.422	1.00	71.30
	5340	CB	VAL	D	96	50.010	50.433	49.657	1.00	83.19
	5341	CG1	VAL	D	96	50.502	49.611	50.812	1.00	83.19
	5342	CG2	VAL	D	96	50.802	50.132	48.410	1.00	83.19
	5343	C	VAL	D	96	47.713	50.869	50.435	1.00	71.30
30	5344	O	VAL	D	96	47.560	52.071	50.347	1.00	71.30
	5345	N	VAL	D	97	47.190	50.159	51.420	1.00	69.41
	5346	CA	VAL	D	97	46.277	50.778	52.365	1.00	69.41
	5347	CB	VAL	D	97	44.849	50.417	51.970	1.00	60.29
	5348	CG1	VAL	D	97	43.889	51.256	52.717	1.00	60.29
35	5349	CG2	VAL	D	97	44.654	50.562	50.501	1.00	60.29
	5350	C	VAL	D	97	46.410	50.374	53.828	1.00	69.41
	5351	O	VAL	D	97	46.540	49.185	54.136	1.00	69.41
	5352	N	MET	D	98	46.316	51.350	54.730	1.00	72.66
	5353	CA	MET	D	98	46.389	51.084	56.169	1.00	72.66
40	5354	CB	MET	D	98	46.498	52.404	56.921	1.00	249.19
	5355	CG	MET	D	98	47.751	53.177	56.594	1.00	249.19
	5356	SD	MET	D	98	49.140	52.518	57.501	1.00	249.19
	5357	CE	MET	D	98	48.761	53.180	59.122	1.00	249.19
	5358	C	MET	D	98	45.110	50.363	56.592	1.00	72.66
45	5359	O	MET	D	98	44.014	50.780	56.201	1.00	72.66
	5360	N	GLU	D	99	45.234	49.288	57.373	1.00	68.49
	5361	CA	GLU	D	99	44.063	48.535	57.828	1.00	68.49
	5362	CB	GLU	D	99	44.441	47.605	58.977	1.00	249.24
	5363	CG	GLU	D	99	43.474	46.454	59.176	1.00	249.24
50	5364	CD	GLU	D	99	43.683	45.744	60.499	1.00	249.24
	5365	OE1	GLU	D	99	44.852	45.590	60.913	1.00	249.24
	5366	OE2	GLU	D	99	42.679	45.331	61.120	1.00	249.24
	5367	C	GLU	D	99	43.007	49.529	58.315	1.00	68.49
	5368	O	GLU	D	99	43.308	50.396	59.129	1.00	68.49
55	5369	N	GLY	D	100	41.786	49.439	57.807	1.00	99.19
	5370	CA	GLY	D	100	40.757	50.360	58.251	1.00	99.19
	5371	C	GLY	D	100	40.336	51.428	57.256	1.00	99.19
	5372	O	GLY	D	100	39.252	52.016	57.398	1.00	99.19
	5373	N	GLN	D	101	41.167	51.678	56.244	1.00	64.03
60	5374	CA	GLN	D	101	40.845	52.709	55.249	1.00	64.03
	5375	CB	GLN	D	101	42.121	53.294	54.653	1.00	115.74
	5376	CG	GLN	D	101	42.956	54.053	55.650	1.00	115.74
	5377	CD	GLN	D	101	42.145	55.055	56.435	1.00	115.74
	5378	OE1	GLN	D	101	41.427	54.698	57.365	1.00	115.74
65	5379	NE2	GLN	D	101	42.246	56.318	56.053	1.00	115.74
	5380	C	GLN	D	101	39.939	52.240	54.118	1.00	64.03
	5381	O	GLN	D	101	39.701	51.050	53.960	1.00	64.03
	5382	N	PRO	D	102	39.411	53.178	53.317	1.00	85.32
	5383	CD	PRO	D	102	39.527	54.647	53.374	1.00	90.00
70	5384	CA	PRO	D	102	38.536	52.761	52.218	1.00	85.32

	5385	CB	PRO	D	102	37.759	54.032	51.911	1.00	90.00
	5386	CG	PRO	D	102	38.814	55.078	52.098	1.00	90.00
	5387	C	PRO	D	102	39.365	52.273	51.026	1.00	85.32
	5388	O	PRO	D	102	40.528	52.659	50.867	1.00	85.32
5	5389	N	LEU	D	103	38.760	51.430	50.194	1.00	84.38
	5390	CA	LEU	D	103	39.424	50.903	49.016	1.00	84.38
	5391	CB	LEU	D	103	39.973	49.525	49.315	1.00	75.67
	5392	CG	LEU	D	103	40.655	48.977	48.070	1.00	75.67
	5393	CD1	LEU	D	103	41.849	49.845	47.739	1.00	75.67
10	5394	CD2	LEU	D	103	41.095	47.543	48.305	1.00	75.67
	5395	C	LEU	D	103	38.467	50.792	47.854	1.00	84.38
	5396	O	LEU	D	103	37.453	50.135	47.974	1.00	84.38
	5397	N	PHE	D	104	38.771	51.419	46.728	1.00	75.73
	5398	CA	PHE	D	104	37.865	51.312	45.586	1.00	75.73
15	5399	CB	PHE	D	104	37.272	52.679	45.208	1.00	163.52
	5400	CG	PHE	D	104	36.530	53.359	46.322	1.00	163.52
	5401	CD1	PHE	D	104	37.222	53.984	47.352	1.00	163.52
	5402	CD2	PHE	D	104	35.139	53.381	46.342	1.00	163.52
	5403	CE1	PHE	D	104	36.542	54.625	48.393	1.00	163.52
20	5404	CE2	PHE	D	104	34.446	54.020	47.381	1.00	163.52
	5405	CZ	PHE	D	104	35.152	54.643	48.407	1.00	163.52
	5406	C	PHE	D	104	38.550	50.717	44.353	1.00	75.73
	5407	O	PHE	D	104	39.617	51.181	43.942	1.00	75.73
	5408	N	LEU	D	105	37.950	49.684	43.769	1.00	46.40
25	5409	CA	LEU	D	105	38.504	49.069	42.561	1.00	46.40
	5410	CB	LEU	D	105	38.633	47.555	42.722	1.00	51.89
	5411	CG	LEU	D	105	39.461	47.169	43.932	1.00	51.89
	5412	CD1	LEU	D	105	39.723	45.660	43.969	1.00	51.89
	5413	CD2	LEU	D	105	40.750	47.942	43.836	1.00	51.89
30	5414	C	LEU	D	105	37.518	49.366	41.456	1.00	46.40
	5415	O	LEU	D	105	36.330	49.413	41.701	1.00	46.40
	5416	N	ARG	D	106	37.988	49.551	40.236	1.00	68.20
	5417	CA	ARG	D	106	37.073	49.852	39.159	1.00	68.20
	5418	CB	ARG	D	106	37.090	51.354	38.922	1.00	103.77
35	5419	CG	ARG	D	106	36.259	51.801	37.762	1.00	103.77
	5420	CD	ARG	D	106	36.514	53.271	37.452	1.00	103.77
	5421	NE	ARG	D	106	35.766	53.701	36.275	1.00	103.77
	5422	CZ	ARG	D	106	36.095	54.738	35.519	1.00	103.77
	5423	NH1	ARG	D	106	37.170	55.458	35.811	1.00	103.77
40	5424	NH2	ARG	D	106	35.353	55.044	34.462	1.00	103.77
	5425	C	ARG	D	106	37.457	49.119	37.876	1.00	68.20
	5426	O	ARG	D	106	38.595	49.240	37.415	1.00	68.20
	5427	N	CYS	D	107	36.535	48.340	37.309	1.00	54.86
	5428	CA	CYS	D	107	36.842	47.659	36.053	1.00	54.86
45	5429	C	CYS	D	107	36.528	48.688	34.983	1.00	54.86
	5430	O	CYS	D	107	35.365	49.000	34.720	1.00	54.86
	5431	CB	CYS	D	107	35.984	46.421	35.850	1.00	81.59
	5432	SG	CYS	D	107	36.664	45.289	34.601	1.00	81.59
	5433	N	HIS	D	108	37.578	49.236	34.384	1.00	77.64
50	5434	CA	HIS	D	108	37.449	50.285	33.386	1.00	77.64
	5435	CB	HIS	D	108	38.460	51.352	33.687	1.00	84.93
	5436	CG	HIS	D	108	38.301	52.573	32.853	1.00	84.93
	5437	CD2	HIS	D	108	39.176	53.230	32.060	1.00	84.93
	5438	ND1	HIS	D	108	37.136	53.301	32.834	1.00	84.93
55	5439	CE1	HIS	D	108	37.306	54.364	32.068	1.00	84.93
	5440	NE2	HIS	D	108	38.534	54.346	31.587	1.00	84.93
	5441	C	HIS	D	108	37.608	49.848	31.945	1.00	77.64
	5442	O	HIS	D	108	38.604	49.229	31.559	1.00	77.64
	5443	N	GLY	D	109	36.618	50.206	31.143	1.00	64.08
60	5444	CA	GLY	D	109	36.637	49.820	29.750	1.00	64.08
	5445	C	GLY	D	109	37.367	50.854	28.945	1.00	64.08
	5446	O	GLY	D	109	37.498	52.002	29.379	1.00	64.08
	5447	N	TRP	D	110	37.858	50.446	27.781	1.00	110.56
65	5448	CA	TRP	D	110	38.575	51.353	26.806	1.00	110.56
	5449	CB	TRP	D	110	39.206	50.578	25.749	1.00	129.78
	5450	CG	TRP	D	110	39.819	51.456	24.721	1.00	129.78
	5451	CD2	TRP	D	110	41.184	51.879	24.659	1.00	129.78
	5452	CE2	TRP	D	110	41.307	52.743	23.557	1.00	129.78
	5453	CE3	TRP	D	110	42.322	51.608	25.434	1.00	129.78
70	5454	CD1	TRP	D	110	39.184	52.062	23.682	1.00	129.78

	5455	NE1	TRP	D	110	40.068	52.836	22.977	1.00	129.78
	5456	CZ2	TRP	D	110	42.514	53.345	23.204	1.00	129.78
	5457	CZ3	TRP	D	110	43.525	52.208	25.083	1.00	129.78
5	5458	CH2	TRP	D	110	43.609	53.068	23.980	1.00	129.78
	5459	C	TRP	D	110	37.623	52.414	26.377	1.00	110.56
	5460	O	TRP	D	110	36.417	52.183	26.252	1.00	110.56
	5461	N	ARG	D	111	38.170	53.591	26.091	1.00	110.12
	5462	CA	ARG	D	111	37.377	54.696	25.564	1.00	110.12
	5463	CB	ARG	D	111	37.068	54.455	24.113	1.00	249.23
10	5464	CG	ARG	D	111	38.127	54.981	23.233	1.00	249.23
	5465	CD	ARG	D	111	37.639	54.963	21.844	1.00	249.23
	5466	NE	ARG	D	111	38.039	56.180	21.160	1.00	249.23
	5467	CZ	ARG	D	111	37.564	57.390	21.444	1.00	249.23
	5468	NH1	ARG	D	111	36.661	57.561	22.411	1.00	249.23
15	5469	NH2	ARG	D	111	38.007	58.437	20.760	1.00	249.23
	5470	C	ARG	D	111	36.070	54.939	26.286	1.00	110.12
	5471	O	ARG	D	111	35.117	55.496	25.736	1.00	110.12
	5472	N	ASN	D	112	36.031	54.502	27.527	1.00	80.55
	5473	CA	ASN	D	112	34.859	54.663	28.349	1.00	80.55
20	5474	CB	ASN	D	112	34.546	56.137	28.546	1.00	69.20
	5475	CG	ASN	D	112	33.765	56.379	29.815	1.00	69.20
	5476	OD1	ASN	D	112	33.075	55.484	30.307	1.00	69.20
	5477	ND2	ASN	D	112	33.863	57.586	30.355	1.00	69.20
	5478	C	ASN	D	112	33.621	53.963	27.813	1.00	80.55
25	5479	O	ASN	D	112	32.500	54.357	28.143	1.00	80.55
	5480	N	TRP	D	113	33.544	52.930	26.998	1.00	104.63
	5481	CA	TRP	D	113	32.649	52.207	26.504	1.00	104.63
	5482	CB	TRP	D	113	33.045	51.128	25.519	1.00	141.29
	5483	CG	TRP	D	113	33.355	51.652	24.198	1.00	141.29
30	5484	CD2	TRP	D	113	34.368	51.180	23.311	1.00	141.29
	5485	CE2	TRP	D	113	34.278	51.944	22.133	1.00	141.29
	5486	CE3	TRP	D	113	35.343	50.182	23.397	1.00	141.29
	5487	CD1	TRP	D	113	32.705	52.655	23.541	1.00	141.29
	5488	NE1	TRP	D	113	33.254	52.837	22.296	1.00	141.29
35	5489	CZ2	TRP	D	113	35.126	51.743	21.057	1.00	141.29
	5490	CZ3	TRP	D	113	36.188	49.984	22.324	1.00	141.29
	5491	CH2	TRP	D	113	36.075	50.761	21.173	1.00	141.29
	5492	C	TRP	D	113	31.928	51.542	27.656	1.00	104.63
	5493	O	TRP	D	113	32.215	51.806	28.828	1.00	104.63
40	5494	N	ASP	D	114	30.990	50.668	27.313	1.00	117.64
	5495	CA	ASP	D	114	30.229	49.960	28.320	1.00	117.64
	5496	CB	ASP	D	114	28.725	50.109	28.065	1.00	192.42
	5497	CG	ASP	D	114	28.176	51.431	28.576	1.00	192.42
	5498	OD1	ASP	D	114	28.288	51.685	29.796	1.00	192.42
45	5499	OD2	ASP	D	114	27.636	52.214	27.764	1.00	192.42
	5500	C	ASP	D	114	30.619	48.498	28.345	1.00	117.64
	5501	O	ASP	D	114	30.831	47.875	27.301	1.00	117.64
	5502	N	VAL	D	115	30.730	47.967	29.559	1.00	73.71
	5503	CA	VAL	D	115	31.084	46.577	29.766	1.00	73.71
50	5504	CB	VAL	D	115	32.340	46.448	30.614	1.00	75.80
	5505	CG1	VAL	D	115	32.827	45.011	30.593	1.00	75.80
	5506	CG2	VAL	D	115	33.403	47.378	30.086	1.00	75.80
	5507	C	VAL	D	115	29.947	45.862	30.481	1.00	73.71
	5508	O	VAL	D	115	29.301	46.431	31.368	1.00	73.71
55	5509	N	TYR	D	116	29.700	44.615	30.078	1.00	69.51
	5510	CA	TYR	D	116	28.642	43.810	30.672	1.00	69.51
	5511	CB	TYR	D	116	27.563	43.539	29.638	1.00	100.20
	5512	CG	TYR	D	116	26.886	44.780	29.133	1.00	100.20
	5513	CD1	TYR	D	116	27.276	45.376	27.942	1.00	100.20
60	5514	CE1	TYR	D	116	26.660	46.549	27.481	1.00	100.20
	5515	CD2	TYR	D	116	25.866	45.375	29.858	1.00	100.20
	5516	CE2	TYR	D	116	25.243	46.545	29.412	1.00	100.20
	5517	CZ	TYR	D	116	25.648	47.127	28.225	1.00	100.20
	5518	OH	TYR	D	116	25.060	48.293	27.795	1.00	100.20
65	5519	C	TYR	D	116	29.179	42.488	31.222	1.00	69.51
	5520	O	TYR	D	116	30.341	42.127	30.986	1.00	69.51
	5521	N	LYS	D	117	28.327	41.766	31.947	1.00	88.92
	5522	CA	LYS	D	117	28.708	40.492	32.541	1.00	88.92
	5523	CB	LYS	D	117	28.772	39.397	31.480	1.00	111.93
70	5524	CG	LYS	D	117	27.453	38.715	31.180	1.00	111.93

5525	CD	LYS	D	117	27.695	37.387	30.471	1.00	111.93
5526	CE	LYS	D	117	28.540	36.435	31.338	1.00	111.93
5527	NZ	LYS	D	117	28.852	35.125	30.675	1.00	111.93
5528	C	LYS	D	117	30.069	40.625	33.213	1.00	88.92
5529	O	LYS	D	117	31.002	39.882	32.909	1.00	88.92
5530	N	VAL	D	118	30.182	41.578	34.129	1.00	81.88
5531	CA	VAL	D	118	31.433	41.816	34.828	1.00	81.88
5532	CB	VAL	D	118	31.524	43.274	35.241	1.00	84.78
5533	CG1	VAL	D	118	32.404	43.434	36.459	1.00	84.78
5534	CG2	VAL	D	118	32.104	44.055	34.101	1.00	84.78
5535	C	VAL	D	118	31.693	40.949	36.052	1.00	81.88
5536	O	VAL	D	118	30.803	40.742	36.893	1.00	81.88
5537	N	ILE	D	119	32.928	40.468	36.171	1.00	56.52
5538	CA	ILE	D	119	33.296	39.637	37.310	1.00	56.52
5539	CB	ILE	D	119	33.364	38.181	36.895	1.00	59.73
5540	CG2	ILE	D	119	33.652	37.309	38.094	1.00	59.73
5541	CG1	ILE	D	119	32.058	37.776	36.217	1.00	59.73
5542	CD1	ILE	D	119	32.154	36.446	35.534	1.00	59.73
5543	C	ILE	D	119	34.662	40.027	37.826	1.00	56.52
5544	O	ILE	D	119	35.611	40.026	37.057	1.00	56.52
5545	N	TYR	D	120	34.785	40.378	39.104	1.00	51.66
5546	CA	TYR	D	120	36.115	40.736	39.618	1.00	51.66
5547	CB	TYR	D	120	36.064	41.770	40.742	1.00	57.63
5548	CG	TYR	D	120	35.658	43.139	40.320	1.00	57.63
5549	CD1	TYR	D	120	34.336	43.470	40.170	1.00	57.63
5550	CE1	TYR	D	120	33.960	44.720	39.744	1.00	57.63
5551	CD2	TYR	D	120	36.599	44.093	40.038	1.00	57.63
5552	CE2	TYR	D	120	36.237	45.353	39.609	1.00	57.63
5553	CZ	TYR	D	120	34.915	45.656	39.464	1.00	57.63
5554	OH	TYR	D	120	34.549	46.902	39.039	1.00	57.63
5555	C	TYR	D	120	36.702	39.486	40.200	1.00	51.66
5556	O	TYR	D	120	35.971	38.657	40.725	1.00	51.66
5557	N	TYR	D	121	38.015	39.353	40.123	1.00	46.59
5558	CA	TYR	D	121	38.667	38.180	40.684	1.00	46.59
5559	CB	TYR	D	121	39.304	37.344	39.572	1.00	81.03
5560	CG	TYR	D	121	38.357	36.640	38.623	1.00	81.03
5561	CD1	TYR	D	121	37.541	37.362	37.761	1.00	81.03
5562	CE1	TYR	D	121	36.705	36.721	36.856	1.00	81.03
5563	CD2	TYR	D	121	38.311	35.244	38.562	1.00	81.03
5564	CE2	TYR	D	121	37.478	34.597	37.666	1.00	81.03
5565	CZ	TYR	D	121	36.672	35.345	36.808	1.00	81.03
5566	OH	TYR	D	121	35.835	34.720	35.894	1.00	81.03
5567	C	TYR	D	121	39.771	38.566	41.683	1.00	46.59
5568	O	TYR	D	121	40.518	39.538	41.473	1.00	46.59
5569	N	LYS	D	122	39.876	37.809	42.770	1.00	72.20
5570	CA	LYS	D	122	40.920	38.054	43.759	1.00	72.20
5571	CB	LYS	D	122	40.357	38.585	45.073	1.00	128.16
5572	CG	LYS	D	122	41.440	38.842	46.100	1.00	128.16
5573	CD	LYS	D	122	40.869	39.066	47.470	1.00	128.16
5574	CE	LYS	D	122	41.973	39.176	48.496	1.00	128.16
5575	NZ	LYS	D	122	41.394	39.233	49.865	1.00	128.16
5576	C	LYS	D	122	41.598	36.736	44.028	1.00	72.20
5577	O	LYS	D	122	40.977	35.813	44.536	1.00	72.20
5578	N	ASP	D	123	42.876	36.658	43.692	1.00	101.46
5579	CA	ASP	D	123	43.660	35.450	43.884	1.00	101.46
5580	CB	ASP	D	123	43.802	35.135	45.375	1.00	177.22
5581	CG	ASP	D	123	44.795	36.049	46.065	1.00	177.22
5582	OD1	ASP	D	123	45.903	36.238	45.518	1.00	177.22
5583	OD2	ASP	D	123	44.477	36.572	47.154	1.00	177.22
5584	C	ASP	D	123	43.079	34.258	43.138	1.00	101.46
5585	O	ASP	D	123	43.017	33.147	43.668	1.00	101.46
5586	N	GLY	D	124	42.661	34.502	41.898	1.00	89.52
5587	CA	GLY	D	124	42.103	33.456	41.056	1.00	89.52
5588	C	GLY	D	124	40.673	33.041	41.346	1.00	89.52
5589	O	GLY	D	124	40.092	32.261	40.587	1.00	89.52
5590	N	GLU	D	125	40.097	33.559	42.428	1.00	72.85
5591	CA	GLU	D	125	38.730	33.206	42.826	1.00	72.85
5592	CB	GLU	D	125	38.599	33.194	44.362	1.00	232.74
5593	CG	GLU	D	125	39.348	32.082	45.103	1.00	232.74
5594	CD	GLU	D	125	38.625	30.746	45.068	1.00	232.74

	5595	OE1	GLU	D	125	37.493	30.662	45.593	1.00	232.74
	5596	OE2	GLU	D	125	39.194	29.780	44.517	1.00	232.74
	5597	C	GLU	D	125	37.706	34.202	42.280	1.00	72.85
5	5598	O	GLU	D	125	37.974	35.404	42.183	1.00	72.85
	5599	N	ALA	D	126	36.527	33.708	41.926	1.00	95.10
	5600	CA	ALA	D	126	35.472	34.595	41.450	1.00	95.10
	5601	CB	ALA	D	126	34.290	33.791	40.991	1.00	132.03
	5602	C	ALA	D	126	35.119	35.403	42.693	1.00	95.10
	5603	O	ALA	D	126	35.153	34.869	43.802	1.00	95.10
10	5604	N	LEU	D	127	34.782	36.678	42.531	1.00	64.20
	5605	CA	LEU	D	127	34.470	37.522	43.697	1.00	64.20
	5606	CB	LEU	D	127	35.559	38.566	43.919	1.00	89.10
	5607	CG	LEU	D	127	35.546	38.957	45.392	1.00	89.10
	5608	CD1	LEU	D	127	35.768	37.691	46.219	1.00	89.10
15	5609	CD2	LEU	D	127	36.612	39.988	45.686	1.00	89.10
	5610	C	LEU	D	127	33.138	38.237	43.722	1.00	64.20
	5611	O	LEU	D	127	32.408	38.098	44.686	1.00	64.20
	5612	N	LYS	D	128	32.859	39.041	42.702	1.00	63.83
	5613	CA	LYS	D	128	31.584	39.742	42.583	1.00	63.83
20	5614	CB	LYS	D	128	31.737	41.203	43.000	1.00	126.01
	5615	CG	LYS	D	128	32.165	41.409	44.431	1.00	126.01
	5616	CD	LYS	D	128	31.058	41.080	45.416	1.00	126.01
	5617	CE	LYS	D	128	31.491	41.410	46.843	1.00	126.01
	5618	NZ	LYS	D	128	30.404	44.252	47.855	1.00	126.01
25	5619	C	LYS	D	128	31.160	39.675	41.109	1.00	63.83
	5620	O	LYS	D	128	32.021	39.580	40.219	1.00	63.83
	5621	N	TYR	D	129	29.857	39.741	40.833	1.00	62.64
	5622	CA	TYR	D	129	29.387	39.683	39.444	1.00	62.64
	5623	CB	TYR	D	129	28.984	38.268	39.098	1.00	80.75
30	5624	CG	TYR	D	129	28.046	38.200	37.928	1.00	80.75
	5625	CD1	TYR	D	129	28.521	38.321	36.629	1.00	80.75
	5626	CE1	TYR	D	129	27.652	38.296	35.533	1.00	80.75
	5627	CD2	TYR	D	129	26.682	38.057	38.118	1.00	80.75
	5628	CE2	TYR	D	129	25.803	38.042	37.037	1.00	80.75
35	5629	CZ	TYR	D	129	26.288	38.160	35.741	1.00	80.75
	5630	OH	TYR	D	129	25.412	38.145	34.662	1.00	80.75
	5631	C	TYR	D	129	28.192	40.564	39.182	1.00	62.64
	5632	O	TYR	D	129	27.268	40.602	39.996	1.00	62.64
	5633	N	TRP	D	130	28.190	41.252	38.042	1.00	93.45
40	5634	CA	TRP	D	130	27.076	42.123	37.680	1.00	93.45
	5635	CB	TRP	D	130	27.356	43.561	38.092	1.00	113.53
	5636	CG	TRP	D	130	27.799	43.749	39.506	1.00	113.53
	5637	CD2	TRP	D	130	27.020	44.284	40.583	1.00	113.53
	5638	CE2	TRP	D	130	27.863	44.336	41.718	1.00	113.53
45	5639	CE3	TRP	D	130	25.690	44.716	40.700	1.00	113.53
	5640	CD1	TRP	D	130	29.043	43.512	40.018	1.00	113.53
	5641	NE1	TRP	D	130	29.092	43.864	41.347	1.00	113.53
	5642	CZ2	TRP	D	130	27.413	44.811	42.961	1.00	113.53
	5643	CZ3	TRP	D	130	25.242	45.191	41.945	1.00	113.53
50	5644	CH2	TRP	D	130	26.104	45.238	43.051	1.00	113.53
	5645	C	TRP	D	130	26.817	42.119	36.181	1.00	93.45
	5646	O	TRP	D	130	27.643	41.649	35.404	1.00	93.45
	5647	N	TYR	D	131	25.667	42.650	35.773	1.00	68.85
	5648	CA	TYR	D	131	25.343	42.732	34.351	1.00	68.85
55	5649	CB	TYR	D	131	23.835	42.746	34.119	1.00	129.65
	5650	CG	TYR	D	131	23.515	42.570	32.657	1.00	129.65
	5651	CD1	TYR	D	131	23.660	41.330	32.046	1.00	129.65
	5652	CE1	TYR	D	131	23.494	41.183	30.685	1.00	129.65
	5653	CD2	TYR	D	131	23.182	43.661	31.862	1.00	129.65
60	5654	CE2	TYR	D	131	23.015	43.523	30.495	1.00	129.65
	5655	CZ	TYR	D	131	23.177	42.282	29.915	1.00	129.65
	5656	OH	TYR	D	131	23.056	42.154	28.555	1.00	129.65
	5657	C	TYR	D	131	25.953	44.035	33.846	1.00	68.85
	5658	O	TYR	D	131	27.035	44.028	33.249	1.00	68.85
65	5659	N	GLU	D	132	25.234	45.142	34.045	1.00	110.47
	5660	CA	GLU	D	132	25.761	46.455	33.684	1.00	110.47
	5661	CB	GLU	D	132	24.715	47.569	33.878	1.00	169.41
	5662	CG	GLU	D	132	23.632	47.688	32.798	1.00	169.41
	5663	CD	GLU	D	132	23.679	49.022	32.059	1.00	169.41
70	5664	OE1	GLU	D	132	24.276	49.981	32.594	1.00	169.41

	5665	OE2	GLU	D	132	23.107	49.114	30.951	1.00	169.41
	5666	C	GLU	D	132	26.765	46.491	34.814	1.00	110.47
	5667	O	GLU	D	132	26.391	46.249	35.965	1.00	110.47
	5668	N	ASN	D	133	28.029	46.777	34.515	1.00	115.67
5	5669	CA	ASN	D	133	29.030	46.736	35.574	1.00	115.67
	5670	CB	ASN	D	133	30.448	46.807	35.003	1.00	113.79
	5671	CG	ASN	D	133	30.911	48.198	34.814	1.00	113.79
	5672	OD1	ASN	D	133	30.200	49.009	34.233	1.00	113.79
	5673	ND2	ASN	D	133	32.110	48.501	35.296	1.00	113.79
10	5674	C	ASN	D	133	28.888	47.723	36.718	1.00	115.67
	5675	O	ASN	D	133	28.054	48.618	36.717	1.00	115.67
	5676	N	HIS	D	134	29.747	47.518	37.702	1.00	133.45
	5677	CA	HIS	D	134	29.748	48.283	38.921	1.00	133.45
	5678	CB	HIS	D	134	29.100	47.430	40.006	1.00	207.58
15	5679	CG	HIS	D	134	28.893	48.141	41.302	1.00	207.58
	5680	CD2	HIS	D	134	29.411	47.919	42.534	1.00	207.58
	5681	ND1	HIS	D	134	28.039	49.213	41.435	1.00	207.58
	5682	CE1	HIS	D	134	28.038	49.620	42.690	1.00	207.58
	5683	NE2	HIS	D	134	28.862	48.851	43.378	1.00	207.58
20	5684	C	HIS	D	134	31.188	48.609	39.290	1.00	133.45
	5685	O	HIS	D	134	32.091	48.473	38.469	1.00	133.45
	5686	N	ASN	D	135	31.388	49.015	40.537	1.00	73.71
	5687	CA	ASN	D	135	32.701	49.394	41.017	1.00	73.71
	5688	CB	ASN	D	135	32.877	50.923	40.922	1.00	127.04
25	5689	CG	ASN	D	135	32.913	51.402	39.490	1.00	127.04
	5690	OD1	ASN	D	135	33.606	50.790	38.668	1.00	127.04
	5691	ND2	ASN	D	135	32.193	52.478	39.170	1.00	127.04
	5692	C	ASN	D	135	32.869	48.930	42.441	1.00	73.71
	5693	O	ASN	D	135	32.604	49.672	43.363	1.00	73.71
30	5694	N	ILE	D	136	33.307	47.689	42.606	1.00	72.93
	5695	CA	ILE	D	136	33.534	47.094	43.918	1.00	72.93
	5696	CB	ILE	D	136	34.435	45.852	43.786	1.00	89.30
	5697	CG2	ILE	D	136	35.652	46.164	42.961	1.00	89.30
	5698	CG1	ILE	D	136	34.828	45.348	45.159	1.00	89.30
35	5699	CD1	ILE	D	136	35.595	44.057	45.088	1.00	89.30
	5700	C	ILE	D	136	34.139	48.097	44.892	1.00	72.93
	5701	O	ILE	D	136	35.241	48.602	44.689	1.00	72.93
	5702	N	SER	D	137	33.393	48.393	45.952	1.00	72.75
	5703	CA	SER	D	137	33.810	49.378	46.952	1.00	72.75
40	5704	CB	SER	D	137	32.797	50.514	46.982	1.00	69.16
	5705	OG	SER	D	137	32.966	51.300	48.135	1.00	69.16
	5706	C	SER	D	137	33.965	48.811	48.356	1.00	72.75
	5707	O	SER	D	137	33.227	47.922	48.765	1.00	72.75
	5708	N	ILE	D	138	34.914	49.348	49.106	1.00	112.14
45	5709	CA	ILE	D	138	35.171	48.888	50.464	1.00	112.14
	5710	CB	ILE	D	138	36.436	48.063	50.515	1.00	65.89
	5711	CG2	ILE	D	138	36.827	47.824	51.962	1.00	65.89
	5712	CG1	ILE	D	138	36.239	46.759	49.745	1.00	65.89
	5713	CD1	ILE	D	138	37.523	46.004	49.492	1.00	65.89
50	5714	C	ILE	D	138	35.359	50.050	51.431	1.00	112.14
	5715	O	ILE	D	138	36.253	50.879	51.244	1.00	112.14
	5716	N	THR	D	139	34.544	50.092	52.483	1.00	70.90
	5717	CA	THR	D	139	34.628	51.172	53.464	1.00	70.90
	5718	CB	THR	D	139	33.330	51.276	54.253	1.00	212.07
55	5719	OG1	THR	D	139	32.988	49.984	54.771	1.00	212.07
	5720	CG2	THR	D	139	32.212	51.772	53.352	1.00	212.07
	5721	C	THR	D	139	35.791	50.913	54.409	1.00	70.90
	5722	O	THR	D	139	36.851	51.523	54.280	1.00	70.90
	5723	N	ASN	D	140	35.586	50.005	55.356	1.00	80.70
60	5724	CA	ASN	D	140	36.606	49.640	56.333	1.00	80.70
	5725	CB	ASN	D	140	35.957	49.206	57.644	1.00	232.63
	5726	CG	ASN	D	140	36.967	48.690	58.636	1.00	232.63
	5727	OD1	ASN	D	140	37.818	47.864	58.318	1.00	232.63
	5728	ND2	ASN	D	140	36.862	49.170	59.865	1.00	232.63
65	5729	C	ASN	D	140	37.344	48.464	55.709	1.00	80.70
	5730	O	ASN	D	140	36.732	47.447	55.411	1.00	80.70
	5731	N	ALA	D	141	38.650	48.593	55.503	1.00	77.89
	5732	CA	ALA	D	141	39.428	47.522	54.870	1.00	77.89
	5733	CB	ALA	D	141	40.437	48.086	53.919	1.00	47.27
70	5734	C	ALA	D	141	40.142	46.600	55.822	1.00	77.89

	5735	O	ALA	D	141	40.885	47.017	56.703	1.00	77.89
	5736	N	THR	D	142	39.941	45.317	55.606	1.00	73.90
	5737	CA	THR	D	142	40.557	44.300	56.434	1.00	73.90
	5738	CB	THR	D	142	39.702	43.013	56.412	1.00	158.80
5	5739	OG1	THR	D	142	38.346	43.343	56.745	1.00	158.80
	5740	CG2	THR	D	142	40.214	42.014	57.416	1.00	158.80
	5741	C	THR	D	142	41.927	44.055	55.837	1.00	73.90
	5742	O	THR	D	142	42.236	44.606	54.779	1.00	73.90
	5743	N	VAL	D	143	42.756	43.268	56.521	1.00	104.07
10	5744	CA	VAL	D	143	44.088	42.953	56.008	1.00	104.07
	5745	CB	VAL	D	143	45.093	42.610	57.127	1.00	127.52
	5746	CG1	VAL	D	143	44.701	41.320	57.807	1.00	127.52
	5747	CG2	VAL	D	143	46.495	42.479	56.545	1.00	127.52
	5748	C	VAL	D	143	43.955	41.736	55.107	1.00	104.07
15	5749	O	VAL	D	143	44.846	41.424	54.322	1.00	104.07
	5750	N	GLU	D	144	42.829	41.046	55.222	1.00	87.28
	5751	CA	GLU	D	144	42.603	39.874	54.400	1.00	87.28
	5752	CB	GLU	D	144	41.492	39.011	55.003	1.00	215.80
	5753	CG	GLU	D	144	41.840	38.428	56.363	1.00	215.80
20	5754	CD	GLU	D	144	40.992	39.001	57.475	1.00	215.80
	5755	OE1	GLU	D	144	39.756	38.856	57.409	1.00	215.80
	5756	OE2	GLU	D	144	41.555	39.596	58.416	1.00	215.80
	5757	C	GLU	D	144	42.245	40.287	52.982	1.00	87.28
	5758	O	GLU	D	144	42.288	39.478	52.074	1.00	87.28
25	5759	N	ASP	D	145	41.898	41.556	52.801	1.00	67.03
	5760	CA	ASP	D	145	41.533	42.083	51.491	1.00	67.03
	5761	CB	ASP	D	145	40.847	43.441	51.634	1.00	129.44
	5762	CG	ASP	D	145	39.448	43.320	52.163	1.00	129.44
	5763	OD1	ASP	D	145	38.636	42.636	51.510	1.00	129.44
30	5764	OD2	ASP	D	145	39.158	43.899	53.228	1.00	129.44
	5765	C	ASP	D	145	42.751	42.217	50.587	1.00	67.03
	5766	O	ASP	D	145	42.634	42.396	49.365	1.00	67.03
	5767	N	SER	D	146	43.932	42.121	51.177	1.00	89.85
	5768	CA	SER	D	146	45.140	42.235	50.383	1.00	89.85
35	5769	CB	SER	D	146	46.366	42.277	51.300	1.00	212.33
	5770	OG	SER	D	146	46.317	43.408	52.152	1.00	212.33
	5771	C	SER	D	146	45.185	41.034	49.452	1.00	89.85
	5772	O	SER	D	146	44.810	39.933	49.836	1.00	89.85
	5773	N	GLY	D	147	45.604	41.256	48.213	1.00	67.51
40	5774	CA	GLY	D	147	45.698	40.164	47.254	1.00	67.51
	5775	C	GLY	D	147	46.000	40.693	45.865	1.00	67.51
	5776	O	GLY	D	147	46.475	41.825	45.724	1.00	67.51
	5777	N	THR	D	148	45.740	39.888	44.835	1.00	62.13
	5778	CA	THR	D	148	45.975	40.327	43.454	1.00	62.13
45	5779	CB	THR	D	148	47.073	39.493	42.770	1.00	85.26
	5780	OG1	THR	D	148	46.483	38.564	41.871	1.00	85.26
	5781	CG2	THR	D	148	47.863	38.729	43.800	1.00	85.26
	5782	C	THR	D	148	44.665	40.210	42.689	1.00	62.13
	5783	O	THR	D	148	44.106	39.134	42.527	1.00	62.13
50	5784	N	TYR	D	149	44.164	41.339	42.230	1.00	42.52
	5785	CA	TYR	D	149	42.894	41.349	41.547	1.00	42.52
	5786	CB	TYR	D	149	42.072	42.518	42.079	1.00	42.86
	5787	CG	TYR	D	149	41.722	42.498	43.543	1.00	42.86
	5788	CD1	TYR	D	149	42.689	42.662	44.522	1.00	42.86
55	5789	CE1	TYR	D	149	42.339	42.702	45.880	1.00	42.86
	5790	CD2	TYR	D	149	40.404	42.373	43.936	1.00	42.86
	5791	CE2	TYR	D	149	40.038	42.412	45.251	1.00	42.86
	5792	CZ	TYR	D	149	40.998	42.570	46.237	1.00	42.86
	5793	OH	TYR	D	149	40.592	42.542	47.568	1.00	42.86
60	5794	C	TYR	D	149	43.028	41.506	40.046	1.00	42.52
	5795	O	TYR	D	149	44.102	41.847	39.556	1.00	42.52
	5796	N	TYR	D	150	41.921	41.262	39.340	1.00	57.99
	5797	CA	TYR	D	150	41.799	41.429	37.892	1.00	57.99
	5798	CB	TYR	D	150	42.675	40.420	37.108	1.00	88.00
65	5799	CG	TYR	D	150	42.197	38.986	36.975	1.00	88.00
	5800	CD1	TYR	D	150	41.124	38.661	36.156	1.00	88.00
	5801	CE1	TYR	D	150	40.693	37.342	36.010	1.00	88.00
	5802	CD2	TYR	D	150	42.840	37.948	37.649	1.00	88.00
	5803	CE2	TYR	D	150	42.422	36.626	37.513	1.00	88.00
70	5804	CZ	TYR	D	150	41.342	36.327	36.692	1.00	88.00

	5805	OH	TYR	D	150	40.898	35.020	36.578	1.00	88.00
	5806	C	TYR	D	150	40.293	41.260	37.623	1.00	57.99
	5807	O	TYR	D	150	39.569	40.702	38.470	1.00	57.99
	5808	N	CYS	D	151	39.793	41.782	36.500	1.00	62.97
5	5809	CA	CYS	D	151	38.365	41.650	36.193	1.00	62.97
	5810	C	CYS	D	151	38.136	41.175	34.780	1.00	62.97
	5811	O	CYS	D	151	39.009	41.229	33.931	1.00	62.97
	5812	CB	CYS	D	151	37.636	42.966	36.413	1.00	102.16
	5813	SG	CYS	D	151	38.287	44.417	35.527	1.00	102.16
10	5814	N	THR	D	152	36.975	40.566	34.538	1.00	73.20
	5815	CA	THR	D	152	36.613	40.055	33.215	1.00	73.20
	5816	CB	THR	D	152	36.437	38.527	33.230	1.00	136.00
	5817	OG1	THR	D	152	35.288	38.183	34.017	1.00	136.00
	5818	CG2	THR	D	152	37.664	37.855	33.814	1.00	136.00
15	5819	C	THR	D	152	35.286	40.688	32.830	1.00	73.20
	5820	O	THR	D	152	34.434	40.945	33.698	1.00	73.20
	5821	N	GLY	D	153	35.105	40.950	31.538	1.00	64.84
	5822	CA	GLY	D	153	33.863	41.572	31.099	1.00	64.84
	5823	C	GLY	D	153	33.682	41.463	29.609	1.00	64.84
20	5824	O	GLY	D	153	34.636	41.184	28.899	1.00	64.84
	5825	N	LYS	D	154	32.462	41.680	29.133	1.00	72.61
	5826	CA	LYS	D	154	32.180	41.576	27.706	1.00	72.61
	5827	CB	LYS	D	154	30.881	40.800	27.484	1.00	205.73
	5828	CG	LYS	D	154	30.546	40.515	26.030	1.00	205.73
25	5829	CD	LYS	D	154	29.274	39.697	25.956	1.00	205.73
	5830	CE	LYS	D	154	?? 825	39.439	24.533	1.00	205.73
	5831	NZ	LYS	D	154	27.516	38.730	24.533	1.00	205.73
	5832	C	LYS	D	154	32.056	42.967	27.134	1.00	72.61
	5833	O	LYS	D	154	31.329	43.802	27.662	1.00	72.61
30	5834	N	VAL	D	155	32.792	43.226	26.065	1.00	92.93
	5835	CA	VAL	D	155	32.751	44.532	25.426	1.00	92.93
	5836	CB	VAL	D	155	34.140	45.153	25.313	1.00	130.27
	5837	CG1	VAL	D	155	34.065	46.494	24.609	1.00	130.27
	5838	CG2	VAL	D	155	34.714	45.331	26.689	1.00	130.27
35	5839	C	VAL	D	155	32.216	44.275	24.040	1.00	92.93
	5840	O	VAL	D	155	32.715	43.395	23.330	1.00	92.93
	5841	N	TRP	D	156	31.205	45.046	23.653	1.00	158.38
	5842	CA	TRP	D	156	30.579	44.860	22.358	1.00	158.38
	5843	CB	TRP	D	156	31.605	44.866	21.235	1.00	243.82
40	5844	CG	TRP	D	156	32.236	46.155	21.100	1.00	243.82
	5845	CD2	TRP	D	156	31.589	47.366	20.812	1.00	243.82
	5846	CE2	TRP	D	156	32.575	48.376	20.781	1.00	243.82
	5847	CE3	TRP	D	156	30.261	47.713	20.608	1.00	243.82
	5848	CD1	TRP	D	156	33.550	46.428	21.198	1.00	243.82
45	5849	NE1	TRP	D	156	33.771	47.767	21.014	1.00	243.82
	5850	CZ2	TRP	D	156	32.278	49.703	20.533	1.00	243.82
	5851	CZ3	TRP	D	156	29.993	49.006	20.358	1.00	243.82
	5852	CH2	TRP	D	156	30.983	49.997	20.320	1.00	243.82
	5853	C	TRP	D	156	29.982	43.492	22.407	1.00	158.38
50	5854	O	TRP	D	156	28.886	43.299	22.908	1.00	158.38
	5855	N	GLN	D	157	30.752	42.528	21.924	1.00	148.04
	5856	CA	GLN	D	157	30.284	41.168	21.881	1.00	148.04
	5857	CB	GLN	D	157	29.612	40.948	20.533	1.00	249.45
	5858	CG	GLN	D	157	28.288	41.684	20.483	1.00	249.45
55	5859	CD	GLN	D	157	27.435	41.306	21.676	1.00	249.45
	5860	OE1	GLN	D	157	27.203	40.132	21.914	1.00	249.45
	5861	NE2	GLN	D	157	26.963	42.292	22.421	1.00	249.45
	5862	C	GLN	D	157	31.348	40.127	22.150	1.00	148.04
	5863	O	GLN	D	157	31.140	38.936	21.912	1.00	148.04
60	5864	N	LEU	D	158	32.488	40.579	22.665	1.00	85.54
	5865	CA	LEU	D	158	33.584	39.676	22.996	1.00	85.54
	5866	CB	LEU	D	158	34.779	39.917	22.073	1.00	127.62
	5867	CG	LEU	D	158	34.714	39.361	20.649	1.00	127.62
	5868	CD1	LEU	D	158	36.094	38.823	20.329	1.00	127.62
65	5869	CD2	LEU	D	158	33.694	38.231	20.514	1.00	127.62
	5870	C	LEU	D	158	34.022	39.797	24.457	1.00	85.54
	5871	O	LEU	D	158	33.857	40.847	25.090	1.00	85.54
	5872	N	ASP	D	159	34.562	38.706	24.986	1.00	91.88
	5873	CA	ASP	D	159	35.024	38.662	26.363	1.00	91.88
70	5874	CB	ASP	D	159	34.915	37.229	26.901	1.00	249.49

	5875	CG	ASP	D	159	33.518	36.644	26.743	1.00	249.49
	5876	OD1	ASP	D	159	32.559	37.204	27.319	1.00	249.49
	5877	OD2	ASP	D	159	33.380	35.620	26.039	1.00	249.49
	5878	C	ASP	D	159	36.476	39.142	26.462	1.00	91.88
5	5879	O	ASP	D	159	37.270	38.921	25.543	1.00	91.88
	5880	N	TYR	D	160	36.818	39.807	27.568	1.00	90.02
	5881	CA	TYR	D	160	38.179	40.298	27.785	1.00	90.02
	5882	CB	TYR	D	160	38.334	41.742	27.323	1.00	132.54
	5883	CG	TYR	D	160	37.907	41.996	25.905	1.00	132.54
10	5884	CD1	TYR	D	160	36.605	42.362	25.617	1.00	132.54
	5885	CE1	TYR	D	160	36.196	42.585	24.315	1.00	132.54
	5886	CD2	TYR	D	160	38.800	41.857	24.851	1.00	132.54
	5887	CE2	TYR	D	160	38.405	42.075	23.539	1.00	132.54
	5888	CZ	TYR	D	160	37.101	42.437	23.278	1.00	132.54
15	5889	OH	TYR	D	160	36.697	42.638	21.977	1.00	132.54
	5890	C	TYR	D	160	38.594	40.222	29.239	1.00	90.02
	5891	O	TYR	D	160	37.782	40.394	30.143	1.00	90.02
	5892	N	GLU	D	161	39.884	39.979	29.436	1.00	92.36
	5893	CA	GLU	D	161	40.492	39.862	30.750	1.00	92.36
20	5894	CB	GLU	D	161	41.247	38.536	30.815	1.00	148.75
	5895	CG	GLU	D	161	42.005	38.266	32.084	1.00	148.75
	5896	CD	GLU	D	161	42.398	36.810	32.189	1.00	148.75
	5897	OE1	GLU	D	161	43.333	36.490	32.957	1.00	148.75
	5898	OE2	GLU	D	161	41.757	35.985	31.506	1.00	148.75
25	5899	C	GLU	D	161	41.448	41.051	30.923	1.00	92.36
	5900	O	GLU	D	161	42.157	41.424	29.985	1.00	92.36
	5901	N	SER	D	162	41.450	41.655	32.110	1.00	74.96
	5902	CA	SER	D	162	42.323	42.789	32.404	1.00	74.96
	5903	CB	SER	D	162	41.652	43.705	33.398	1.00	62.82
30	5904	OG	SER	D	162	41.377	42.998	34.594	1.00	62.82
	5905	C	SER	D	162	43.671	42.370	32.989	1.00	74.96
	5906	O	SER	D	162	43.876	41.208	33.354	1.00	74.96
	5907	N	GLU	D	163	44.593	43.325	33.088	1.00	68.26
	5908	CA	GLU	D	163	45.929	43.034	33.625	1.00	68.26
35	5909	CB	GLU	D	163	46.877	44.206	33.368	1.00	242.79
	5910	CG	GLU	D	163	47.352	44.338	31.925	1.00	242.79
	5911	CD	GLU	D	163	48.358	43.266	31.540	1.00	242.79
	5912	OE1	GLU	D	163	49.400	43.158	32.222	1.00	242.79
	5913	OE2	GLU	D	163	48.113	42.537	30.556	1.00	242.79
40	5914	C	GLU	D	163	45.768	42.820	35.117	1.00	68.26
	5915	O	GLU	D	163	44.970	43.504	35.751	1.00	68.26
	5916	N	PRO	D	164	46.511	41.863	35.698	1.00	51.48
	5917	CD	PRO	D	164	47.539	40.983	35.148	1.00	112.85
	5918	CA	PRO	D	164	46.359	41.659	37.137	1.00	51.48
45	5919	CB	PRO	D	164	47.112	40.364	37.367	1.00	112.85
	5920	CG	PRO	D	164	48.211	40.465	36.404	1.00	112.85
	5921	C	PRO	D	164	46.955	42.827	37.920	1.00	51.48
	5922	O	PRO	D	164	47.839	43.536	37.411	1.00	51.48
	5923	N	LEU	D	165	46.480	43.045	39.145	1.00	58.03
50	5924	CA	LEU	D	165	46.988	44.134	39.944	1.00	58.03
	5925	CB	LEU	D	165	46.085	45.333	39.824	1.00	67.82
	5926	CG	LEU	D	165	46.417	46.436	40.816	1.00	67.82
	5927	CD1	LEU	D	165	47.878	46.685	40.736	1.00	67.82
	5928	CD2	LEU	D	165	45.653	47.711	40.495	1.00	67.82
55	5929	C	LEU	D	165	47.080	43.744	41.384	1.00	58.03
	5930	O	LEU	D	165	46.082	43.313	41.957	1.00	58.03
	5931	N	ASN	D	166	48.274	43.892	41.964	1.00	50.98
	5932	CA	ASN	D	166	48.513	43.551	43.367	1.00	50.98
	5933	CB	ASN	D	166	49.984	43.249	43.618	1.00	110.65
60	5934	CG	ASN	D	166	50.324	41.777	43.461	1.00	110.65
	5935	OD1	ASN	D	166	49.514	40.900	43.700	1.00	110.65
	5936	ND2	ASN	D	166	51.557	41.517	43.077	1.00	110.65
	5937	C	ASN	D	166	48.084	44.660	44.311	1.00	50.98
	5938	O	ASN	D	166	48.175	45.818	43.992	1.00	50.98
65	5939	N	ILE	D	167	47.626	44.290	45.489	1.00	69.36
	5940	CA	ILE	D	167	47.167	45.267	46.443	1.00	69.36
	5941	CB	ILE	D	167	45.659	45.375	46.397	1.00	42.00
	5942	CG2	ILE	D	167	45.152	46.062	47.661	1.00	42.00
	5943	CG1	ILE	D	167	45.241	46.105	45.129	1.00	42.00
70	5944	CD1	ILE	D	167	43.748	46.402	45.115	1.00	42.00

	5945	C	ILE	D	167	47.557	44.842	47.833	1.00	69.36
	5946	O	ILE	D	167	47.366	43.682	48.218	1.00	69.36
	5947	N	THR	D	168	48.090	45.774	48.603	1.00	69.22
5	5948	CA .	THR	D	168	48.480	45.418	49.945	1.00	69.22
	5949	CB	THR	D	168	49.988	45.453	50.107	1.00	70.81
	5950	OG1	THR	D	168	50.575	44.544	49.169	1.00	70.81
	5951	CG2	THR	D	168	50.372	45.030	51.511	1.00	70.81
	5952	C	THR	D	168	47.84:	46.301	50.987	1.00	69.22
	5953	O	THR	D	168	47.754	47.509	50.828	1.00	69.22
10	5954	N	VAL	D	169	47.387	45.670	52.051	1.00	66.57
	5955	CA	VAL	D	169	46.774	46.361	53.155	1.00	66.57
	5956	CB	VAL	D	169	45.379	45.806	53.417	1.00	62.74
	5957	CG1	VAL	D	169	44.945	46.137	54.819	1.00	62.74
	5958	CG2	VAL	D	169	44.418	46.381	52.416	1.00	62.74
15	5959	C	VAL	D	169	47.693	46.061	54.334	1.00	66.57
	5960	O	VAL	D	169	47.740	44.932	54.805	1.00	66.57
	5961	N	ILE	D	170	48.460	47.051	54.780	1.00	82.22
	5962	CA	ILE	D	170	49.360	46.864	55.913	1.00	82.22
	5963	CB	ILE	D	170	50.599	47.738	55.759	1.00	114.31
20	5964	CG2	ILE	D	170	51.201	47.504	54.406	1.00	114.31
	5965	CG1	ILE	D	170	50.232	49.218	55.860	1.00	114.31
	5966	CD1	ILE	D	170	51.416	50.187	55.670	1.00	114.31
	5967	C	ILE	D	170	48.613	47.237	57.189	1.00	82.22
	5968	O	ILE	D	170	47.459	47.676	57.122	1.00	82.22
25	5969	N	LYS	D	171	49.245	47.053	58.347	1.00	108.79
	5970	CA	LYS	D	171	48.598	47.390	59.620	1.00	108.79
	5971	CB	LYS	D	171	48.214	46.117	60.360	1.00	188.56
	5972	CG	LYS	D	171	49.380	45.194	60.614	1.00	188.56
	5973	CD	LYS	D	171	48.910	43.762	60.800	1.00	188.56
30	5974	CE	LYS	D	171	47.946	43.624	61.976	1.00	188.56
	5975	NZ	LYS	D	171	47.459	42.220	62.130	1.00	188.56
	5976	C	LYS	D	171	49.453	48.270	60.524	1.00	108.79
	5977	O	LYS	D	171	48.981	48.761	61.549	1.00	108.79
	5978	C1	NAG	D	221	40.344	65.629	28.022	1.00	249.77
35	5979	C2	NAG	D	221	39.010	64.922	27.810	1.00	249.77
	5980	N2	NAG	D	221	39.203	63.489	27.903	1.00	249.77
	5981	C7	NAG	D	221	38.191	62.705	28.261	1.00	249.77
	5982	O7	NAG	D	221	37.073	63.139	28.545	1.00	249.77
	5983	C8	NAG	D	221	38.462	61.211	28.324	1.00	249.77
40	5984	C3	NAG	D	221	38.434	65.256	26.441	1.00	249.77
	5985	O3	NAG	D	221	37.116	64.735	26.342	1.00	249.77
	5986	C4	NAG	D	221	38.404	66.763	26.173	1.00	249.77
	5987	O4	NAG	D	221	38.077	66.947	24.777	1.00	249.77
	5988	C5	NAG	D	221	39.780	67.394	26.498	1.00	249.77
45	5989	O5	NAG	D	221	40.191	67.042	27.838	1.00	249.77
	5990	C6	NAG	D	221	39.770	68.913	26.439	1.00	249.77
	5991	O6	NAG	D	221	38.854	69.459	27.379	1.00	249.77
	5992	C1	NAG	D	222	37.835	68.189	24.343	1.00	233.91
	5993	C2	NAG	D	222	36.436	68.019	23.396	1.00	233.91
50	5994	N2	NAG	D	222	35.346	67.346	24.082	1.00	233.91
	5995	C7	NAG	D	222	34.173	67.955	24.234	1.00	233.91
	5996	O7	NAG	D	222	33.947	69.093	23.816	1.00	233.91
	5997	C8	NAG	D	222	33.082	67.183	24.963	1.00	233.91
	5998	C3	NAG	D	222	36.855	67.215	22.156	1.00	233.91
55	5999	O3	NAG	D	222	35.790	67.196	21.217	1.00	233.91
	6000	C4	NAG	D	222	38.102	67.829	21.503	1.00	233.91
	6001	O4	NAG	D	222	38.567	66.974	20.471	1.00	233.91
	6002	C5	NAG	D	222	39.211	68.020	22.542	1.00	233.91
	6003	O5	NAG	D	222	38.722	68.817	23.644	1.00	233.91
60	6004	C6	NAG	D	222	40.435	68.722	21.989	1.00	233.91
	6005	O6	NAG	D	222	41.628	68.076	22.406	1.00	233.91
	6006	C1	NAG	D	242	59.627	58.578	32.960	1.00	107.57
	6007	C2	NAG	D	242	59.450	58.871	31.486	1.00	107.57
	6008	N2	NAG	D	242	59.010	60.232	31.316	1.00	107.57
65	6009	C7	NAG	D	242	59.707	61.044	30.534	1.00	107.57
	6010	O7	NAG	D	242	60.732	60.679	29.950	1.00	107.57
	6011	C8	NAG	D	242	59.199	62.478	30.373	1.00	107.57
	6012	C3	NAG	D	242	58.412	57.932	30.887	1.00	107.57
	6013	O3	NAG	D	242	58.316	58.138	29.483	1.00	107.57
70	6014	C4	NAG	D	242	58.806	56.496	31.148	1.00	107.57

6015	O4	NAG D	242	57.728	55.629	30.752	1.00	107.57
6016	C5	NAG D	242	59.118	56.268	32.625	1.00	107.57
8017	O5	NAG D	242	60.064	57.236	33.114	1.00	107.57
6018	C6	NAG D	242	59.783	54.930	32.783	1.00	107.57
6019	O6	NAG D	242	59.082	54.107	33.697	1.00	107.57
6020	C1	NAG D	243	57.985	54.762	29.705	1.00	125.30
6021	C2	NAG D	243	57.074	53.527	29.789	1.00	125.30
6022	N2	NAG D	243	57.321	52.782	31.013	1.00	125.30
6023	C7	NAG D	243	56.303	52.357	31.758	1.00	125.30
6024	O7	NAG D	243	55.129	52.583	31.473	1.00	125.30
6025	C8	NAG D	243	56.634	51.574	33.018	1.00	125.30
6026	C3	NAG D	243	57.345	52.629	28.586	1.00	125.30
6027	O3	NAG D	243	56.458	51.521	28.595	1.00	125.30
6028	C4	NAG D	243	57.191	53.414	27.277	1.00	125.30
6029	O4	NAG D	243	57.612	52.582	26.156	1.00	125.30
6030	C5	NAG D	243	58.083	54.659	27.339	1.00	125.30
6031	O5	NAG D	243	57.744	55.459	28.483	1.00	125.30
6032	C6	NAG D	243	57.985	55.549	26.119	1.00	125.30
6033	O6	NAG D	243	56.713	56.172	26.043	1.00	125.30
6034	C1	MAN D	244	56.846	52.424	25.031	1.00	205.85
6035	C2	MAN D	244	55.417	51.844	25.171	1.00	205.85
6036	O2	MAN D	244	54.487	52.897	25.184	1.00	205.85
6037	C3	MAN D	244	55.275	51.012	23.858	1.00	205.85
6038	O3	MAN D	244	54.016	50.380	23.757	1.00	205.85
6039	C4	MAN D	244	55.586	51.831	22.569	1.00	205.85
6040	O4	MAN D	244	55.419	51.015	21.411	1.00	205.85
6041	C5	MAN D	244	57.054	52.305	22.669	1.00	205.85
6042	O5	MAN D	244	57.244	53.154	23.833	1.00	205.85
6043	C6	MAN D	244	57.597	52.991	21.412	1.00	205.85
6044	O6	MAN D	244	57.221	54.349	21.357	1.00	205.85
6045	C1	NAG D	250	45.992	76.510	37.679	1.00	248.68
6046	C2	NAG D	250	44.579	76.931	38.128	1.00	248.68
6047	N2	NAG D	250	44.536	77.116	39.567	1.00	248.68
6048	C7	NAG D	250	44.384	78.333	40.083	1.00	248.68
6049	O7	NAG D	250	44.277	79.347	39.391	1.00	248.68
6050	C8	NAG D	250	44.348	78.442	41.599	1.00	248.68
6051	C3	NAG D	250	43.573	75.849	37.715	1.00	248.68
6052	O3	NAG D	250	42.252	76.265	38.034	1.00	248.68
6053	C4	NAG D	250	43.682	75.570	36.213	1.00	248.68
6054	O4	NAG D	250	42.841	74.477	35.869	1.00	248.68
6055	C5	NAG D	250	45.139	75.244	35.834	1.00	248.68
6056	O5	NAG D	250	46.017	76.312	36.259	1.00	248.68
6057	C6	NAG D	250	45.335	75.070	34.335	1.00	248.68
6058	O6	NAG D	250	46.713	75.089	33.986	1.00	248.68
6059	C1	NAG D	274	63.247	69.025	55.540	1.00	209.92
6060	C2	NAG D	274	62.953	68.056	56.695	1.00	209.92
6061	N2	NAG D	274	61.768	68.477	57.416	1.00	209.92
6062	C7	NAG D	274	61.053	67.585	58.098	1.00	209.92
6063	O7	NAG D	274	61.342	66.390	58.145	1.00	209.92
6064	C8	NAG D	274	59.826	68.096	58.835	1.00	209.92
6065	C3	NAG D	274	64.147	68.007	57.654	1.00	209.92
6066	O3	NAG D	274	63.927	67.009	58.639	1.00	209.92
6067	C4	NAG D	274	65.443	67.703	56.893	1.00	209.92
6068	O4	NAG D	274	66.552	67.817	57.775	1.00	209.92
6069	C5	NAG D	274	65.610	68.683	55.725	1.00	209.92
6070	O5	NAG D	274	64.452	68.631	54.865	1.00	209.92
6071	C6	NAG D	274	66.820	68.373	54.862	1.00	209.92
6072	O6	NAG D	274	66.810	69.142	53.667	1.00	209.92
6073	C1	NAG D	335	32.860	53.594	38.525	1.00	187.23
6074	C2	NAG D	335	32.657	54.924	39.281	1.00	187.23
6075	N2	NAG D	335	32.302	54.604	40.651	1.00	187.23
6076	C7	NAG D	335	33.089	54.970	41.656	1.00	187.23
6077	O7	NAG D	335	34.133	55.601	41.498	1.00	187.23
6078	C8	NAG D	335	32.640	54.583	43.054	1.00	187.23
6079	C3	NAG D	335	31.561	55.826	38.691	1.00	187.23
6080	O3	NAG D	335	31.736	57.155	39.169	1.00	187.23
6081	C4	NAG D	335	31.606	55.833	37.168	1.00	187.23
6082	O4	NAG D	335	30.534	56.616	36.658	1.00	187.23
6083	C5	NAG D	335	31.498	54.394	36.668	1.00	187.23
6084	O5	NAG D	335	32.666	53.657	37.089	1.00	187.23

	6085	C6	NAG	D	335	31.442	54.317	35.144	1.00	187.23
	6086	O6	NAG	D	335	30.243	53.705	34.692	1.00	187.23
	6087	C1	NAG	D	340	36.447	48.280	60.935	1.00	247.88
	6088	C2	NAG	D	340	37.563	48.157	61.941	1.00	247.88
5	6089	N2	NAG	D	340	38.786	47.736	61.296	1.00	247.88
	6090	C7	NAG	D	340	39.907	48.420	61.502	1.00	247.88
	6091	O7	NAG	D	340	39.959	49.402	62.248	1.00	247.88
	6092	C8	NAG	D	340	41.160	47.954	60.781	1.00	247.88
	6093	C3	NAG	D	340	37.180	47.173	63.025	1.00	247.88
10	6094	O3	NAG	D	340	38.213	47.101	64.002	1.00	247.88
	6095	C4	NAG	D	340	35.881	47.637	63.677	1.00	247.88
	6096	O4	NAG	D	340	35.406	46.605	64.547	1.00	247.88
	6097	C5	NAG	D	340	34.778	47.988	62.613	1.00	247.88
15	6098	O5	NAG	D	340	35.305	48.810	61.587	1.00	247.88
	6099	C6	NAG	D	340	33.729	48.850	63.239	1.00	247.88
	6100	O6	NAG	D	340	33.003	49.565	62.297	1.00	247.88
	6101	C1	NAG	D	366	51.975	40.156	42.859	1.00	179.92
	6102	C2	NAG	D	366	53.015	40.152	41.753	1.00	179.92
	6103	N2	NAG	D	366	52.433	40.714	40.551	1.00	179.92
20	6104	C7	NAG	D	366	52.553	42.013	40.303	1.00	179.92
	6105	O7	NAG	D	366	53.160	42.786	41.048	1.00	179.92
	6106	C8	NAG	D	366	51.908	42.532	39.029	1.00	179.92
	6107	C3	NAG	D	366	53.483	38.733	41.488	1.00	179.92
	6108	O3	NAG	D	366	54.558	38.758	40.562	1.00	179.92
25	6109	C4	NAG	D	366	53.939	38.053	42.783	1.00	179.92
	6110	O4	NAG	D	366	54.150	36.651	42.516	1.00	179.92
	6111	C5	NAG	D	366	52.883	38.216	43.899	1.00	179.92
	6112	O5	NAG	D	366	52.522	39.602	44.056	1.00	179.92
	6113	C6	NAG	D	366	53.364	37.740	45.257	1.00	179.92
30	6114	O6	NAG	D	366	52.346	37.880	46.242	1.00	179.92
	6115	C1	NAG	D	367	55.386	36.120	42.861	1.00	249.52
	6116	C2	NAG	D	367	55.270	34.606	43.041	1.00	249.52
	6117	N2	NAG	D	367	54.288	34.289	44.061	1.00	249.52
35	6118	C7	NAG	D	367	53.121	33.757	43.710	1.00	249.52
	6119	O7	NAG	D	367	52.823	33.510	42.539	1.00	249.52
	6120	C8	NAG	D	367	52.132	33.450	44.825	1.00	249.52
	6121	C3	NAG	D	367	56.643	34.041	43.413	1.00	249.52
	6122	O3	NAG	D	367	56.568	32.629	43.535	1.00	249.52
40	6123	C4	NAG	D	367	57.655	34.411	42.327	1.00	249.52
	6124	O4	NAG	D	367	58.951	33.973	42.709	1.00	249.52
	6125	C5	NAG	D	367	57.659	35.931	42.108	1.00	249.52
	6126	O5	NAG	D	367	56.321	36.405	41.807	1.00	249.52
	6127	C6	NAG	D	367	58.553	36.343	40.953	1.00	249.52
45	6128	O6	NAG	D	367	57.795	36.836	39.858	1.00	249.52
	6129	CB	LYS	E	4	12.130	63.790	1.727	1.00	181.25
	6130	CG	LYS	E	4	10.709	63.348	1.434	1.00	181.25
	6131	CD	LYS	E	4	9.964	63.056	2.721	1.00	181.25
	6132	CE	LYS	E	4	8.534	62.631	2.447	1.00	181.25
50	6133	NZ	LYS	E	4	7.791	62.349	3.709	1.00	181.25
	6134	C	LYS	E	4	12.157	65.259	-0.281	1.00	249.30
	6135	O	LYS	E	4	11.355	65.991	0.294	1.00	249.30
	6136	N	LYS	E	4	14.286	64.661	0.874	1.00	249.30
	6137	CA	LYS	E	4	12.924	64.186	0.485	1.00	249.30
55	6138	N	PRO	E	5	12.400	65.365	-1.597	1.00	120.68
	6139	CD	PRO	E	5	13.529	64.775	-2.329	1.00	144.78
	6140	CA	PRO	E	5	11.713	66.365	-2.422	1.00	120.68
	6141	CB	PRO	E	5	12.699	66.600	-3.566	1.00	144.78
	6142	CG	PRO	E	5	13.298	65.263	-3.751	1.00	144.78
60	6143	C	PRO	E	5	10.345	65.902	-2.912	1.00	120.68
	6144	O	PRO	E	5	10.065	64.705	-2.963	1.00	120.68
	6145	N	LYS	E	6	9.489	66.856	-3.263	1.00	141.31
	6146	CA	LYS	E	6	8.153	66.534	-3.743	1.00	141.31
	6147	CB	LYS	E	6	7.152	66.622	-2.590	1.00	196.63
65	6148	CG	LYS	E	6	5.747	66.182	-2.959	1.00	196.63
	6149	CD	LYS	E	6	4.834	66.110	-1.741	1.00	196.63
	6150	CE	LYS	E	6	3.443	65.623	-2.137	1.00	196.63
	6151	NZ	LYS	E	6	2.521	65.453	-0.973	1.00	196.63
	6152	C	LYS	E	6	7.735	67.460	-4.883	1.00	141.31
	6153	O	LYS	E	6	7.596	68.669	-4.698	1.00	141.31
70	6154	N	VAL	E	7	7.526	66.874	-6.059	1.00	81.07

	6155	CA	VAL	E	7.	7.145	67.622	-7.259	1.00	81.07
	6156	CB	VAL	E	7	7.188	66.745	-8.530	1.00	76.53
	6157	CG1	VAL	E	7	6.965	67.610	-9.757	1.00	76.53
	6158	CG2	VAL	E	7	8.488	66.003	-8.626	1.00	76.53
5	6159	C	VAL	E	7	5.738	68.181	-7.212	1.00	81.07
	6160	O	VAL	E	7	4.778	67.426	-7.151	1.00	81.07
	6161	N	SER	E	8	5.606	69.498	-7.268	1.00	146.33
	6162	CA	SER	E	8	4.287	70.111	-7.266	1.00	146.33
	6163	CB	SER	E	8	4.268	71.325	-6.332	1.00	208.51
10	6164	OG	SER	E	8	5.288	72.253	-6.669	1.00	208.51
	6165	C	SER	E	8	3.948	70.536	-8.692	1.00	146.33
	6166	O	SER	E	8	4.829	70.605	-9.548	1.00	146.33
	6167	N	LEU	E	9	2.671	70.806	-8.946	1.00	130.86
	6168	CA	LEU	E	9	2.221	71.236	-10.269	1.00	130.86
15	6169	CB	LEU	E	9	1.358	70.166	-10.929	1.00	129.83
	6170	CG	LEU	E	9	1.921	68.783	-11.217	1.00	129.83
	6171	CD1	LEU	E	9	1.089	68.115	-12.291	1.00	129.83
	6172	CD2	LEU	E	9	3.337	68.911	-11.693	1.00	129.83
	6173	C	LEU	E	9	1.393	72.513	-10.206	1.00	130.86
20	6174	O	LEU	E	9	0.783	72.822	-9.184	1.00	130.86
	6175	N	ASN	E	10	1.356	73.248	-11.311	1.00	238.98
	6176	CA	ASN	E	10	0.572	74.473	-11.372	1.00	238.98
	6177	CB	ASN	E	10	1.327	75.629	-10.726	1.00	166.05
	6178	CG	ASN	E	10	0.451	76.844	-10.530	1.00	166.05
25	6179	OD1	ASN	E	10	-0.489	76.822	-9.737	1.00	166.05
	6180	ND2	ASN	E	10	0.745	77.911	-11.263	1.00	166.05
	6181	C	ASN	E	10	0.235	74.821	-12.817	1.00	238.98
	6182	O	ASN	E	10	1.112	75.191	-13.598	1.00	238.98
	6183	N	PRO	E	11	-1.053	74.715	-13.195	1.00	125.56
30	6184	CD	PRO	E	11	-1.439	74.939	-14.595	1.00	163.67
	6185	CA	PRO	E	11	-2.214	74.304	-12.392	1.00	125.56
	6186	CB	PRO	E	11	-3.341	74.258	-13.429	1.00	163.67
	6187	CG	PRO	E	11	-2.903	75.247	-14.467	1.00	163.67
	6188	C	PRO	E	11	-2.053	72.952	-11.676	1.00	125.56
35	6189	O	PRO	E	11	-1.179	72.163	-12.027	1.00	125.56
	6190	N	PRO	E	12	-2.887	72.668	-10.663	1.00	68.14
	6191	CD	PRO	E	12	-3.978	73.517	-10.138	1.00	156.84
	6192	CA	PRO	E	12	-2.826	71.412	-9.907	1.00	68.14
	6193	CB	PRO	E	12	-3.863	71.600	-8.802	1.00	156.84
40	6194	CG	PRO	E	12	-4.037	73.077	-8.709	1.00	156.84
	6195	C	PRO	E	12	-3.214	70.234	-10.814	1.00	68.14
	6196	O	PRO	E	12	-2.835	69.084	-10.562	1.00	68.14
	6197	N	TRP	E	13	-3.987	70.547	-11.857	1.00	90.03
	6198	CA	TRP	E	13	-4.488	69.551	-12.800	1.00	90.03
45	6199	CB	TRP	E	13	-5.267	70.231	-13.916	1.00	120.89
	6200	CG	TRP	E	13	-6.235	71.215	-13.407	1.00	120.89
	6201	CD2	TRP	E	13	-7.024	71.111	-12.227	1.00	120.89
	6202	CE2	TRP	E	13	-7.750	72.310	-12.102	1.00	120.89
	6203	CE3	TRP	E	13	-7.191	70.121	-11.255	1.00	120.89
50	6204	CD1	TRP	E	13	-6.509	72.430	-13.945	1.00	120.89
	6205	NE1	TRP	E	13	-7.418	73.100	-13.167	1.00	120.89
	6206	CZ2	TRP	E	13	-8.627	72.548	-11.042	1.00	120.89
	6207	CZ3	TRP	E	13	-8.065	70.359	-10.204	1.00	120.89
	6208	CH2	TRP	E	13	-8.768	71.561	-10.104	1.00	120.89
55	6209	C	TRP	E	13	-3.377	68.727	-13.398	1.00	90.03
	6210	O	TRP	E	13	-2.479	69.264	-14.031	1.00	90.03
	6211	N	ASN	E	14	-3.443	67.415	-13.192	1.00	80.76
	6212	CA	ASN	E	14	-2.431	66.516	-13.720	1.00	80.76
	6213	CB	ASN	E	14	-1.883	65.579	-12.622	1.00	101.28
60	6214	CG	ASN	E	14	-2.896	64.571	-12.133	1.00	101.28
	6215	OD1	ASN	E	14	-3.979	64.933	-11.674	1.00	101.28
	6216	ND2	ASN	E	14	-2.542	63.293	-12.211	1.00	101.28
	6217	C	ASN	E	14	-2.917	65.715	-14.921	1.00	80.76
	6218	O	ASN	E	14	-2.303	64.709	-15.288	1.00	80.76
65	6219	N	ARG	E	15	-4.026	66.154	-15.523	1.00	74.26
	6220	CA	ARG	E	15	-4.554	65.520	-16.732	1.00	74.26
	6221	CB	ARG	E	15	-5.855	64.779	-16.490	1.00	82.67
	6222	CG	ARG	E	15	-5.888	63.896	-15.236	1.00	82.67
	6223	CD	ARG	E	15	-7.202	63.278	-15.142	1.00	82.67
70	6224	NE	ARG	E	15	-7.314	62.199	-16.114	1.00	82.67

	6225	CZ	ARG	E	15	-8.470	61.801	-16.627	1.00	82.67
	6226	NH1	ARG	E	15	-9.582	62.415	-16.260	1.00	82.67
	6227	NH2	ARG	E	15	-8.523	60.784	-17.483	1.00	82.67
	6228	C	ARG	E	15	-4.860	66.730	-17.570	1.00	74.26
5	6229	O	ARG	E	15	-5.753	67.509	-17.232	1.00	74.26
	6230	N	ILE	E	16	-4.116	66.920	-18.647	1.00	117.86
	6231	CA	ILE	E	16	-4.363	68.085	-19.460	1.00	117.86
	6232	CB	ILE	E	16	-3.213	69.070	-19.378	1.00	89.68
	6233	CG2	ILE	E	16	-3.128	69.663	-17.980	1.00	89.68
10	6234	CG1	ILE	E	16	-1.917	68.359	-19.758	1.00	89.68
	6235	CD1	ILE	E	16	-0.707	69.252	-19.676	1.00	89.68
	6236	C	ILE	E	16	-4.589	67.773	-20.909	1.00	117.86
	6237	O	ILE	E	16	-4.302	66.678	-21.390	1.00	117.86
	6238	N	PHE	E	17	-5.103	68.784	-21.591	1.00	150.96
15	6239	CA	PHE	E	17	-5.417	68.746	-23.003	1.00	150.96
	6240	CB	PHE	E	17	-6.466	69.815	-23.287	1.00	92.59
	6241	CG	PHE	E	17	-7.872	69.337	-23.168	1.00	92.59
	6242	CD1	PHE	E	17	-8.846	70.151	-22.597	1.00	92.59
	6243	CD2	PHE	E	17	-8.251	68.120	-23.724	1.00	92.59
20	6244	CE1	PHE	E	17	-10.193	69.757	-22.577	1.00	92.59
	6245	CE2	PHE	E	17	-9.588	67.717	-23.711	1.00	92.59
	6246	CZ	PHE	E	17	-10.567	68.546	-23.141	1.00	92.59
	6247	C	PHE	E	17	-4.169	69.021	-23.835	1.00	150.96
	6248	O	PHE	E	17	-3.184	69.562	-23.333	1.00	150.96
25	6249	N	LYS	E	18	-4.222	68.665	-25.112	1.00	145.64
	6250	CA	LYS	E	18	-3.099	68.891	-26.010	1.00	145.64
	6251	CB	LYS	E	18	-3.370	68.206	-27.350	1.00	192.00
	6252	CG	LYS	E	18	-2.210	68.241	-28.329	1.00	192.00
	6253	CD	LYS	E	18	-2.457	67.244	-29.441	1.00	192.00
30	6254	CE	LYS	E	18	-1.359	67.245	-30.495	1.00	192.00
	6255	NZ	LYS	E	18	-1.218	68.567	-31.165	1.00	192.00
	6256	C	LYS	E	18	-2.878	70.388	-26.224	1.00	145.64
	6257	O	LYS	E	18	-3.814	71.129	-26.517	1.00	145.64
	6258	N	GLY	E	19	-1.638	70.835	-26.061	1.00	249.22
35	6259	CA	GLY	E	19	-1.339	72.237	-26.278	1.00	249.22
	6260	C	GLY	E	19	-1.364	73.144	-25.065	1.00	249.22
	6261	O	GLY	E	19	-0.954	74.298	-25.156	1.00	249.22
	6262	N	GLU	E	20	-1.837	72.648	-23.930	1.00	144.61
	6263	CA	GLU	E	20	-1.882	73.481	-22.732	1.00	144.61
40	6264	CB	GLU	E	20	-2.930	72.929	-21.759	1.00	147.82
	6265	CG	GLU	E	20	-4.288	72.690	-22.425	1.00	147.82
	6266	CD	GLU	E	20	-5.371	72.257	-21.449	1.00	147.82
	6267	OE1	GLU	E	20	-5.166	71.259	-20.729	1.00	147.82
	6268	OE2	GLU	E	20	-6.435	72.910	-21.411	1.00	147.82
45	6269	C	GLU	E	20	-0.501	73.546	-22.071	1.00	144.61
	6270	O	GLU	E	20	0.412	72.815	-22.466	1.00	144.61
	6271	N	ASN	E	21	-0.335	74.432	-21.089	1.00	165.65
	6272	CA	ASN	E	21	0.951	74.549	-20.407	1.00	165.65
	6273	CB	ASN	E	21	1.551	75.953	-20.547	1.00	216.79
50	6274	CG	ASN	E	21	1.361	76.551	-21.918	1.00	216.79
	6275	OD1	ASN	E	21	1.528	75.886	-22.943	1.00	216.79
	6276	ND2	ASN	E	21	1.027	77.836	-21.921	1.00	216.79
	6277	C	ASN	E	21	0.837	74.248	-18.917	1.00	165.65
	6278	O	ASN	E	21	-0.147	74.602	-18.268	1.00	165.65
55	6279	N	VAL	E	22	1.868	73.608	-18.380	1.00	160.77
	6280	CA	VAL	E	22	1.912	73.265	-16.968	1.00	160.77
	6281	CB	VAL	E	22	1.497	71.820	-16.737	1.00	158.92
	6282	CG1	VAL	E	22	2.481	70.881	-17.426	1.00	158.92
	6283	CG2	VAL	E	22	1.448	71.543	-15.256	1.00	158.92
60	6284	C	VAL	E	22	3.342	73.442	-16.467	1.00	160.77
	6285	O	VAL	E	22	4.306	73.287	-17.229	1.00	160.77
	6286	N	THR	E	23	3.478	73.743	-15.180	1.00	119.61
	6287	CA	THR	E	23	4.789	73.972	-14.581	1.00	119.61
	6288	CB	THR	E	23	4.862	75.412	-14.037	1.00	249.32
65	6289	OG1	THR	E	23	4.505	76.335	-15.075	1.00	249.32
	6290	CG2	THR	E	23	6.255	75.728	-13.537	1.00	249.32
	6291	C	THR	E	23	5.089	73.004	-13.434	1.00	119.61
	6292	O	THR	E	23	4.291	72.881	-12.515	1.00	119.61
	6293	N	LEU	E	24	6.233	72.326	-13.467	1.00	105.17
70	6294	CA	LEU	E	24	6.556	71.397	-12.387	1.00	105.17

	#	Atom	Res	Chain	Seq	X	Y	Z	Occ	B
	6295	CB	LEU	E	24	7.032	70.045	-12.922	1.00	144.47
	6296	CG	LEU	E	24	6.394	69.466	-14.178	1.00	144.47
	6297	CD1	LEU	E	24	6.782	68.008	-14.314	1.00	144.47
	6298	CD2	LEU	E	24	4.904	69.607	-14.118	1.00	144.47
5	6299	C	LEU	E	24	7.635	71.944	-11.482	1.00	105.17
	6300	O	LEU	E	24	8.814	71.943	-11.821	1.00	105.17
	6301	N	THR	E	25	7.238	72.386	-10.306	1.00	95.95
	6302	CA	THR	E	25	8.206	72.926	-9.380	1.00	95.95
	6303	CB	THR	E	25	7.552	74.012	-8.528	1.00	178.12
10	6304	OG1	THR	E	25	6.961	74.986	-9.397	1.00	178.12
	6305	CG2	THR	E	25	8.578	74.689	-7.639	1.00	178.12
	6306	C	THR	E	25	8.786	71.833	-8.486	1.00	95.95
	6307	O	THR	E	25	8.062	70.964	-8.004	1.00	95.95
	6308	N	CYS	E	26	10.098	71.858	-8.279	1.00	175.10
15	6309	CA	CYS	E	26	10.709	70.859	-7.421	1.00	175.10
	6310	C	CYS	E	26	10.598	71.335	-5.991	1.00	175.10
	6311	O	CYS	E	26	10.769	72.518	-5.698	1.00	175.10
	6312	CB	CYS	E	26	12.178	70.637	-7.771	1.00	230.60
	6313	SG	CYS	E	26	12.906	69.220	-6.890	1.00	230.60
20	6314	N	ASN	E	27	10.293	70.392	-5.114	1.00	159.04
	6315	CA	ASN	E	27	10.141	70.641	-3.696	1.00	159.04
	6316	CB	ASN	E	27	10.980	69.628	-2.940	1.00	118.85
	6317	CG	ASN	E	27	10.546	69.486	-1.511	1.00	118.85
	6318	OD1	ASN	E	27	9.351	69.537	-1.211	1.00	118.85
25	6319	ND2	ASN	E	27	11.506	69.298	-0.613	1.00	118.85
	6320	C	ASN	E	27	10.502	72.054	-3.237	1.00	159.04
	6321	O	ASN	E	27	11.646	72.331	-2.882	1.00	159.04
	6322	N	GLY	E	28	9.516	72.944	-3.238	1.00	225.84
	6323	CA	GLY	E	28	9.750	74.315	-2.824	1.00	225.84
30	6324	C	GLY	E	28	8.487	75.101	-3.091	1.00	225.84
	6325	O	GLY	E	28	8.021	75.153	-4.227	1.00	225.84
	6326	N	ASN	E	29	7.929	75.722	-2.059	1.00	249.43
	6327	CA	ASN	E	29	6.693	76.466	-2.228	1.00	249.43
	6328	CB	ASN	E	29	6.026	76.682	-0.870	1.00	249.43
35	6329	CG	ASN	E	29	4.607	77.193	-0.996	1.00	249.43
	6330	OD1	ASN	E	29	3.999	77.145	-2.066	1.00	249.43
	6331	ND2	ASN	E	29	4.067	77.674	0.104	1.00	249.43
	6332	C	ASN	E	29	6.820	77.799	-2.962	1.00	249.43
	6333	O	ASN	E	29	6.084	78.052	-3.920	1.00	249.43
40	6334	N	ASN	E	30	7.746	78.649	-2.530	1.00	249.58
	6335	CA	ASN	E	30	7.903	79.952	-3.169	1.00	249.58
	6336	CB	ASN	E	30	7.420	81.060	-2.229	1.00	249.27
	6337	CG	ASN	E	30	5.941	80.965	-1.929	1.00	249.27
	6338	OD1	ASN	E	30	5.532	80.984	-0.770	1.00	249.27
45	6339	ND2	ASN	E	30	5.128	80.865	-2.974	1.00	249.27
	6340	C	ASN	E	30	9.313	80.279	-3.633	1.00	249.58
	6341	O	ASN	E	30	9.589	80.313	-4.833	1.00	249.58
	6342	N	PHE	E	31	10.206	80.526	-2.682	1.00	249.39
	6343	CA	PHE	E	31	11.567	80.882	-3.038	1.00	249.39
50	6344	CB	PHE	E	31	11.939	82.212	-2.368	1.00	249.51
	6345	CG	PHE	E	31	10.976	83.336	-2.673	1.00	249.51
	6346	CD1	PHE	E	31	9.760	83.431	-2.003	1.00	249.51
	6347	CD2	PHE	E	31	11.275	84.285	-3.649	1.00	249.51
	6348	CE1	PHE	E	31	8.855	84.455	-2.294	1.00	249.51
55	6349	CE2	PHE	E	31	10.278	85.313	-3.949	1.00	249.51
	6350	CZ	PHE	E	31	9.164	85.396	-3.270	1.00	249.51
	6351	C	PHE	E	31	12.602	79.806	-2.729	1.00	249.39
	6352	O	PHE	E	31	12.696	79.305	-1.605	1.00	249.39
	6353	N	PHE	E	32	13.374	79.462	-3.760	1.00	249.36
60	6354	CA	PHE	E	32	14.421	78.447	-3.678	1.00	249.36
	6355	CB	PHE	E	32	14.088	77.296	-4.623	1.00	231.13
	6356	CG	PHE	E	32	14.910	76.075	-4.386	1.00	231.13
	6357	CD1	PHE	E	32	14.771	75.366	-3.200	1.00	231.13
	6358	CD2	PHE	E	32	15.844	75.644	-5.325	1.00	231.13
65	6359	CE1	PHE	E	32	15.547	74.245	-2.944	1.00	231.13
	6360	CE2	PHE	E	32	16.628	74.520	-5.079	1.00	231.13
	6361	CZ	PHE	E	32	16.477	73.819	-3.881	1.00	231.13
	6362	C	PHE	E	32	15.779	79.040	-4.063	1.00	249.36
	6363	O	PHE	E	32	15.849	80.171	-4.540	1.00	249.36
70	6364	N	GLU	E	33	16.857	78.277	-3.876	1.00	249.65

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6365	CA	GLU	E	33	18.190	78.784	-4.212	1.00	249.65
6366	CB	GLU	E	33	19.035	78.993	-2.958	1.00	249.51
6367	CG	GLU	E	33	20.347	79.715	-3.258	1.00	249.51
6368	CD	GLU	E	33	20.106	81.122	-3.769	1.00	249.51
6369	OE1	GLU	E	33	19.170	81.769	-3.253	1.00	249.51
6370	OE2	GLU	E	33	20.849	81.591	-4.659	1.00	249.51
6371	C	GLU	E	33	19.038	77.975	-5.180	1.00	249.65
6372	O	GLU	E	33	19.533	78.510	-6.173	1.00	249.65
6373	N	VAL	E	34	19.242	76.699	-4.873	1.00	249.34
6374	CA	VAL	E	34	20.073	75.864	-5.721	1.00	249.34
6375	CB	VAL	E	34	20.055	74.399	-5.244	1.00	177.29
6376	CG1	VAL	E	34	20.927	73.540	-6.146	1.00	177.29
6377	CG2	VAL	E	34	20.562	74.325	-3.815	1.00	177.29
6378	C	VAL	E	34	19.694	75.933	-7.196	1.00	249.34
6379	O	VAL	E	34	18.530	76.142	-7.555	1.00	249.34
6380	N	SER	E	35	20.705	75.782	-8.040	1.00	249.49
6381	CA	SER	E	35	20.523	75.809	-9.479	1.00	249.49
6382	CB	SER	E	35	21.517	76.779	-10.122	1.00	217.44
6383	OG	SER	E	35	22.845	76.294	-10.006	1.00	217.44
6384	C	SER	E	35	20.763	74.397	-10.001	1.00	249.49
6385	O	SER	E	35	20.658	74.144	-11.199	1.00	249.49
6386	N	SER	E	36	21.094	73.480	-9.092	1.00	249.36
6387	CA	SER	E	36	21.335	72.089	-9.464	1.00	249.36
6388	CB	SER	E	36	22.586	71.540	-8.769	1.00	172.90
6389	OG	SER	E	36	22.371	71.370	-7.379	1.00	172.90
6390	C	SER	E	36	20.128	71.242	-9.085	1.00	249.36
6391	O	SER	E	36	20.020	70.741	-7.964	1.00	249.36
6392	N	THR	E	37	19.214	71.104	-10.036	1.00	210.16
6393	CA	THR	E	37	18.007	70.321	-9.849	1.00	210.16
6394	CB	THR	E	37	16.754	71.225	-9.905	1.00	202.55
6395	OG1	THR	E	37	16.859	72.253	-8.913	1.00	202.55
6396	CG2	THR	E	37	15.499	70.414	-9.647	1.00	202.55
6397	C	THR	E	37	17.982	69.325	-11.000	1.00	210.16
6398	O	THR	E	37	18.352	69.662	-12.126	1.00	210.16
6399	N	LYS	E	38	17.565	68.098	-10.718	1.00	223.06
6400	CA	LYS	E	38	17.517	67.070	-11.749	1.00	223.06
6401	CB	LYS	E	38	18.234	65.818	-11.256	1.00	249.17
6402	CG	LYS	E	38	19.660	66.069	-10.828	1.00	249.17
6403	CD	LYS	E	38	20.313	64.794	-10.338	1.00	249.17
6404	CE	LYS	E	38	21.769	65.032	-9.996	1.00	249.17
6405	NZ	LYS	E	38	22.436	63.783	-9.543	1.00	249.17
6406	C	LYS	E	38	16.086	66.711	-12.133	1.00	223.06
6407	O	LYS	E	38	15.204	66.678	-11.281	1.00	223.06
6408	N	TRP	E	39	15.858	66.451	-13.418	1.00	178.64
6409	CA	TRP	E	39	14.530	66.068	-13.895	1.00	178.64
6410	CB	TRP	E	39	13.911	67.160	-14.768	1.00	178.88
6411	CG	TRP	E	39	13.622	68.431	-14.049	1.00	178.88
6412	CD2	TRP	E	39	12.634	68.651	-13.034	1.00	178.88
6413	CE2	TRP	E	39	12.721	70.008	-12.652	1.00	178.88
6414	CE3	TRP	E	39	11.685	67.832	-12.407	1.00	178.88
6415	CD1	TRP	E	39	14.249	69.627	-14.235	1.00	178.88
6416	NE1	TRP	E	39	13.712	70.580	-13.400	1.00	178.88
6417	CZ2	TRP	E	39	11.896	70.564	-11.678	1.00	178.88
6418	CZ3	TRP	E	39	10.865	68.390	-11.436	1.00	178.88
6419	CH2	TRP	E	39	10.978	69.744	-11.081	1.00	178.88
6420	C	TRP	E	39	14.641	64.796	-14.710	1.00	178.64
6421	O	TRP	E	39	15.495	64.687	-15.582	1.00	178.64
6422	N	PHE	E	40	13.771	63.838	-14.432	1.00	223.76
6423	CA	PHE	E	40	13.811	62.585	-15.159	1.00	223.76
6424	CB	PHE	E	40	14.209	61.445	-14.223	1.00	188.15
6425	CG	PHE	E	40	15.514	61.660	-13.529	1.00	188.15
6426	CD1	PHE	E	40	15.592	62.472	-12.407	1.00	188.15
6427	CD2	PHE	E	40	16.663	61.029	-13.984	1.00	188.15
6428	CE1	PHE	E	40	16.797	62.656	-11.746	1.00	188.15
6429	CE2	PHE	E	40	17.875	61.204	-13.333	1.00	188.15
6430	CZ	PHE	E	40	17.942	62.020	-12.207	1.00	188.15
6431	C	PHE	E	40	12.490	62.235	-15.834	1.00	223.76
6432	O	PHE	E	40	11.665	61.521	-15.266	1.00	223.76
6433	N	HIS	E	41	12.294	62.737	-17.048	1.00	123.84
6434	CA	HIS	E	41	11.080	62.448	-17.801	1.00	123.84

	6435	CB	HIS	E	41	10.940	63.454	-18.937	1.00	124.43
	6436	CG	HIS	E	41	9.749	63.222	-19.801	1.00	124.43
	6437	CD2	HIS	E	41	9.597	63.290	-21.144	1.00	124.43
	6438	ND1	HIS	E	41	8.510	62.907	-19.289	1.00	124.43
5	6439	CE1	HIS	E	41	7.645	62.789	-20.278	1.00	124.43
	6440	NE2	HIS	E	41	8.280	63.016	-21.415	1.00	124.43
	6441	C	HIS	E	41	11.136	61.013	-18.349	1.00	123.84
	6442	O	HIS	E	41	11.924	60.715	-19.243	1.00	123.84
	6443	N	ASN	E	42	10.298	60.132	-17.809	1.00	190.21
10	6444	CA	ASN	E	42	10.269	58.717	-18.206	1.00	190.21
	6445	CB	ASN	E	42	10.027	58.550	-19.720	1.00	194.75
	6446	CG	ASN	E	42	8.588	58.839	-20.123	1.00	194.75
	6447	OD1	ASN	E	42	8.009	59.813	-19.653	1.00	194.75
	6448	ND2	ASN	E	42	8.017	58.019	-21.005	1.00	194.75
15	6449	C	ASN	E	42	11.593	58.050	-17.826	1.00	190.21
	6450	O	ASN	E	42	12.003	57.072	-18.446	1.00	190.21
	6451	N	GLY	E	43	12.263	58.580	-16.806	1.00	203.91
	6452	CA	GLY	E	43	13.533	58.010	-16.386	1.00	203.91
	6453	C	GLY	E	43	14.734	58.697	-17.020	1.00	203.91
20	6454	O	GLY	E	43	15.758	58.901	-16.364	1.00	203.91
	6455	N	SER	E	44	14.609	59.053	-18.297	1.00	245.20
	6456	CA	SER	E	44	15.683	59.723	-19.030	1.00	245.20
	6457	CB	SER	E	44	15.312	59.846	-20.512	1.00	220.02
	6458	OG	SER	E	44	14.940	58.591	-21.055	1.00	220.02
25	6459	C	SER	E	44	15.929	61.114	-18.452	1.00	245.20
	6460	O	SER	E	44	14.999	61.907	-18.326	1.00	245.20
	6461	N	LEU	E	45	17.177	61.412	-18.101	1.00	174.49
	6462	CA	LEU	E	45	17.519	62.718	-17.541	1.00	174.49
	6463	CB	LEU	E	45	19.028	62.804	-17.280	1.00	249.38
30	6464	CG	LEU	E	45	19.550	64.104	-16.660	1.00	249.38
	6465	CD1	LEU	E	45	18.785	64.404	-15.381	1.00	249.38
	6466	CD2	LEU	E	45	21.043	63.982	-16.375	1.00	249.38
	6467	C	LEU	E	45	17.095	63.834	-18.498	1.00	174.49
	6468	O	LEU	E	45	17.140	63.672	-19.717	1.00	174.49
35	6469	N	SER	E	46	16.673	64.965	-17.945	1.00	153.34
	6470	CA	SER	E	46	16.247	66.094	-18.766	1.00	153.34
	6471	CB	SER	E	46	15.016	66.766	-18.148	1.00	249.33
	6472	OG	SER	E	46	14.541	67.822	-18.971	1.00	249.33
	6473	C	SER	E	46	17.394	67.088	-18.845	1.00	153.34
40	6474	O	SER	E	46	18.345	66.994	-18.072	1.00	153.34
	6475	N	GLU	E	47	17.310	68.043	-19.768	1.00	221.85
	6476	CA	GLU	E	47	18.371	69.035	-19.903	1.00	221.85
	6477	CB	GLU	E	47	18.589	69.401	-21.384	1.00	249.45
	6478	CG	GLU	E	47	18.515	68.232	-22.369	1.00	249.45
45	6479	CD	GLU	E	47	18.351	68.687	-23.823	1.00	249.45
	6480	OE1	GLU	E	47	17.207	68.973	-24.239	1.00	249.45
	6481	OE2	GLU	E	47	19.372	68.774	-24.540	1.00	249.45
	6482	C	GLU	E	47	18.128	70.317	-19.081	1.00	221.85
	6483	O	GLU	E	47	18.974	71.207	-19.091	1.00	221.85
50	6484	N	GLU	E	48	16.993	70.438	-18.387	1.00	204.14
	6485	CA	GLU	E	48	16.775	71.643	-17.573	1.00	204.14
	6486	CB	GLU	E	48	15.275	71.939	-17.355	1.00	206.52
	6487	CG	GLU	E	48	14.973	73.087	-16.352	1.00	206.52
	6488	CD	GLU	E	48	15.418	74.469	-16.823	1.00	206.52
55	6489	OE1	GLU	E	48	14.812	74.995	-17.778	1.00	206.52
	6490	OE2	GLU	E	48	16.370	75.032	-16.236	1.00	206.52
	6491	C	GLU	E	48	17.471	71.443	-16.221	1.00	204.14
	6492	O	GLU	E	48	17.724	70.311	-15.798	1.00	204.14
	6493	N	THR	E	49	17.803	72.545	-15.556	1.00	206.12
60	6494	CA	THR	E	49	18.472	72.476	-14.266	1.00	206.12
	6495	CB	THR	E	49	19.947	72.928	-14.386	1.00	224.40
	6496	OG1	THR	E	49	20.006	74.247	-14.942	1.00	224.40
	6497	CG2	THR	E	49	20.721	71.972	-15.288	1.00	224.40
	6498	C	THR	E	49	17.747	73.335	-13.233	1.00	206.12
65	6499	O	THR	E	49	17.781	73.043	-12.035	1.00	206.12
	6500	N	ASN	E	50	17.081	74.388	-13.702	1.00	231.11
	6501	CA	ASN	E	50	16.330	75.272	-12.819	1.00	231.11
	6502	CB	ASN	E	50	15.602	76.349	-13.640	1.00	176.85
	6503	CG	ASN	E	50	15.085	77.491	-12.783	1.00	176.85
70	6504	OD1	ASN	E	50	14.962	77.346	-11.568	1.00	176.85

	6505	ND2	ASN	E	50	14.770	78.622	-13.410	1.00	176.85
	6506	C	ASN	E	50	15.316	74.396	-12.076	1.00	231.11
	6507	O	ASN	E	50	14.884	73.368	-12.597	1.00	231.11
	6508	N	SER	E	51	14.942	74.792	-10.863	1.00	235.89
5	6509	CA	SER	E	51	13.985	74.015	-10.077	1.00	235.89
	6510	CB	SER	E	51	13.895	74.561	-8.645	1.00	153.05
	6511	OG	SER	E	51	13.254	75.826	-8.609	1.00	153.05
	6512	C	SER	E	51	12.587	73.995	-10.696	1.00	235.89
	6513	O	SER	E	51	11.765	73.145	-10.358	1.00	235.89
10	6514	N	SER	E	52	12.314	74.932	-11.597	1.00	154.90
	6515	CA	SER	E	52	11.009	74.997	-12.245	1.00	154.90
	6516	CB	SER	E	52	10.435	76.415	-12.157	1.00	199.68
	6517	OG	SER	E	52	10.195	76.786	-10.809	1.00	199.68
	6518	C	SER	E	52	11.109	74.569	-13.700	1.00	154.90
15	6519	O	SER	E	52	11.656	75.288	-14.538	1.00	154.90
	6520	N	LEU	E	53	10.582	73.385	-13.985	1.00	130.79
	6521	CA	LEU	E	53	10.590	72.827	-15.332	1.00	130.79
	6522	CB	LEU	E	53	10.833	71.315	-15.264	1.00	134.25
	6523	CG	LEU	E	53	10.394	70.457	-16.457	1.00	134.25
20	6524	CD1	LEU	E	53	10.802	71.095	-17.779	1.00	134.25
	6525	CD2	LEU	E	53	10.999	69.065	-16.304	1.00	134.25
	6526	C	LEU	E	53	9.271	73.112	-16.044	1.00	130.79
	6527	O	LEU	E	53	8.279	72.435	-15.810	1.00	130.79
	6528	N	ASN	E	54	9.258	74.109	-16.920	1.00	200.88
25	6529	CA	ASN	E	54	8.031	74.440	-17.632	1.00	200.88
	6530	CB	ASN	E	54	8.095	75.864	-18.181	1.00	249.13
	6531	CG	ASN	E	54	7.990	76.907	-17.096	1.00	249.13
	6532	OD1	ASN	E	54	7.029	76.923	-16.328	1.00	249.13
	6533	ND2	ASN	E	54	8.975	77.790	-17.026	1.00	249.13
30	6534	C	ASN	E	54	7.719	73.486	-18.771	1.00	200.88
	6535	O	ASN	E	54	8.589	72.769	-19.265	1.00	200.88
	6536	N	ILE	E	55	6.453	73.481	-19.168	1.00	204.06
	6537	CA	ILE	E	55	5.985	72.657	-20.269	1.00	204.06
	6538	CB	ILE	E	55	5.212	71.417	-19.770	1.00	202.84
35	6539	CG2	ILE	E	55	4.367	70.839	-20.896	1.00	202.84
	6540	CG1	ILE	E	55	6.205	70.376	-19.246	1.00	202.84
	6541	CD1	ILE	E	55	5.569	69.111	-18.716	1.00	202.84
	6542	C	ILE	E	55	5.065	73.547	-21.080	1.00	204.06
	6543	O	ILE	E	55	4.086	74.074	-20.559	1.00	204.06
40	6544	N	VAL	E	56	5.395	73.739	-22.349	1.00	244.52
	6545	CA	VAL	E	56	4.580	74.585	-23.202	1.00	244.52
	6546	CB	VAL	E	56	5.458	75.494	-24.072	1.00	219.78
	6547	CG1	VAL	E	56	4.629	76.643	-24.618	1.00	219.78
	6548	CG2	VAL	E	56	6.622	76.026	-23.246	1.00	219.78
45	6549	C	VAL	E	56	3.711	73.696	-24.073	1.00	244.52
	6550	O	VAL	E	56	3.545	72.522	-23.758	1.00	244.52
	6551	N	ASN	E	57	3.160	74.247	-25.152	1.00	153.88
	6552	CA	ASN	E	57	2.290	73.486	-26.047	1.00	153.88
50	6553	CB	ASN	E	57	2.564	73.854	-27.506	1.00	249.23
	6554	CG	ASN	E	57	2.105	75.254	-27.843	1.00	249.23
	6555	OD1	ASN	E	57	0.954	75.617	-27.601	1.00	249.23
	6556	ND2	ASN	E	57	3.003	76.051	-28.404	1.00	249.23
	6557	C	ASN	E	57	2.438	71.983	-25.847	1.00	153.88
55	6558	O	ASN	E	57	3.263	71.323	-26.489	1.00	153.88
	6559	N	ALA	E	58	1.624	71.458	-24.936	1.00	183.15
	6560	CA	ALA	E	58	1.638	70.047	-24.587	1.00	183.15
	6561	CB	ALA	E	58	0.552	69.763	-23.565	1.00	127.72
	6562	C	ALA	E	58	1.492	69.103	-25.766	1.00	183.15
60	6563	O	ALA	E	58	0.486	69.115	-26.474	1.00	183.15
	6564	N	LYS	E	59	2.510	68.281	-25.968	1.00	111.87
	6565	CA	LYS	E	59	2.495	67.293	-27.035	1.00	111.87
	6566	CB	LYS	E	59	3.816	67.338	-27.815	1.00	249.40
	6567	CG	LYS	E	59	4.115	68.702	-28.436	1.00	249.40
65	6568	CD	LYS	E	59	5.489	68.753	-29.090	1.00	249.40
	6569	CE	LYS	E	59	5.764	70.129	-29.691	1.00	249.40
	6570	NZ	LYS	E	59	7.117	70.219	-30.310	1.00	249.40
	6571	C	LYS	E	59	2.319	65.942	-26.334	1.00	111.87
	6572	O	LYS	E	59	2.824	65.746	-25.226	1.00	111.87
	6573	N	PHE	E	60	1.597	65.020	-26.960	1.00	223.03
70	6574	CA	PHE	E	60	1.368	63.703	-26.366	1.00	223.03

	6575	CB	PHE	E	60	0.846	62.744	-27.427	1.00	249.06
	6576	CG	PHE	E	60	-0.496	63.120	-27.953	1.00	249.06
	6577	CD1	PHE	E	60	-0.876	62.774	-29.237	1.00	249.06
	6578	CD2	PHE	E	60	-1.390	63.823	-27.155	1.00	249.06
5	6579	CE1	PHE	E	60	-2.124	63.119	-29.727	1.00	249.06
	6580	CE2	PHE	E	60	-2.640	64.176	-27.633	1.00	249.06
	6581	CZ	PHE	E	60	-3.010	63.822	-28.922	1.00	249.06
	6582	C	PHE	E	60	2.610	63.115	-25.720	1.00	223.03
	6583	O	PHE	E	60	2.520	62.404	-24.721	1.00	223.03
10	6584	N	GLU	E	61	3.771	63.417	-26.296	1.00	190.77
	6585	CA	GLU	E	61	5.044	62.917	-25.783	1.00	190.77
	6586	CB	GLU	E	61	6.196	63.299	-26.718	1.00	249.27
	6587	CG	GLU	E	61	6.096	62.728	-28.116	1.00	249.27
	6588	CD	GLU	E	61	4.851	63.190	-28.838	1.00	249.27
15	6589	OE1	GLU	E	61	4.635	64.418	-28.924	1.00	249.27
	6590	OE2	GLU	E	61	4.090	62.327	-29.320	1.00	249.27
	6591	C	GLU	E	61	5.357	63.449	-24.395	1.00	190.77
	6592	O	GLU	E	61	6.140	62.842	-23.663	1.00	190.77
	6593	N	ASP	E	62	4.765	64.588	-24.040	1.00	156.70
20	6594	CA	ASP	E	62	5.006	65.174	-22.727	1.00	156.70
	6595	CB	ASP	E	62	4.489	66.613	-22.678	1.00	165.21
	6596	CG	ASP	E	62	5.062	67.477	-23.792	1.00	165.21
	6597	OD1	ASP	E	62	6.251	67.299	-24.133	1.00	·· 165.21
	6598	OD2	ASP	E	62	4.329	68.341	-24.320	1.00	165.21
25	6599	C	ASP	E	62	4.341	64.324	-21.643	1.00	156.70
	6600	O	ASP	E	62	4.711	64.394	-20.470	1.00	156.70
	6601	N	SER	E	63	3.358	63.523	-22.045	1.00	· 140.02
	6602	CA	SER	E	63	2.672	62.635	-21.118	1.00	140.02
	6603	CB	SER	E	63	1.618	61.796	-21.856	1.00	116.21
30	6604	OG	SER	E	63	0.557	62.589	-22.368	1.00	116.21
	6605	C	SER	E	63	3.744	61.710	-20.557	1.00	140.02
	6606	O	SER	E	63	4.509	61.128	-21.315	1.00	140.02
	6607	N	GLY	E	64	3.818	61.572	-19.243	1.00	94.90
	6608	CA	GLY	E	64	4.835	60.694	-18.698	1.00	94.90
35	6609	C	GLY	E	64	5.050	60.749	-17.195	1.00	94.90
	6610	O	GLY	E	64	4.252	61.333	-16.462	1.00	94.90
	6611	N	GLU	E	65	6.127	60.121	-16.737	1.00	137.73
	6612	CA	GLU	E	65	6.476	60.071	-15.323	1.00	137.73
	6613	CB	GLU	E	65	6.875	58.635	-14.971	1.00	170.42
40	6614	CG	GLU	E	65	7.492	58.437	-13.609	1.00	170.42
	6615	CD	GLU	E	65	8.153	57.072	-13.484	1.00	170.42
	6616	OE1	GLU	E	65	9.121	56.807	-14.233	1.00	170.42
	6617	OE2	GLU	E	65	7.706	56.263	-12.644	1.00	170.42
	6618	C	GLU	E	65	7.645	61.025	-15.096	1.00	137.73
45	6619	O	GLU	E	65	8.653	60.925	-15.789	1.00	137.73
	6620	N	TYR	E	66	7.513	61.952	-14.147	1.00	117.13
	6621	CA	TYR	E	66	8.588	62.908	-13.864	1.00	117.13
	6622	CB	TYR	E	66	8.123	64.321	-14.112	1.00	93.74
	6623	CG	TYR	E	66	7.767	64.647	-15.528	1.00	93.74
50	6624	CD1	TYR	E	66	6.586	64.214	-16.090	1.00	93.74
	6625	CE1	TYR	E	66	6.220	64.609	-17.382	1.00	93.74
	6626	CD2	TYR	E	66	8.582	65.471	-16.285	1.00	93.74
	6627	CE2	TYR	E	66	8.230	65.873	-17.564	1.00	93.74
	6628	CZ	TYR	E	66	7.050	65.445	-18.110	1.00	93.74
55	6629	OH	TYR	E	66	6.702	65.872	-19.376	1.00	93.74
	6630	C	TYR	E	66	9.062	62.852	-12.426	1.00	117.13
	6631	O	TYR	E	66	8.359	62.335	-11.564	1.00	117.13
	6632	N	LYS	E	67	10.248	63.402	-12.169	1.00	125.36
	6633	CA	LYS	E	67	10.802	63.443	-10.815	1.00	125.36
60	6634	CB	LYS	E	67	11.186	62.037	-10.352	1.00	181.51
	6635	CG	LYS	E	67	12.026	61.282	-11.345	1.00	181.51
	6636	CD	LYS	E	67	12.264	59.876	-10.876	1.00	181.51
	6637	CE	LYS	E	67	12.938	59.066	-11.956	1.00	181.51
	6638	NZ	LYS	E	67	13.120	57.655	-11.522	1.00	181.51
65	6639	C	LYS	E	67	12.014	64.362	-10.732	1.00	125.36
	6640	O	LYS	E	67	12.671	64.622	-11.737	1.00	125.36
	6641	N	CYS	E	68	12.289	64.881	-9.541	1.00	114.74
	6642	CA	CYS	E	68	13.451	65.729	-9.370	1.00	114.74
	6643	C	CYS	E	68	14.297	65.211	-8.210	1.00	114.74
70	6644	O	CYS	E	68	13.824	64.428	-7.388	1.00	114.74

	6645	CB	CYS	E	68	13.047	67.197	-9.159	1.00	167.12
	6646	SG	CYS	E	68	12.001	67.607	-7.729	1.00	167.12
	6647	N	GLN	E	69	15.561	65.619	-8.180	1.00	152.39
	6648	CA	GLN	E	69	16.493	65.217	-7.139	1.00	152.39
5	6649	CB	GLN	E	69	17.120	63.861	-7.482	1.00	180.76
	6650	CG	GLN	E	69	18.398	63.553	-6.725	1.00	180.76
	6651	CD	GLN	E	69	19.065	62.274	-7.191	1.00	180.76
	6652	OE1	GLN	E	69	19.315	62.089	-8.383	1.00	180.76
	6653	NE2	GLN	E	69	19.364	61.386	-6.250	1.00	180.76
10	6654	C	GLN	E	69	17.566	66.292	-7.067	1.00	152.39
	6655	O	GLN	E	69	17.822	66.998	-8.048	1.00	152.39
	6656	N	HIS	E	70	18.186	66.429	-5.902	1.00	249.25
	6657	CA	HIS	E	70	19.226	67.429	-5.730	1.00	249.25
	6658	CB	HIS	E	70	18.911	68.308	-4.519	1.00	185.63
15	6659	CG	HIS	E	70	17.717	69.187	-4.713	1.00	185.63
	6660	CD2	HIS	E	70	16.426	69.026	-4.338	1.00	185.63
	6661	ND1	HIS	E	70	17.769	70.377	-5.406	1.00	185.63
	6662	CE1	HIS	E	70	16.560	70.915	-5.449	1.00	185.63
	6663	NE2	HIS	E	70	15.729	70.114	-4.806	1.00	185.63
20	6664	C	HIS	E	70	20.605	66.806	-5.583	1.00	249.25
	6665	O	HIS	E	70	20.793	65.603	-5.787	1.00	249.25
	6666	N	GLN	E	71	21.568	67.644	-5.225	1.00	214.79
	6667	CA	GLN	E	71	22.945	67.209	-5.061	1.00	214.79
	6668	CB	GLN	E	71	23.787	68.387	-4.553	1.00	249.44
25	6669	CG	GLN	E	71	25.227	68.347	-5.024	1.00	249.44
	6670	CD	GLN	E	71	25.359	68.172	-6.526	1.00	249.44
	6671	OE1	GLN	E	71	25.049	69.077	-7.304	1.00	249.44
	6672	NE2	GLN	E	71	25.815	67.001	-6.940	1.00	249.44
	6673	C	GLN	E	71	23.055	66.005	-4.119	1.00	214.79
30	6674	O	GLN	E	71	23.602	64.967	-4.496	1.00	214.79
	6675	N	GLN	E	72	22.517	66.140	-2.906	1.00	224.12
	6676	CA	GLN	E	72	22.569	65.060	-1.906	1.00	224.12
	6677	CB	GLN	E	72	23.396	65.488	-0.694	1.00	220.92
	6678	CG	GLN	E	72	23.660	64.401	0.347	1.00	220.92
35	6879	CD	GLN	E	72	24.599	64.863	1.460	1.00	220.92
	6680	OE1	GLN	E	72	25.746	65.260	1.224	1.00	220.92
	6681	NE2	GLN	E	72	24.108	64.811	2.684	1.00	220.92
	6682	C	GLN	E	72	21.190	64.677	-1.396	1.00	224.12
	6683	O	GLN	E	72	20.938	64.719	-0.192	1.00	224.12
40	6684	N	VAL	E	73	20.301	64.293	-2.298	1.00	249.50
	6685	CA	VAL	E	73	18.953	63.928	-1.899	1.00	249.50
	6686	CB	VAL	E	73	18.006	65.126	-2.032	1.00	213.59
	6687	CG1	VAL	E	73	16.699	64.850	-1.308	1.00	213.59
	6688	CG2	VAL	E	73	18.676	66.352	-1.536	1.00	213.59
45	6689	C	VAL	E	73	18.410	62.814	-2.776	1.00	249.50
	6690	O	VAL	E	73	18.724	62.740	-3.964	1.00	249.50
	6691	N	ASN	E	74	17.584	61.952	-2.192	1.00	249.52
	6692	CA	ASN	E	74	16.994	60.858	-2.946	1.00	249.52
	6693	CB	ASN	E	74	16.515	59.760	-1.994	1.00	169.17
50	6694	CG	ASN	E	74	17.620	59.273	-1.081	1.00	169.17
	6695	OD1	ASN	E	74	18.757	59.080	-1.522	1.00	169.17
	6696	ND2	ASN	E	74	17.291	59.065	0.192	1.00	169.17
	6697	C	ASN	E	74	15.838	61.389	-3.787	1.00	249.52
	6698	O	ASN	E	74	14.956	62.085	-3.283	1.00	249.52
55	6699	N	GLU	E	75	15.870	61.071	-5.077	1.00	220.79
	6700	CA	GLU	E	75	14.851	61.501	-6.025	1.00	220.79
	6701	CB	GLU	E	75	14.992	60.694	-7.316	1.00	206.72
	6702	CG	GLU	E	75	15.456	59.259	-7.100	1.00	206.72
	6703	CD	GLU	E	75	15.805	58.557	-8.399	1.00	206.72
60	6704	OE1	GLU	E	75	16.636	59.096	-9.159	1.00	206.72
	6705	OE2	GLU	E	75	15.254	57.465	-8.660	1.00	206.72
	6706	C	GLU	E	75	13.420	61.414	-5.488	1.00	220.79
	6707	O	GLU	E	75	13.071	60.495	-4.747	1.00	220.79
	6708	N	SER	E	76	12.604	62.385	-5.885	1.00	123.65
65	6709	CA	SER	E	76	11.211	62.502	-5.457	1.00	123.65
	6710	CB	SER	E	76	10.646	63.837	-5.918	1.00	156.05
	6711	OG	SER	E	76	10.583	63.854	-7.332	1.00	156.05
	6712	C	SER	E	76	10.310	61.422	-5.997	1.00	123.65
	6713	O	SER	E	76	10.623	60.793	-7.006	1.00	123.65
70	6714	N	GLU	E	77	9.172	61.235	-5.333	1.00	207.91

	6715	CA	GLU	E	77	8.193	60.247	-5.762	1.00	207.91
	6716	CB	GLU	E	77	7.055	60.135	-4.744	1.00	181.88
	6717	CG	GLU	E	77	7.495	59.613	-3.388	1.00	181.88
	6718	CD	GLU	E	77	8.000	58.181	-3.440	1.00	181.88
5	6719	OE1	GLU	E	77	8.281	57.684	-4.551	1.00	181.88
	6720	OE2	GLU	E	77	8.127	57.550	-2.369	1.00	181.88
	6721	C	GLU	E	77	7.645	60.711	-7.103	1.00	207.91
	6722	O	GLU	E	77	7.050	61.788	-7.189	1.00	207.91
	6723	N	PRO	E	78	7.857	59.919	-8.171	1.00	80.79
10	6724	CD	PRO	E	78	8.716	58.718	-8.203	1.00	240.65
	6725	CA	PRO	E	78	7.390	60.237	-9.522	1.00	80.79
	6726	CB	PRO	E	78	7.588	58.930	-10.260	1.00	240.65
	6727	CG	PRO	E	78	8.884	58.468	-9.599	1.00	240.65
	6728	C	PRO	E	78	5.967	60.738	-9.594	1.00	80.79
15	6729	O	PRO	E	78	5.145	60.436	-8.738	1.00	80.79
	6730	N	VAL	E	79	5.681	61.517	-10.622	1.00	112.90
	6731	CA	VAL	E	79	4.351	62.067	-10.801	1.00	112.90
	6732	CB	VAL	E	79	4.314	63.550	-10.455	1.00	137.47
	6733	CG1	VAL	E	79	3.032	64.176	-10.987	1.00	137.47
20	6734	CG2	VAL	E	79	4.403	63.715	-8.951	1.00	137.47
	6735	C	VAL	E	79	3.978	61.908	-12.251	1.00	112.90
	6736	O	VAL	E	79	4.737	62.312	-13.132	1.00	112.90
	6737	N	TYR	E	80	2.807	61.334	-12.508	1.00	70.76
	6738	CA	TYR	E	80	2.402	61.134	-13.886	1.00	70.76
25	6739	CB	TYR	E	80	1.630	59.841	-14.062	1.00	159.99
	6740	CG	TYR	E	80	1.595	59.441	-15.510	1.00	159.99
	6741	CD1	TYR	E	80	2.763	59.078	-16.169	1.00	159.99
	6742	CE1	TYR	E	80	2.758	58.714	-17.498	1.00	159.99
	6743	CD2	TYR	E	80	0.408	59.437	-16.231	1.00	159.99
30	6744	CE2	TYR	E	80	0.395	59.076	-17.589	1.00	159.99
	6745	CZ	TYR	E	80	1.583	58.712	-18.206	1.00	159.99
	6746	OH	TYR	E	80	1.597	58.323	-19.528	1.00	159.99
	6747	C	TYR	E	80	1.562	62.238	-14.446	1.00	70.76
	6748	O	TYR	E	80	0.661	62.746	-13.795	1.00	70.76
35	6749	N	LEU	E	81	1.838	62.587	-15.684	1.00	117.40
	6750	CA	LEU	E	81	1.086	63.620	-16.343	1.00	117.40
	6751	CB	LEU	E	81	2.037	64.731	-16.752	1.00	104.60
	6752	CG	LEU	E	81	1.348	65.795	-17.590	1.00	104.60
	6753	CD1	LEU	E	81	0.269	66.455	-16.750	1.00	104.60
40	6754	CD2	LEU	E	81	2.357	66.811	-18.058	1.00	104.60
	6755	C	LEU	E	81	0.455	62.990	-17.575	1.00	117.40
	6756	O	LEU	E	81	1.148	62.313	-18.325	1.00	117.40
	6757	N	GLU	E	82	-0.844	63.186	-17.792	1.00	85.04
	6758	CA	GLU	E	82	-1.474	62.609	-18.982	1.00	85.04
45	6759	CB	GLU	E	82	-2.520	61.566	-18.598	1.00	152.39
	6760	CG	GLU	E	82	-2.736	60.525	-19.684	1.00	152.39
	6761	CD	GLU	E	82	-3.765	59.482	-19.297	1.00	152.30
	6762	OE1	GLU	E	82	-3.785	59.083	-18.107	1.00	152.39
	6763	OE2	GLU	E	82	-4.542	59.055	-20.185	1.00	152.39
50	6764	C	GLU	E	82	-2.112	63.691	-19.854	1.00	85.04
	6765	O	GLU	E	82	-2.843	64.562	-19.363	1.00	85.04
	6766	N	VAL	E	83	-1.829	63.634	-21.152	1.00	88.74
	6767	CA	VAL	E	83	-2.355	64.628	-22.085	1.00	88.74
	6768	CB	VAL	E	83	-1.258	65.146	-23.010	1.00	170.11
55	6769	CG1	VAL	E	83	-1.862	66.064	-24.054	1.00	170.11
	6770	CG2	VAL	E	83	-0.213	65.878	-22.197	1.00	170.11
	6771	C	VAL	E	83	-3.482	64.102	-22.949	1.00	88.74
	6772	O	VAL	E	83	-3.391	63.013	-23.507	1.00	88.74
	6773	N	PHE	E	84	-4.534	64.895	-23.091	1.00	98.95
60	6774	CA	PHE	E	84	-5.675	64.451	-23.873	1.00	98.95
	6775	CB	PHE	E	84	-6.917	64.273	-22.986	1.00	118.45
	6776	CG	PHE	E	84	-6.734	63.316	-21.864	1.00	118.45
	6777	CD1	PHE	E	84	-5.997	63.674	-20.749	1.00	118.45
	6778	CD2	PHE	E	84	-7.324	62.065	-21.911	1.00	118.45
65	6779	CE1	PHE	E	84	-5.839	62.795	-19.701	1.00	118.45
	6780	CE2	PHE	E	84	-7.172	61.173	-20.865	1.00	118.45
	6781	CZ	PHE	E	84	-6.434	61.541	-19.756	1.00	118.45
	6782	C	PHE	E	84	-6.114	65.318	-25.034	1.00	98.95
	6783	O	PHE	E	84	-5.736	66.484	-25.178	1.00	98.95
70	6784	N	SER	E	85	-6.967	64.697	-25.837	1.00	152.83

	6785	CA	SER	E	85	-7.592	65.304	-26.990	1.00	152.83
	6786	CB	SER	E	85	-6.937	64.819	-28.279	1.00	197.25
	6787	OG	SER	E	85	-7.565	65.403	-29.405	1.00	197.25
	6788	C	SER	E	85	-9.030	64.791	-26.914	1.00	152.83
5	6789	O	SER	E	85	-9.279	63.598	-27.101	1.00	152.83
	6790	N	ASP	E	86	-9.962	65.685	-26.600	1.00	101.99
	6791	CA	ASP	E	86	-11.375	65.330	-26.494	1.00	101.99
	6792	CB	ASP	E	86	-11.573	64.296	-25.386	1.00	136.02
	6793	CG	ASP	E	86	-12.655	63.310	-25.715	1.00	136.02
10	6794	OD1	ASP	E	86	-13.782	63.752	-26.031	1.00	136.02
	6795	OD2	ASP	E	86	-12.375	62.095	-25.664	1.00	136.02
	6796	C	ASP	E	86	-12.199	66.594	-26.197	1.00	101.99
	6797	O	ASP	E	86	-11.646	67.635	-25.830	1.00	101.99
	6798	N	TRP	E	87	-13.516	66.516	-26.356	1.00	94.76
15	6799	CA	TRP	E	87	-14.351	67.689	-26.106	1.00	94.76
	6800	CB	TRP	E	87	-15.806	67.417	-26.477	1.00	229.11
	6801	CG	TRP	E	87	-16.051	67.695	-27.896	1.00	229.11
	6802	CD2	TRP	E	87	-15.956	66.755	-28.964	1.00	229.11
	6803	CE2	TRP	E	87	-16.120	67.470	-30.165	1.00	229.11
20	6804	CE3	TRP	E	87	-15.735	65.372	-29.026	1.00	229.11
	6805	CD1	TRP	E	87	-16.281	68.917	-28.471	1.00	229.11
	6806	NE1	TRP	E	87	-16.319	68.787	-29.837	1.00	229.11
	6807	CZ2	TRP	E	87	-16.070	66.850	-31.411	1.00	229.11
	6808	CZ3	TRP	E	87	-15.685	64.755	-30.265	1.00	229.11
25	6809	CH2	TRP	E	87	-15.855	65.491	-31.438	1.00	229.11
	6810	C	TRP	E	87	-14.273	68.108	-24.671	1.00	94.76
	6811	O	TRP	E	87	-13.962	69.260	-24.355	1.00	94.76
	6812	N	LEU	E	88	-14.546	67.147	-23.802	1.00	160.64
	6813	CA	LEU	E	88	-14.527	67.385	-22.379	1.00	160.64
30	6814	CB	LEU	E	88	-15.912	67.160	-21.803	1.00	93.36
	6815	CG	LEU	E	88	-16.950	68.149	-22.276	1.00	93.36
	6816	CD1	LEU	E	88	-18.247	67.872	-21.532	1.00	93.36
	6817	CD2	LEU	E	88	-16.456	69.560	-22.001	1.00	93.36
	6818	C	LEU	E	88	-13.553	66.490	-21.645	1.00	160.64
35	6819	O	LEU	E	88	-13.401	65.314	-21.968	1.00	160.64
	6820	N	LEU	E	89	-12.908	67.057	-20.635	1.00	107.53
	6821	CA	LEU	E	89	-11.961	66.321	-19.828	1.00	107.53
	6822	CB	LEU	E	89	-10.552	66.785	-20.131	1.00	83.31
	6823	CG	LEU	E	89	-9.538	66.057	-19.267	1.00	83.31
40	6824	CD1	LEU	E	89	-9.821	64.541	-19.311	1.00	83.31
	6825	CD2	LEU	E	89	-8.138	66.385	-19.757	1.00	83.31
	6826	C	LEU	E	89	-12.252	66.573	-18.366	1.00	107.53
	6827	O	LEU	E	89	-12.378	67.718	-17.954	1.00	107.53
	6828	N	LEU	E	90	-12.366	65.510	-17.576	1.00	62.89
45	6829	CA	LEU	E	90	-12.629	65.676	-16.142	1.00	62.89
	6830	CB	LEU	E	90	-13.400	64.487	-15.588	1.00	49.26
	6831	CG	LEU	E	90	-13.609	64.523	-14.077	1.00	49.26
	6832	CD1	LEU	E	90	-14.422	65.760	-13.775	1.00	49.26
	6833	CD2	LEU	E	90	-14.308	63.261	-13.579	1.00	49.26
50	6834	C	LEU	E	90	-11.300	65.773	-15.404	1.00	62.89
	6835	O	LEU	E	90	-10.515	64.830	-15.410	1.00	62.89
	6836	N	GLN	E	91	-11.043	66.907	-14.764	1.00	69.52
	6837	CA	GLN	E	91	-9.785	67.083	-14.064	1.00	69.52
	6838	CB	GLN	E	91	-9.210	68.449	-14.388	1.00	103.30
55	6839	CG	GLN	E	91	-8.977	68.644	-15.857	1.00	103.30
	6840	CD	GLN	E	91	-8.226	69.921	-16.149	1.00	103.30
	6841	OE1	GLN	E	91	-8.750	71.021	-15.967	1.00	103.30
	6842	NE2	GLN	E	91	-6.979	69.783	-16.599	1.00	103.30
	6843	C	GLN	E	91	-9.965	66.953	-12.584	1.00	69.52
60	6844	O	GLN	E	91	-10.984	67.372	-12.033	1.00	69.52
	6845	N	ALA	E	92	-8.972	66.375	-11.925	1.00	61.94
	6846	CA	ALA	E	92	-9.070	66.223	-10.483	1.00	61.94
	6847	CB	ALA	E	92	-9.241	64.773	-10.125	1.00	129.56
	6848	C	ALA	E	92	-7.838	66.792	-9.794	1.00	61.94
65	6849	O	ALA	E	92	-6.715	66.663	-10.314	1.00	61.94
	6850	N	SER	E	93	-8.045	67.437	-8.643	1.00	82.97
	6851	CA	SER	E	93	-6.930	68.004	-7.904	1.00	82.97
	6852	CB	SER	E	93	-7.388	68.550	-6.552	1.00	72.43
	6853	OG	SER	E	93	-8.203	67.620	-5.871	1.00	72.43
70	6854	C	SER	E	93	-5.965	66.855	-7.717	1.00	82.97

	6855	O	SER	E	93	-4.873	66.846	-8.282	1.00	82.97
	6856	N	ALA	E	94	-6.395	65.865	-6.948	1.00	109.69
	6857	CA	ALA	E	94	-5.588	64.680	-6.683	1.00	109.69
	6858	CB	ALA	E	94	-5.086	64.711	-5.262	1.00	145.34
5	6859	C	ALA	E	94	-6.468	63.455	-6.910	1.00	109.69
	6860	O	ALA	E	94	-7.652	63.488	-6.620	1.00	109.69
	6861	N	GLU	E	95	-5.902	62.372	-7.431	1.00	77.50
	6862	CA	GLU	E	95	-6.688	61.172	-7.711	1.00	77.50
	6863	CB	GLU	E	95	-6.065	60.391	-8.859	1.00	137.79
10	6864	CG	GLU	E	95	-5.979	61.195	-10.136	1.00	137.79
	6865	CD	GLU	E	95	-5.700	60.335	-11.358	1.00	137.79
	6866	OE1	GLU	E	95	-5.582	60.901	-12.468	1.00	137.79
	6867	OE2	GLU	E	95	-5.607	59.094	-11.210	1.00	137.79
	6868	C	GLU	E	95	-6.869	60.258	-6.514	1.00	77.50
15	6869	O	GLU	E	95	-7.723	59.376	-6.538	1.00	77.50
	6870	N	VAL	E	96	-6.067	60.468	-5.470	1.00	83.99
	6871	CA	VAL	E	96	-6.148	59.673	-4.241	1.00	83.99
	6872	CB	VAL	E	96	-5.042	58.641	-4.191	1.00	76.64
	6873	CG1	VAL	E	96	-5.384	57.579	-3.164	1.00	76.64
20	6874	CG2	VAL	E	96	-4.856	58.037	-5.568	1.00	76.64
	6875	C	VAL	E	96	-6.009	60.634	-3.071	1.00	83.99
	6876	O	VAL	E	96	-5.127	61.491	-3.057	1.00	83.99
	6877	N	VAL	E	97	-6.863	60.475	-2.071	1.00	86.29
	6878	CA	VAL	E	97	-6.880	61.409	-0.959	1.00	86.29
25	6879	CB	VAL	E	97	-8.028	62.389	-1.152	1.00	80.14
	6880	CG1	VAL	E	97	-7.861	63.550	-0.242	1.00	80.14
	6881	CG2	VAL	E	97	-8.102	62.821	-2.571	1.00	80.14
	6882	C	VAL	E	97	-7.073	60.838	0.440	1.00	86.29
	6883	O	VAL	E	97	-7.940	59.988	0.646	1.00	86.29
30	6884	N	MET	E	98	-6.305	61.349	1.405	1.00	72.65
	6885	CA	MET	E	98	-6.430	60.922	2.799	1.00	72.65
	6886	CB	MET	E	98	-5.268	61.476	3.603	1.00	162.98
	6887	CG	MET	E	98	-3.950	60.925	3.147	1.00	162.98
	6888	SD	MET	E	98	-3.643	59.309	3.816	1.00	162.98
35	6889	CE	MET	E	98	-3.249	59.757	5.511	1.00	162.98
	6890	C	MET	E	98	-7.747	61.457	3.359	1.00	72.65
	6891	O	MET	E	98	-8.065	62.625	3.165	1.00	72.65
	6892	N	GLU	E	99	-8.515	60.612	4.042	1.00	91.21
	6893	CA	GLU	E	99	-9.789	61.038	4.615	1.00	91.21
40	6894	CB	GLU	E	99	-10.288	60.011	5.630	1.00	221.21
	6895	CG	GLU	E	99	-11.780	60.081	5.888	1.00	221.21
	6896	CD	GLU	E	99	-12.193	59.288	7.112	1.00	221.21
	6897	OE1	GLU	E	99	-11.617	58.201	7.342	1.00	221.21
	6898	OE2	GLU	E	99	-13.102	59.747	7.836	1.00	221.21
45	6899	C	GLU	E	99	-9.575	62.376	5.322	1.00	91.21
	6900	O	GLU	E	99	-8.664	62.499	6.140	1.00	91.21
	6901	N	GLY	E	100	-10.388	63.379	4.993	1.00	149.52
	6902	CA	GLY	E	100	-10.248	64.679	5.632	1.00	149.52
	6903	C	GLY	E	100	-9.666	65.799	4.782	1.00	149.52
50	6904	O	GLY	E	100	-9.830	66.974	5.111	1.00	149.52
	6905	N	GLN	E	101	-8.982	65.450	3.697	1.00	88.18
	6906	CA	GLN	E	101	-8.381	66.447	2.803	1.00	88.18
	6907	CB	GLN	E	101	-7.183	65.843	2.072	1.00	168.37
	6908	CG	GLN	E	101	-6.053	65.456	2.988	1.00	168.37
55	6909	CD	GLN	E	101	-5.680	66.573	3.934	1.00	168.37
	6910	OE1	GLN	E	101	-6.363	66.812	4.923	1.00	168.37
	6911	NE2	GLN	E	101	-4.598	67.272	3.630	1.00	168.37
	6912	C	GLN	E	101	-9.334	67.070	1.767	1.00	88.18
	6913	O	GLN	E	101	-10.447	66.597	1.540	1.00	88.18
60	6914	N	PRO	E	102	-8.894	68.148	1.116	1.00	90.47
	6915	CD	PRO	E	102	-7.628	68.898	1.252	1.00	130.24
	6916	CA	PRO	E	102	-9.766	68.772	0.125	1.00	90.47
	6917	CB	PRO	E	102	-9.195	70.179	0.022	1.00	130.24
	6918	CG	PRO	E	102	-7.727	69.923	0.124	1.00	130.24
65	6919	C	PRO	E	102	-9.708	68.020	-1.203	1.00	90.47
	6920	O	PRO	E	102	-8.713	67.360	-1.510	1.00	90.47
	6921	N	LEU	E	103	-10.775	68.133	-1.988	1.00	92.93
	6922	CA	LEU	E	103	-10.853	67.475	-3.283	1.00	92.93
	6923	CB	LEU	E	103	-11.638	66.186	-3.160	1.00	78.05
70	6924	CG	LEU	E	103	-11.718	65.529	-4.528	1.00	78.05

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	6925	CD1	LEU	E	103	-10.330	65.172	-4.969	1.00	78.05
	6926	CD2	LEU	E	103	-12.618	64.299	-4.466	1.00	78.05
	6927	C	LEU	E	103	-11.556	68.364	-4.296	1.00	92.93
	6928	O	LEU	E	103	-12.690	68.784	-4.071	1.00	92.93
5	6929	N	PHE	E	104	-10.906	68.654	-5.413	1.00	62.11
	6930	CA	PHE	E	104	-11.557	69.491	-6.406	1.00	62.11
	6931	CB	PHE	E	104	-10.792	70.814	-6.607	1.00	152.14
	6932	CG	PHE	E	104	-10.639	71.636	-5.354	1.00	152.14
	6933	CD1	PHE	E	104	-9.688	71.298	-4.401	1.00	152.14
10	6934	CD2	PHE	E	104	-11.439	72.760	-5.132	1.00	152.14
	6935	CE1	PHE	E	104	-9.537	72.054	-3.235	1.00	152.14
	6936	CE2	PHE	E	104	-11.297	73.526	-3.967	1.00	152.14
	6937	CZ	PHE	E	104	-10.338	73.173	-3.020	1.00	152.14
	6938	C	PHE	E	104	-11.672	68.775	-7.759	1.00	62.11
15	6939	O	PHE	E	104	-10.686	68.246	-8.269	1.00	62.11
	6940	N	LEU	E	105	-12.871	68.748	-8.336	1.00	83.91
	6941	CA	LEU	E	105	-13.074	68.140	-9.651	1.00	83.91
	6942	CB	LEU	E	105	-14.208	67.119	-9.618	1.00	47.95
	6943	CG	LEU	E	105	-14.010	66.057	-8.551	1.00	47.95
20	6944	CD1	LEU	E	105	-15.076	64.958	-8.677	1.00	47.95
	6945	CD2	LEU	E	105	-12.633	65.508	-8.729	1.00	47.95
	6946	C	LEU	E	105	-13.454	69.279	-10.565	1.00	83.91
	6947	O	LEU	E	105	-14.110	70.224	-10.133	1.00	83.91
	6948	N	ARG	E	106	-13.063	69.201	-11.824	1.00	105.55
25	6949	CA	ARG	E	106	-13.391	70.273	-12.737	1.00	105.55
	6950	CB	ARG	E	106	-12.132	71.181	-12.874	1.00	149.26
	6951	CG	ARG	E	106	-12.358	72.290	-13.865	1.00	149.26
	6952	CD	ARG	E	106	-11.036	72.987	-14.126	1.00	149.26
	6953	NE	ARG	E	106	-11.165	74.010	-15.158	1.00	149.26
30	6954	CZ	ARG	E	106	-10.153	74.477	-15.880	1.00	149.26
	6955	NH1	ARG	E	106	-8.925	74.013	-15.691	1.00	149.26
	6956	NH2	ARG	E	106	-10.374	75.404	-16.800	1.00	149.26
	6957	C	ARG	E	106	-13.804	69.761	-14.110	1.00	105.55
	6958	O	ARG	E	106	-13.044	69.027	-14.734	1.00	105.55
35	6959	N	CYS	E	107	-15.000	70.118	-14.585	1.00	115.02
	6960	CA	CYS	E	107	-15.400	69.665	-15.913	1.00	115.02
	6961	C	CYS	E	107	-14.789	70.673	-16.856	1.00	115.02
	6962	O	CYS	E	107	-15.230	71.813	-16.932	1.00	115.02
	6963	CB	CYS	E	107	-16.914	69.630	-16.079	1.00	134.10
40	6964	SG	CYS	E	107	-17.441	68.605	-17.498	1.00	134.10
	6965	N	HIS	E	108	-13.755	70.242	-17.562	1.00	96.54
	6966	CA	HIS	E	108	-13.017	71.109	-18.460	1.00	96.54
	6967	CB	HIS	E	108	-11.535	70.876	-18.240	1.00	124.72
	6968	CG	HIS	E	108	-10.657	71.846	-18.959	1.00	124.72
45	6969	CD2	HIS	E	108	-9.644	71.651	-19.836	1.00	124.72
	6970	ND1	HIS	E	108	-10.737	73.207	-18.759	1.00	124.72
	6971	CE1	HIS	E	108	-9.806	73.807	-19.480	1.00	124.72
	6972	NE2	HIS	E	108	-9.128	72.886	-20.142	1.00	124.72
	6973	C	HIS	E	108	-13.328	70.954	-19.938	1.00	96.54
50	6974	O	HIS	E	108	-13.224	69.864	-20.506	1.00	96.54
	6975	N	GLY	E	109	-13.680	72.070	-20.563	1.00	176.91
	6976	CA	GLY	E	109	-13.999	72.050	-21.973	1.00	177.91
	6977	C	GLY	E	109	-12.753	72.194	-22.815	1.00	176.91
	6978	O	GLY	E	109	-11.737	72.706	-22.349	1.00	176.91
55	6979	N	TRP	E	110	-12.826	71.732	-24.056	1.00	146.96
	6980	CA	TRP	E	110	-11.696	71.836	-24.956	1.00	146.96
	6981	CB	TRP	E	110	-11.982	71.061	-26.241	1.00	177.84
	6982	CG	TRP	E	110	-10.936	71.248	-27.286	1.00	177.84
	6983	CD2	TRP	E	110	-9.797	70.415	-27.514	1.00	177.84
60	6984	CE2	TRP	E	110	-9.056	70.996	-28.564	1.00	177.84
	6985	CE3	TRP	E	110	-9.331	69.226	-26.932	1.00	177.84
	6986	CD1	TRP	E	110	-10.845	72.273	-28.180	1.00	177.84
	6987	NE1	TRP	E	110	-9.718	72.131	-28.953	1.00	177.84
	6988	CZ2	TRP	E	110	-7.875	70.433	-29.047	1.00	177.84
65	6989	CZ3	TRP	E	110	-8.153	68.667	-27.413	1.00	177.84
	6990	CH2	TRP	E	110	-7.439	69.273	-28.459	1.00	177.84
	6991	C	TRP	E	110	-11.404	73.303	-25.275	1.00	146.96
	6992	O	TRP	E	110	-12.300	74.154	-25.255	1.00	146.96
	6993	N	ARG	E	111	-10.136	73.594	-25.551	1.00	199.97
70	6994	CA	ARG	E	111	-9.716	74.948	-25.887	1.00	199.97

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	6995	CB	ARG	E	111	-10.136	75.282	-27.295	1.00	249.42
	6996	CG	ARG	E	111	-9.116	74.871	-28.285	1.00	249.42
	6997	CD	ARG	E	111	-9.462	75.454	-29.595	1.00	249.42
	6998	NE	ARG	E	111	-8.270	75.956	-30.249	1.00	249.42
5	6999	CZ	ARG	E	111	-7.559	76.996	-29.814	1.00	249.42
	7000	NH1	ARG	E	111	-7.918	77.656	-28.711	1.00	249.42
	7001	NH2	ARG	E	111	-6.472	77.367	-30.483	1.00	249.42
	7002	C	ARG	E	111	-10.262	76.009	-24.972	1.00	199.97
	7003	O	ARG	E	111	-10.388	77.173	-25.350	1.00	199.97
10	7004	N	ASN	E	112	-10.597	75.590	-23.767	1.00	112.19
	7005	CA	ASN	E	112	-11.129	76.482	-22.769	1.00	112.19
	7006	CB	ASN	E	112	-10.101	77.553	-22.432	1.00	133.79
	7007	CG	ASN	E	112	-10.330	78.144	-21.061	1.00	133.79
	7008	OD1	ASN	E	112	-11.446	78.097	-20.531	1.00	133.79
15	7009	ND2	ASN	E	112	-9.280	78.710	-20.478	1.00	133.79
	7010	C	ASN	E	112	-12.445	77.147	-23.163	1.00	112.19
	7011	O	ASN	E	112	-12.776	78.218	-22.651	1.00	112.19
	7012	N	TRP	E	113	-13.200	76.532	-24.067	1.00	154.00
	7013	CA	TRP	E	113	-14.478	77.116	-24.441	1.00	154.00
20	7014	CB	TRP	E	113	-15.153	76.326	-25.542	1.00	235.27
	7015	CG	TRP	E	113	-14.586	76.595	-26.860	1.00	235.27
	7016	CD2	TRP	E	113	-14.400	75.651	-27.909	1.00	235.27
	7017	CE2	TRP	E	113	-13.885	76.353	-29.018	1.00	235.27
	7018	CE3	TRP	E	113	-14.628	74.270	-28.027	1.00	235.27
25	7019	CD1	TRP	E	113	-14.180	77.804	-27.348	1.00	235.27
	7020	NE1	TRP	E	113	-13.758	77.667	-28.647	1.00	235.27
	7021	CZ2	TRP	E	113	-13.592	75.726	-30.229	1.00	235.27
	7022	CZ3	TRP	E	113	-14.335	73.643	-29.233	1.00	235.27
	7023	CH2	TRP	E	113	-13.818	74.373	-30.318	1.00	235.27
30	7024	C	TRP	E	113	-15.400	77.133	-23.246	1.00	154.00
	7025	O	TRP	E	113	-14.983	76.886	-22.116	1.00	154.00
	7026	N	ASP	E	114	-16.664	77.430	-23.503	1.00	242.58
	7027	CA	ASP	E	114	-17.649	77.470	-22.442	1.00	242.58
	7028	CB	ASP	E	114	-18.418	78.794	-22.471	1.00	249.32
35	7029	CG	ASP	E	114	-17.656	79.922	-21.803	1.00	249.32
	7030	OD1	ASP	E	114	-17.348	79.791	-20.599	1.00	249.32
	7031	OD2	ASP	E	114	-17.365	80.933	-22.475	1.00	249.32
	7032	C	ASP	E	114	-18.606	76.306	-22.572	1.00	242.58
	7033	O	ASP	E	114	-19.027	75.942	-23.672	1.00	242.58
40	7034	N	VAL	E	115	-18.931	75.717	-21.430	1.00	148.92
	7035	CA	VAL	E	115	-19.846	74.594	-21.391	1.00	148.92
	7036	CB	VAL	E	115	-19.199	73.377	-20.746	1.00	243.92
	7037	CG1	VAL	E	115	-20.086	72.162	-20.949	1.00	243.92
	7038	CG2	VAL	E	115	-17.821	73.161	-21.331	1.00	243.92
45	7039	C	VAL	E	115	-21.075	74.959	-20.581	1.00	148.92
	7040	O	VAL	E	115	-20.985	75.672	-19.577	1.00	148.92
	7041	N	TYR	E	116	-22.226	74.466	-21.020	1.00	86.50
	7042	CA	TYR	E	116	-23.470	74.752	-20.320	1.00	86.50
	7043	CB	TYR	E	116	-24.374	75.633	-21.192	1.00	249.77
50	7044	CG	TYR	E	116	-23.782	76.991	-21.517	1.00	249.77
	7045	CD1	TYR	E	116	-23.088	77.210	-22.709	1.00	249.77
	7046	CE1	TYR	E	116	-22.513	78.454	-22.994	1.00	249.77
	7047	CD2	TYR	E	116	-23.889	78.048	-20.616	1.00	249.77
	7048	CE2	TYR	E	116	-23.319	79.293	-20.886	1.00	249.77
55	7049	CZ	TYR	E	116	-22.631	79.488	-22.075	1.00	249.77
	7050	OH	TYR	E	116	-22.051	80.710	-22.336	1.00	249.77
	7051	C	TYR	E	116	-24.208	73.466	-19.940	1.00	86.50
	7052	O	TYR	E	116	-23.829	72.356	-20.362	1.00	86.50
	7053	N	LYS	E	117	-25.277	73.630	-19.164	1.00	217.77
60	7054	CA	LYS	E	117	-26.078	72.500	-18.707	1.00	217.77
	7055	CB	LYS	E	117	-26.963	71.967	-19.832	1.00	191.92
	7056	CG	LYS	E	117	-28.295	72.674	-19.997	1.00	191.92
	7057	CD	LYS	E	117	-29.246	71.813	-20.819	1.00	191.92
	7058	CE	LYS	E	117	-29.481	70.462	-20.143	1.00	191.92
65	7059	NZ	LYS	E	117	-30.376	69.560	-20.915	1.00	191.92
	7060	C	LYS	E	117	-25.161	71.387	-18.230	1.00	217.77
	7061	O	LYS	E	117	-25.228	70.262	-18.724	1.00	217.77
	7062	N	VAL	E	118	-24.306	71.709	-17.268	1.00	181.28
	7063	CA	VAL	E	118	-23.356	70.743	-16.731	1.00	181.28
70	7064	CB	VAL	E	118	-22.089	71.444	-16.254	1.00	157.61

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	7065	CG1	VAL	E	118	-21.427	70.628	-15.171	1.00	157.61
	7066	CG2	VAL	E	118	-21.141	71.619	-17.420	1.00	157.61
	7067	C	VAL	E	118	-23.857	69.864	-15.598	1.00	181.28
5	7068	O	VAL	E	118	-24.500	70.335	-14.661	1.00	181.28
	7069	N	ILE	E	119	-23.514	68.585	-15.674	1.00	95.37
	7070	CA	ILE	E	119	-23.932	67.630	-14.665	1.00	95.37
	7071	CB	ILE	E	119	-25.093	66.783	-15.184	1.00	80.86
	7072	CG2	ILE	E	119	-25.598	65.858	-14.102	1.00	80.86
	7073	CG1	ILE	E	119	-26.198	67.695	-15.696	1.00	80.86
10	7074	CD1	ILE	E	119	-27.227	66.956	-16.527	1.00	80.86
	7075	C	ILE	E	119	-22.791	66.678	-14.348	1.00	95.37
	7076	O	ILE	E	119	-22.280	66.017	-15.249	1.00	95.37
	7077	N	TYR	E	120	-22.373	66.602	13.088	1.00	103.71
	7078	CA	TYR	E	120	-21.315	65.664	-12.732	1.00	103.71
15	7079	CB	TYR	E	120	-20.499	66.128	-11.550	1.00	87.63
	7080	CG	TYR	E	120	-19.634	67.303	-11.821	1.00	87.63
	7081	CD1	TYR	E	120	-20.141	68.575	-11.746	1.00	87.63
	7082	CE1	TYR	E	120	-19.351	69.666	-12.010	1.00	87.63
	7083	CD2	TYR	E	120	-18.300	67.141	-12.171	1.00	87.63
20	7084	CE2	TYR	E	120	-17.486	68.226	-12.447	1.00	87.63
	7085	CZ	TYR	E	120	-18.017	69.490	-12.366	1.00	87.63
	7086	OH	TYR	E	120	-17.220	70.579	-12.651	1.00	87.63
	7087	C	TYR	E	120	-21.972	64.380	-12.305	1.00	103.71
	7088	O	TYR	E	120	-23.037	64.401	-11.694	1.00	103.71
25	7089	N	TYR	E	121	-21.324	63.263	-12.596	1.00	62.69
	7090	CA	TYR	E	121	-21.857	61.963	-12.221	1.00	62.69
	7091	CB	TYR	E	121	-22.202	61.148	-13.476	1.00	95.66
	7092	CG	TYR	E	121	-23.364	61.653	-14.309	1.00	95.66
	7093	CD1	TYR	E	121	-23.288	62.865	-14.992	1.00	95.66
30	7094	CE1	TYR	E	121	-24.334	63.305	-15.806	1.00	95.66
	7095	CD2	TYR	E	121	-24.522	60.885	-14.455	1.00	95.66
	7096	CE2	TYR	E	121	-25.576	61.315	-15.269	1.00	95.66
	7097	CZ	TYR	E	121	-25.477	62.527	-15.945	1.00	95.66
	7098	OH	TYR	E	121	-26.515	62.943	-16.761	1.00	95.66
35	7099	C	TYR	E	121	-20.873	61.165	-11.368	1.00	62.69
	7100	O	TYR	E	121	-19.667	61.179	-11.620	1.00	62.69
	7101	N	LYS	E	122	-21.391	60.478	-10.356	1.00	76.05
	7102	CA	LYS	E	122	-20.562	59.633	-9.521	1.00	76.05
	7103	CB	LYS	E	122	-20.410	60.198	-8.114	1.00	107.43
40	7104	CG	LYS	E	122	-19.516	59.339	-7.238	1.00	107.43
	7105	CD	LYS	E	122	-19.635	59.698	-5.779	1.00	107.43
	7106	CE	LYS	E	122	-18.887	58.706	-4.914	1.00	107.43
	7107	NZ	LYS	E	122	-19.161	58.998	-3.484	1.00	107.43
	7108	C	LYS	E	122	-21.223	58.263	-9.440	1.00	76.05
45	7109	O	LYS	E	122	-22.325	58.127	-8.898	1.00	76.05
	7110	N	ASP	E	123	-20.543	57.252	-9.973	1.00	138.97
	7111	CA	ASP	E	123	-21.059	55.892	-9.976	1.00	138.97
	7112	CB	ASP	E	123	-21.188	55.363	-8.545	1.00	185.30
	7113	CG	ASP	E	123	-19.849	54.991	-7.945	1.00	185.30
50	7114	OD1	ASP	E	123	-19.068	54.303	-8.638	1.00	185.30
	7115	OD2	ASP	E	123	-19.578	55.374	-6.785	1.00	185.30
	7116	C	ASP	E	123	-22.396	55.792	-10.702	1.00	138.97
	7117	O	ASP	E	123	-23.333	55.147	-10.225	1.00	138.97
	7118	N	GLY	E	124	-22.472	56.443	-11.862	1.00	163.35
55	7119	CA	GLY	E	124	-23.675	56.412	-12.675	1.00	163.35
	7120	C	GLY	E	124	-24.838	57.262	-12.200	1.00	163.35
	7121	O	GLY	E	124	-25.840	57.388	-12.907	1.00	163.35
	7122	N	GLU	E	125	-24.711	57.854	-11.016	1.00	131.17
	7123	CA	GLU	E	125	-25.777	58.684	-10.447	1.00	131.17
60	7124	CB	GLU	E	125	-25.822	58.535	-8.911	1.00	143.41
	7125	CG	GLU	E	125	-26.269	57.168	-8.368	1.00	143.41
	7126	CD	GLU	E	125	-27.780	56.971	-8.384	1.00	143.41
	7127	OE1	GLU	E	125	-28.492	57.744	-7.700	1.00	143.41
	7128	OE2	GLU	E	125	-28.249	56.040	-9.077	1.00	143.41
65	7129	C	GLU	E	125	-25.597	60.160	-10.771	1.00	131.17
	7130	O	GLU	E	125	-24.483	60.656	-10.809	1.00	131.17
	7131	N	ALA	E	126	-26.695	60.864	-11.006	1.00	115.32
	7132	CA	ALA	E	126	-26.604	62.290	-11.265	1.00	115.32
	7133	CB	ALA	E	126	-27.979	62.844	-11.605	1.00	168.61
70	7134	C	ALA	E	126	-26.104	62.855	-9.935	1.00	115.32

	7135	O	ALA	E	126	-26.467	62.339	-8.876	1.00	115.32
	7136	N	LEU	E	127	-25.275	63.897	-9.967	1.00	118.41
	7137	CA	LEU	E	127	-24.752	64.458	-8.714	1.00	118.41
	7138	CB	LEU	E	127	-23.271	64.162	-8.577	1.00	111.80
5	7139	CG	LEU	E	127	-22.934	64.190	-7.090	1.00	111.80
	7140	CD1	LEU	E	127	-23.811	63.158	-6.384	1.00	111.80
	7141	CD2	LEU	E	127	-21.465	63.889	-6.868	1.00	111.80
	7142	C	LEU	E	127	-24.957	65.947	-8.453	1.00	118.41
	7143	O	LEU	E	127	-25.470	66.328	-7.404	1.00	118.41
10	7144	N	LYS	E	128	-24.498	66.785	-9.373	1.00	133.41
	7145	CA	LYS	E	128	-24.677	68.228	-9.259	1.00	133.41
	7146	CB	LYS	E	128	-23.405	68.893	-8.760	1.00	171.72
	7147	CG	LYS	E	128	-22.965	68.445	-7.388	1.00	171.72
	7148	CD	LYS	E	128	-23.865	68.977	-6.284	1.00	171.72
15	7149	CE	LYS	E	128	-23.287	68.616	-4.917	1.00	171.72
	7150	NZ	LYS	E	128	-24.024	69.227	-3.779	1.00	171.72
	7151	C	LYS	E	128	-25.015	68.757	-10.653	1.00	133.41
	7152	O	LYS	E	128	-24.626	68.153	-11.657	1.00	133.41
	7153	N	TYR	E	129	-25.733	69.87˜	-10.729	1.00	159.58
20	7154	CA	TYR	E	129	-26.106	70.442	-12.029	1.00	159.58
	7155	CB	TYR	E	129	-27.496	69.983	-12.438	1.00	246.12
	7156	CG	TYR	E	129	-28.122	70.887	-13.441	1.00	246.12
	7157	CD1	TYR	E	129	-27.756	70.809	-14.781	1.00	246.12
	7158	CE1	TYR	E	129	-28.298	71.675	-15.715	1.00	246.12
25	7159	CD2	TYR	E	129	-29.063	71.857	-13.055	1.00	246.12
	7160	CE2	TYR	E	129	-29.624	72.721	-13.990	1.00	246.12
	7161	CZ	TYR	E	129	-29.236	72.624	-15.326	1.00	246.12
	7162	OH	TYR	E	129	-29.822	73.442	-16.274	1.00	246.12
	7163	C	TYR	E	129	-26.106	71.953	-12.048	1.00	159.58
30	7164	O	TYR	E	129	-26.579	72.589	-11.112	1.00	159.58
	7165	N	TRP	E	130	-25.600	72.526	-13.137	1.00	184.49
	7166	CA	TRP	E	130	-25.557	73.976	-13.280	1.00	184.49
	7167	CB	TRP	E	130	-24.211	74.535	-12.817	1.00	245.42
	7168	CG	TRP	E	130	-23.751	74.067	-11.472	1.00	245.42
35	7169	CD2	TRP	E	130	-23.750	74.828	-10.257	1.00	245.42
	7170	CE2	TRP	E	130	-23.186	74.005	-9.254	1.00	245.42
	7171	CE3	TRP	E	130	-24.179	76.119	-9.918	1.00	245.42
	7172	CD1	TRP	E	130	-23.202	72.856	-11.166	1.00	245.42
	7173	NE1	TRP	E	130	-22.859	72.811	-9.835	1.00	245.42
40	7174	CZ2	TRP	E	130	-23.034	74.438	-7.930	1.00	245.42
	7175	CZ3	TRP	E	130	-24.028	76.548	-8.600	1.00	245.42
	7176	CH2	TRP	E	130	-23.454	75.709	-7.626	1.00	245.42
	7177	C	TRP	E	130	-25.768	74.407	-14.725	1.00	184.49
	7178	O	TRP	E	130	-25.711	73.584	-15.638	1.00	184.49
45	7179	N	TYR	E	131	-26.014	75.701	-14.930	1.00	185.41
	7180	CA	TYR	E	131	-26.187	76.228	-16.277	1.00	185.41
	7181	CB	TYR	E	131	-27.063	77.477	-16.282	1.00	249.42
	7182	CG	TYR	E	131	-27.438	77.858	-17.685	1.00	249.42
	7183	CD1	TYR	E	131	-28.391	77.125	-18.389	1.00	249.42
50	7184	CE1	TYR	E	131	-28.654	77.384	-19.728	1.00	249.42
	7185	CD2	TYR	E	131	-26.755	78.869	-18.358	1.00	249.42
	7186	CE2	TYR	E	131	-26.997	79.127	-19.703	1.00	249.42
	7187	CZ	TYR	E	131	-27.951	78.384	-20.380	1.00	249.42
	7188	OH	TYR	E	131	-28.189	78.642	-21.710	1.00	249.42
55	7189	C	TYR	E	131	-24.780	76.577	-16.758	1.00	185.41
	7190	O	TYR	E	131	-24.141	75.784	-17.455	1.00	185.41
	7191	N	GLU	E	132	-24.310	77.777	-16.431	1.00	229.70
	7192	CA	GLU	E	132	-22.942	78.159	-16.751	1.00	229.70
	7193	CB	GLU	E	132	-22.638	79.608	-16.344	1.00	249.20
60	7194	CG	GLU	E	132	-23.207	80.700	-17.258	1.00	249.20
	7195	CD	GLU	E	132	-22.123	81.565	-17.898	1.00	249.20
	7196	OE1	GLU	E	132	-20.982	81.562	-17.392	1.00	249.20
	7197	OE2	GLU	E	132	-22.412	82.255	-18.899	1.00	249.20
	7198	C	GLU	E	132	-22.290	77.200	-15.773	1.00	229.70
65	7199	O	GLU	E	132	-22.652	77.190	-14.595	1.00	229.70
	7200	N	ASN	E	133	-21.348	76.385	-16.233	1.00	219.94
	7201	CA	ASN	E	133	-20.764	75.401	-15.332	1.00	219.94
	7202	CB	ASN	E	133	-19.878	74.415	-16.095	1.00	129.08
	7203	CG	ASN	E	133	-18.469	74.898	-16.252	1.00	129.08
70	7204	OD1	ASN	E	133	-18.235	76.020	-16.692	1.00	129.08

	7205	ND2	ASN	E	133	-17.510	74.046	-15.904	1.00	129.08
	7206	C	ASN	E	133	-20.023	75.919	-14.118	1.00	219.94
	7207	O	ASN	E	133	-19.802	77.115	-13.944	1.00	219.94
	7208	N	HIS	E	134	-19.638	74.965	-13.286	1.00	192.14
5	7209	CA	HIS	E	134	-18.970	75.231	-12.036	1.00	192.14
	7210	CB	HIS	E	134	-20.007	75.079	-10.924	1.00	214.14
	7211	CG	HIS	E	134	-19.514	75.463	-9.567	1.00	214.14
	7212	CD2	HIS	E	134	-19.356	74.731	-8.436	1.00	214.14
	7213	ND1	HIS	E	134	-19.138	76.749	-9.245	1.00	214.14
10	7214	CE1	HIS	E	134	-18.771	76.794	-7.976	1.00	214.14
	7215	NE2	HIS	E	134	-18.895	75.584	-7.463	1.00	214.14
	7216	C	HIS	E	134	-17.828	74.231	-11.860	1.00	192.14
	7217	O	HIS	E	134	-17.412	73.574	-12.820	1.00	192.14
	7218	N	ASN	E	135	-17.336	74.114	-10.630	1.00	109.49
15	7219	CA	ASN	E	135	-16.246	73.208	-10.311	1.00	109.49
	7220	CB	ASN	E	135	-14.921	73.967	-10.346	1.00	216.32
	7221	CG	ASN	E	135	-14.571	74.433	-11.741	1.00	216.32
	7222	OD1	ASN	E	135	-14.694	73.661	-12.691	1.00	216.32
	7223	ND2	ASN	E	135	-14.125	75.677	-11.883	1.00	216.32
20	7224	C	ASN	E	135	-16.462	72.573	-8.957	1.00	109.49
	7225	O	ASN	E	135	-15.960	73.058	-7.948	1.00	109.49
	7226	N	ILE	E	136	-17.223	71.484	-8.949	1.00	98.56
	7227	CA	ILE	E	136	-17.541	70.753	-7.725	1.00	98.56
	7228	CB	ILE	E	136	-18.026	69.322	-8.063	1.00	164.42
25	7229	CG2	ILE	E	136	-17.070	68.654	-9.020	1.00	164.42
	7230	CG1	ILE	E	136	-18.182	68.505	-6.792	1.00	164.42
	7231	CD1	ILE	E	136	-18.771	67.146	-7.055	1.00	164.42
	7232	C	ILE	E	136	-16.351	70.717	-6.779	1.00	98.56
	7233	O	ILE	E	136	-15.300	70.168	-7.104	1.00	98.56
30	7234	N	SER	E	137	-16.524	71.329	-5.613	1.00	114.80
	7235	CA	SER	E	137	-15.462	71.405	-4.622	1.00	114.80
	7236	CB	SER	E	137	-15.128	72.866	-4.360	1.00	96.11
	7237	OG	SER	E	137	-14.336	72.997	-3.196	1.00	96.11
	7238	C	SER	E	137	-15.798	70.714	-3.303	1.00	114.80
35	7239	O	SER	E	137	-16.955	70.690	-2.879	1.00	114.80
	7240	N	ILE	E	138	-14.773	70.169	-2.652	1.00	105.32
	7241	CA	ILE	E	138	-14.939	69.466	-1.382	1.00	105.32
	7242	CB	ILE	E	138	-14.851	67.969	-1.577	1.00	81.88
	7243	CG2	ILE	E	138	-14.767	67.296	-0.223	1.00	81.88
40	7244	CG1	ILE	E	138	-16.049	67.484	-2.408	1.00	81.88
	7245	CD1	ILE	E	138	-15.917	66.048	-2.912	1.00	81.88
	7246	C	ILE	E	138	-13.869	69.833	-0.374	1.00	105.32
	7247	O	ILE	E	138	-12.686	69.614	-0.619	1.00	105.32
	7248	N	THR	E	139	-14.283	70.362	0.772	1.00	128.39
45	7249	CA	THR	E	139	-13.333	70.758	1.807	1.00	128.39
	7250	CB	THR	E	139	-13.986	71.743	2.788	1.00	173.9~
	7251	OG1	THR	E	139	-15.220	71.194	3.265	1.00	173.94
	7252	CG2	THR	E	139	-14.267	73.071	2.094	1.00	173.94
	7253	C	THR	E	139	-12.825	69.535	2.566	1.00	128.39
50	7254	O	THR	E	139	-11.709	69.058	2.337	1.00	128.39
	7255	N	ASN	E	140	-13.650	69.041	3.480	1.00	224.25
	7256	CA	ASN	E	140	-13.323	67.859	4.263	1.00	224.25
	7257	CB	ASN	E	140	-14.012	67.918	5.625	1.00	231.48
	7258	CG	ASN	E	140	-13.813	66.656	6.429	1.00	231.48
55	72.9	OD1	ASN	E	140	-13.998	65.547	5.923	1.00	231.4C
	72ô0	ND2	ASN	E	140	-13.443	66.823	7.692	1.00	231.4.
	7261	C	ASN	E	140	-13.874	66.691	3.464	1.00	224.25
	7262	O	ASN	E	140	-15.073	66.629	3.204	1.00	224.25
	7263	N	ALA	E	141	-13.004	65.763	3.086	1.00	132.13
60	7264	CA	ALA	E	141	-13.420	64.623	2.289	1.00	132.13
	7265	CB	ALA	E	141	-12.374	64.323	1.257	1.00	95.25
	7266	C	ALA	E	141	-13.730	63.367	3.072	1.00	132.13
	7267	O	ALA	E	141	-12.932	62.901	3.884	1.00	132.13
	7268	N	THR	E	142	-14.903	62.811	2.802	1.00	103.70
65	7269	CA	THR	E	142	-15.339	61.588	3.454	1.00	103.70
	7270	CB	THR	E	142	-16.873	61.526	3.477	1.00	152.79
	7271	OG1	THR	E	142	-17.384	62.747	4.028	1.00	152.79
	7272	CG2	THR	E	142	-17.346	60.376	4.329	1.00	152.79
	7273	C	THR	E	142	-14.767	60.417	2.650	1.00	103.70
70	7274	O	THR	E	142	-14.198	60.624	1.575	1.00	103.70

7275	N	VAL	E	143	-14.887	59.197	3.164	1.00	124.54
7276	CA	VAL	E	143	-14.369	58.042	2.437	1.00	124.54
7277	CB	VAL	E	143	-14.026	56.863	3.365	1.00	132.81
7278	CG1	VAL	E	143	-15.292	56.315	3.999	1.00	132.81
7279	CG2	VAL	E	143	-13.310	55.773	2.577	1.00	132.81
7280	C	VAL	E	143	-15.448	57.583	1.484	1.00	124.54
7281	O	VAL	E	143	-15.187	56.822	0.555	1.00	124.54
7282	N	GLU	E	144	-16.668	58.047	1.722	1.00	123.03
7283	CA	GLU	E	144	-17.781	57.678	0.863	1.00	123.03
7284	CB	GLU	E	144	-19.108	57.964	1.558	1.00	249.45
7285	CG	GLU	E	144	-19.323	57.136	2.812	1.00	249.45
7286	CD	GLU	E	144	-19.316	57.978	4.073	1.00	249.45
7287	OE1	GLU	E	144	-20.163	58.892	4.176	1.00	249.45
7288	OE2	GLU	E	144	-18.470	57.730	4.958	1.00	249.45
7289	C	GLU	E	144	-17.709	58.428	-0.460	1.00	123.03
7290	O	GLU	E	144	-18.373	58.051	-1.416	1.00	123.03
7291	N	ASP	E	145	-16.897	59.485	-0.509	1.00	78.25
7292	CA	ASP	E	145	-16.721	60.284	-1.726	1.00	78.25
7293	CB	ASP	E	145	-16.017	61.593	-1.396	1.00	126.03
7294	CG	ASP	E	145	-16.912	62.551	-0.679	1.00	126.03
7295	OD1	ASP	E	145	-17.955	62.900	-1.272	1.00	126.03
7296	OD2	ASP	E	145	-16.581	62.944	0.465	1.00	126.03
7297	C	ASP	E	145	-15.918	59.528	-2.789	1.00	78.25
7298	O	ASP	E	145	-15.889	59.920	-3.952	1.00	78.25
7299	N	SER	E	146	-15.263	58.442	-2.388	1.00	91.78
7300	CA	SER	E	146	-14.482	57.660	-3.331	1.00	91.78
7301	CB	SER	E	146	-13.708	56.568	-2.591	1.00	200.20
7302	OG	SER	E	146	-12.805	57.145	-1.661	1.00	200.20
7303	C	SER	E	146	-15.448	57.065	-4.335	1.00	91.78
7304	O	SER	E	146	-16.558	56.675	-3.981	1.00	91.78
7305	N	GLY	E	147	-15.039	57.020	-5.592	1.00	97.94
7306	CA	GLY	E	147	-15.910	56.484	-6.622	1.00	97.94
7307	C	GLY	E	147	-15.365	56.777	-8.007	1.00	97.94
7308	O	GLY	E	147	-14.177	57.079	-8.146	1.00	97.94
7309	N	THR	E	148	-16.211	56.677	-9.033	1.00	66.84
7310	CA	THR	E	148	-15.767	56.955	-10.399	1.00	66.84
7311	CB	THR	E	148	-15.794	55.674	-11.285	1.00	76.59
7312	OG1	THR	E	148	-16.932	55.699	-12.141	1.00	76.59
7313	CG2	THR	E	148	-15.880	54.450	-10.424	1.00	76.59
7314	C	THR	E	148	-16.662	58.055	-10.978	1.00	66.84
7315	O	THR	E	148	-17.884	57.889	-11.145	1.00	66.84
7316	N	TYR	E	149	-16.041	59.187	-11.273	1.00	55.84
7317	CA	TYR	E	149	-16.768	60.335	-11.774	1.00	55.84
7318	CB	TYR	E	149	-16.262	61.585	-11.070	1.00	63.87
7319	CG	TYR	E	149	-16.445	61.611	-9.575	1.00	63.87
7320	CD1	TYR	E	149	-15.728	60.766	-8.730	1.00	63.87
7321	CE1	TYR	E	149	-15.895	60.837	-7.342	1.00	63.87
7322	CD2	TYR	E	149	-17.326	62.515	-9.003	1.00	63.87
7323	CE2	TYR	E	149	-17.502	62.597	-7.639	1.00	63.87
7324	CZ	TYR	E	149	-16.793	61.761	-6.812	1.00	63.87
7325	OH	TYR	E	149	-17.022	61.871	-5.455	1.00	63.87
7326	C	TYR	E	149	-16.630	60.541	-13.274	1.00	55.84
7327	O	TYR	E	149	-15.789	59.909	-13.918	1.00	55.84
7328	N	TYR	E	150	-17.478	61.414	-13.817	1.00	90.25
7329	CA	TYR	E	150	-17.463	61.805	-15.227	1.00	90.25
7330	CB	TYR	E	150	-17.811	60.622	-16.175	1.00	141.76
7331	CG	TYR	E	150	-19.266	60.196	-16.334	1.00	141.76
7332	CD1	TYR	E	150	-20.183	60.995	-17.006	1.00	141.76
7333	CE1	TYR	E	150	-21.503	60.584	-17.180	1.00	141.76
7334	CD2	TYR	E	150	-19.711	58.965	-15.839	1.00	141.76
7335	CE2	TYR	E	150	-21.030	58.545	-16.010	1.00	141.76
7336	CZ	TYR	E	150	-21.924	59.359	-16.678	1.00	141.76
7337	OH	TYR	E	150	-23.239	58.958	-16.823	1.00	141.76
7338	C	TYR	E	150	-18.481	62.934	-15.293	1.00	90.25
7339	O	TYR	E	150	-19.308	63.056	-14.388	1.00	90.25
7340	N	CYS	E	151	-18.404	63.792	-16.309	1.00	89.54
7341	CA	CYS	E	151	-19.360	64.895	-16.421	1.00	89.54
7342	C	CYS	E	151	-19.945	65.031	-17.811	1.00	89.54
7343	O	CYS	E	151	-19.354	64.573	-18.778	1.00	89.54
7344	CB	CYS	E	151	-18.713	66.218	-16.017	1.00	116.04

	7345	SG	CYS	E	151	-17.189	66.664	-16.901	1.00	116.04
	7346	N	THR	E	152	-21.118	65.650	-17.904	1.00	145.06
	7347	CA	THR	E	152	-21.783	65.851	-19.186	1.00	145.06
	7348	CB	THR	E	152	-23.138	65.100	-19.247	1.00	246.19
5	7349	OG1	THR	E	152	-24.059	65.683	-18.316	1.00	246.19
	7350	CG2	THR	E	152	-22.944	63.634	-18.897	1.00	246.19
	7351	C	THR	E	152	-22.032	67.345	-19.332	1.00	145.06
	7352	O	THR	E	152	-22.255	68.039	-18.337	1.00	145.06
	7353	N	GLY	E	153	-21.984	67.845	-20.562	1.00	193.40
10	7354	CA	GLY	E	153	-22.209	69.263	-20.777	1.00	193.40
	7355	C	GLY	E	153	-22.478	69.578	-22.227	1.00	193.40
	7356	O	GLY	E	153	-22.181	68.768	-23.105	1.00	193.40
	7357	N	LYS	E	154	-23.044	70.751	-22.486	1.00	120.13
	7358	CA	LYS	E	154	-23.331	71.135	-23.857	1.00	120.13
15	7359	CB	LYS	E	154	-24.722	71.763	-23.950	1.00	168.61
	7360	CG	LYS	E	154	-25.193	72.073	-25.366	1.00	168.61
	7361	CD	LYS	E	154	-26.607	72.634	-25.316	1.00	168.61
	7362	CE	LYS	E	154	-27.120	73.053	-26.682	1.00	168.61
	7363	NZ	LYS	E	154	-28.455	73.682	-26.542	1.00	168.61
20	7364	C	LYS	E	154	-22.271	72.122	-24.309	1.00	120.13
	7365	O	LYS	E	154	-21.969	73.090	-23.596	1.00	120.13
	7366	N	VAL	E	155	-21.685	71.856	-25.475	1.00	169.05
	7367	CA	VAL	E	155	-20.666	72.731	-26.041	1.00	169.05
	7368	CB	VAL	E	155	-19.362	71.985	-26.310	1.00	148.26
25	7369	CG1	VAL	E	155	-18.328	72.927	-26.910	1.00	148.26
	7370	CG2	VAL	E	155	-18.847	71.420	-25.025	1.00	148.26
	7371	C	VAL	E	155	-21.235	73.223	-27.351	1.00	169.05
	7372	O	VAL	E	155	-21.684	72.425	-28.174	1.00	169.05
	7373	N	TRP	E	156	-21.207	74.537	-27.537	1.00	249.39
30	7374	CA	TRP	E	156	-21.767	75.132	-28.733	1.00	249.39
	7375	CB	TRP	E	156	-21.199	74.494	-29.991	1.00	249.75
	7376	CG	TRP	E	156	-19.797	74.775	-30.144	1.00	249.75
	7377	CD2	TRP	E	156	-19.204	76.069	-30.193	1.00	249.75
	7378	CE2	TRP	E	156	-17.813	75.880	-30.292	1.00	249.75
35	7379	CE3	TRP	E	156	-19.720	77.368	-30.164	1.00	249.75
	7380	CD1	TRP	E	156	-18.784	73.875	-30.220	1.00	249.75
	7381	NE1	TRP	E	156	-17.583	74.533	-30.307	1.00	249.75
	7382	CZ2	TRP	E	156	-16.919	76.947	-30.375	1.00	249.75
	7383	CZ3	TRP	E	156	-18.838	78.426	-30.229	1.00	249.75
40	7384	CH2	TRP	E	156	-17.440	78.210	-30.344	1.00	249.75
	7385	C	TRP	E	156	-23.225	74.814	-28.688	1.00	249.39
	7386	O	TRP	E	156	-24.004	75.512	-28.053	1.00	249.39
	7387	N	GLN	E	157	-23.571	73.711	-29.338	1.00	249.35
	7388	CA	GLN	E	157	-24.945	73.299	-29.404	1.00	249.35
45	7389	CB	GLN	E	157	-25.559	73.927	-30.645	1.00	249.42
	7390	CG	GLN	E	157	-25.723	75.415	-30.458	1.00	249.42
	7391	CD	GLN	E	157	-26.491	75.691	-29.186	1.00	249.42
	7392	OE1	GLN	E	157	-27.538	75.108	-28.977	1.00	249.42
	7393	NE2	GLN	E	157	-25.980	76.575	-28.340	1.00	249.42
50	7394	C	GLN	E	157	-25.152	71.797	-29.367	1.00	249.35
	7395	O	GLN	E	157	-26.238	71.302	-29.670	1.00	249.35
	7396	N	LEU	E	158	-24.109	71.074	-28.973	1.00	232.10
	7397	CA	LEU	E	158	-24.192	69.626	-28.872	1.00	232.10
	7398	CB	LEU	E	158	-23.321	68.956	-29.935	1.00	212.17
55	7399	CG	LEU	E	158	-23.853	68.895	-31.367	1.00	212.17
	7400	CD1	LEU	E	158	-23.486	67.531	-31.928	1.00	212.17
	7401	CD2	LEU	E	158	-25.370	69.079	-31.415	1.00	212.17
	7402	C	LEU	E	158	-23.788	69.124	-27.492	1.00	232.10
	7403	O	LEU	E	158	-23.007	69.767	-26.784	1.00	232.10
60	7404	N	ASP	E	159	-24.333	67.969	-27.122	1.00	245.44
	7405	CA	ASP	E	159	-24.058	67.353	-25.830	1.00	245.44
	7406	CB	ASP	E	159	-25.270	66.525	-25.381	1.00	211.53
	7407	CG	ASP	E	159	-26.567	67.329	-25.373	1.00	211.53
65	7408	OD1	ASP	E	159	-26.659	68.326	-24.626	1.00	211.53
	7409	OD2	ASP	E	159	-27.502	66.961	-26.118	1.00	211.53
	7410	C	ASP	E	159	-22.822	66.454	-25.908	1.00	245.44
	7411	O	ASP	E	159	-22.578	65.818	-26.936	1.00	245.44
	7412	N	TYR	E	160	-22.046	66.411	-24.824	1.00	168.54
70	7413	CA	TYR	E	160	-20.842	65.579	-24.759	1.00	168.54
	7414	CB	TYR	E	160	-19.592	66.368	-25.140	1.00	216.78

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	7415	CG	TYR	E	160	-19.684	67.078	-26.461	1.00	216.78
	7416	CD1	TYR	E	160	-20.168	68.381	-26.533	1.00	216.78
	7417	CE1	TYR	E	160	-20.270	69.041	-27.747	1.00	216.78
	7418	CD2	TYR	E	160	-19.301	66.446	-27.644	1.00	216.78
5	7419	CE2	TYR	E	160	-19.401	67.097	-28.868	1.00	216.78
	7420	CZ	TYR	E	160	-19.887	68.395	-28.909	1.00	216.78
	7421	OH	TYR	E	160	-20.003	69.045	-30.114	1.00	216.78
	7422	C	TYR	E	160	-20.609	64.973	-23.383	1.00	168.54
	7423	O	TYR	E	160	-20.898	65.581	-22.351	1.00	168.54
10	7424	N	GLU	E	161	-20.048	63.771	-23.399	1.00	118.65
	7425	CA	GLU	E	161	-19.738	63.004	-22.200	1.00	118.65
	7426	CB	GLU	E	161	-20.378	61.624	-22.330	1.00	174.81
	7427	CG	GLU	E	161	-20.107	60.665	-21.205	1.00	174.81
	7428	CD	GLU	E	161	-21.068	59.496	-21.241	1.00	174.81
15	7429	OE1	GLU	E	161	-20.765	58.447	-20.632	1.00	174.81
	7430	OE2	GLU	E	161	-22.138	59.638	-21.876	1.00	174.81
	7431	C	GLU	E	161	-18.214	62.890	-22.087	1.00	·118.65
	7432	O	GLU	E	161	-17.529	62.655	-23.085	1.00	118.65
	7433	N	SER	E	162	-17.688	63.066	-20.877	1.00	111.13
20	7434	CA	SER	E	162	-16.249	63.005	-20.643	1.00	111.13
	7435	CB	SER	E	162	-15.864	63.955	-19.512	1.00	104.26
	7436	OG	SER	E	162	-16.548	63.616	-18.315	1.00	104.26
	7437	C	SER	E	162	-15.790	61.603	-20.296	1.00	111.13
	7438	O	SER	E	162	-16.609	60.725	-20.057	1.00	111.13
25	7439	N	GLU	E	163	-14.478	61.391	-20.272	1.00	89.90
	7440	CA	GLU	E	163	-13.915	60.079	-19.943	1.00	89.90
	7441	CB	GLU	E	163	-12.417	60.050	-20.253	1.00	240.41
	7442	CG	GLU	E	163	-12.072	59.972	-21.731	1.00	240.41
	7443	CD	GLU	E	163	-12.359	58.606	-22.321	1.00	240.41
30	7444	OE1	GLU	E	163	-11.812	57.609	-21.802	1.00	240.41
	7445	OE2	GLU	E	163	-13.128	58.527	-23.303	1.00	240.41
	7446	C	GLU	E	163	-14.131	59.856	-18.455	1.00	89.90
	7447	O	GLU	E	163	-14.028	60.795	-17.668	1.00	89.90
	7448	N	PRO	E	164	-14.433	58.609	-18.041	1.00	64.59
35	7449	CD	PRO	E	164	-14.576	57.360	-18.788	1.00	100.06
	7450	CA	PRO	E	164	-14.639	58.395	-16.606	1.00	64.59
	7451	CB	PRO	E	164	-15.248	57.008	-16.568	1.00	100.06
	7452	CG	PRO	E	164	-14.564	56.333	-17.682	1.00	100.06
	7453	C	PRO	E	164	-13.327	58.488	-15.846	1.00	64.59
40	7454	O	PRO	E	164	-12.243	58.317	-16.415	1.00	64.59
	7455	N	LEU	E	165	-13.405	58.777	-14.554	1.00	77.47
	7456	CA	LEU	E	165	-12.197	58.901	-13.758	1.00	77.47
	7457	CB	LEU	E	165	-11.771	60.364	-13.685	1.00	63.52
	7458	CG	LEU	E	165	-10.647	60.607	-12.688	1.00	63.52
45	7459	CD1	LEU	E	165	-9.568	59.589	-12.978	1.00	63.52
	7460	CD2	LEU	E	165	-10.088	61.981	-12.800	1.00	63.52
	7461	C	LEU	E	165	-12.415	58.362	-12.360	1.00	77.47
	7462	O	LEU	E	165	-13.328	58.803	-11.665	1.00	77.47
	7463	N	ASN	E	166	-11.580	57.407	-11.959	1.00	93.16
50	7464	CA	ASN	E	166	-11.684	56.801	-10.635	1.00	93.16
	7465	CB	ASN	E	166	-11.050	55.421	-10.614	1.00	96.38
	7466	CG	ASN	E	166	-12.037	54.314	-10.900	1.00	96.38
	7467	OD1	ASN	E	166	-13.220	54.408	-10.581	1.00	96.38
	7468	ND2	ASN	E	166	-11.534	53.242	-11.486	1.00	96.38
55	7469	C	ASN	E	166	-10.999	57.633	-9.582	1.00	93.16
	7470	O	ASN	E	166	-9.975	58.232	-9.837	1.00	93.16
	7471	N	ILE	E	167	-11.544	57.639	-8.380	1.00	64.50
	7472	CA	ILE	E	167	-10.971	58.424	-7.303	1.00	64.50
	7473	CB	ILE	E	167	-11.751	59.709	-7.114	1.00	67.49
60	7474	CG2	ILE	E	167	-11.452	60.314	-5.762	1.00	67.49
	7475	CG1	ILE	E	167	-11.427	60.672	-8.243	1.00	67.49
	7476	CD1	ILE	E	167	-12.043	62.011	-8.046	1.00	67.49
	7477	C	ILE	E	167	-11.054	57.651	-6.012	1.00	64.50
	7478	O	ILE	E	167	-12.117	57.081	-5.675	1.00	64.50
65	7479	N	THR	E	168	-9.963	57.632	-5.266	1.00	85.23
	7480	CA	THR	E	168	-9.997	56.899	-4.025	1.00	85.23
	7481	CB	THR	E	168	-9.077	55.692	-4.075	1.00	118.46
	7482	OG1	THR	E	168	-9.470	54.848	-5.162	1.00	118.46
	7483	CG2	THR	E	168	-9.178	54.910	-2.787	1.00	118.46
70	7484	C	THR	E	168	-9.621	57.759	-2.856	1.00	85.23

	7485	O	THR	E	168	-8.681	58.558	-2.931	1.00	85.23
	7486	N	VAL	E	169	-10.379	57.600	-1.781	1.00	97.28
	7487	CA	VAL	E	169	-10.150	58.320	-0.544	1.00	97.28
5	7488	CB	VAL	E	169	-11.420	59.087	-0.122	1.00	79.18
	7489	CG1	VAL	E	169	-11.346	59.434	1.333	1.00	79.18
	7490	CG2	VAL	E	169	-11.565	60.340	-0.927	1.00	79.18
	7491	C	VAL	E	169	-9.809	57.241	0.489	1.00	97.28
	7492	O	VAL	E	169	-10.681	56.475	0.905	1.00	97.28
	7493	N	ILE	E	170	-8.538	57.156	0.876	1.00	87.96
10	7494	CA	ILE	E	170	-8.113	56.159	1.856	1.00	87.96
	7495	CB	ILE	E	170	-6.663	55.682	1.574	1.00	99.84
	7496	CG2	ILE	E	170	-6.530	55.259	0.124	1.00	99.84
	7497	CG1	ILE	E	170	-5.666	56.808	1.822	1.00	99.84
	7498	CD1	ILE	E	170	-4.217	56.427	1.528	1.00	99.84
15	7499	C	ILE	E	170	-8.209	56.759	3.253	1.00	87.96
	7500	O	ILE	E	170	-8.544	57.933	3.392	1.00	87.96
	7501	N	LYS	E	171	-7.932	55.970	4.286	1.00	171.73
	7502	CA	LYS	E	171	-8.001	56.486	5.650	1.00	171.73
	7503	CB	LYS	E	171	-9.242	55.303	6.353	1.00	217.19
20	7504	CG	LYS	E	171	-9.308	54.421	6.380	1.00	217.19
	7505	CD	LYS	E	171	-10.739	53.932	6.537	1.00	217.19
	7506	CE	LYS	E	171	-11.376	54.437	7.821	1.00	217.19
	7507	NZ	LYS	E	171	-12.786	53.971	7.947	1.00	217.19
	7508	C	LYS	E	171	-6.749	56.162	6.454	1.00	171.73
25	7509	O	LYS	E	171	-6.573	56.658	7.565	1.00	171.73
	7510	C1	NAG	E	221	0.947	78.578	-23.161	1.00	249.29
	7511	C2	NAG	E	221	-0.412	79.265	-23.224	1.00	249.29
	7512	N2	NAG	E	221	-1.456	78.261	-23.255	1.00	249.29
	7513	C7	NAG	E	221	-2.671	78.553	-22.807	1.00	249.29
30	7514	O7	NAG	E	221	-2.963	79.651	-22.339	1.00	249.29
	7515	C8	NAG	E	221	-3.720	77.456	-22.880	1.00	249.29
	7516	C3	NAG	E	221	-0.518	80.128	-24.473	1.00	249.29
	7517	O3	NAG	E	221	-1.714	80.890	-24.425	1.00	249.29
	7518	C4	NAG	E	221	0.670	81.073	-24.631	1.00	249.29
35	7519	O4	NAG	E	221	0.579	81.653	-25.947	1.00	249.29
	7520	C5	NAG	E	221	1.997	80.296	-24.470	1.00	249.29
	7521	O5	NAG	E	221	1.994	79.555	-23.228	1.00	249.29
	7522	C6	NAG	E	221	3.222	81.198	-24.429	1.00	249.29
	7523	O6	NAG	E	221	3.160	82.105	-23.335	1.00	249.29
40	7524	C1	NAG	E	222	1.316	82.790	-26.227	1.00	249.77
	7525	C2	NAG	E	222	0.449	83.797	-27.008	1.00	249.77
	7526	N2	NAG	E	222	-0.713	84.171	-26.221	1.00	249.77
	7527	C7	NAG	E	222	-0.903	85.441	-25.867	1.00	249.77
	7528	O7	NAG	E	222	-0.130	86.350	-26.178	1.00	249.77
45	7529	C8	NAG	E	222	-2.140	85.750	-25.043	1.00	249.77
	7530	C3	NAG	E	222	0.003	83.194	-28.351	1.00	249.77
	7531	O3	NAG	E	222	-0.664	84.182	-29.124	1.00	249.77
	7532	C4	NAG	E	222	1.211	82.656	-29.133	1.00	249.77
	7533	O4	NAG	E	222	0.762	81.952	-30.285	1.00	249.77
50	7534	C5	NAG	E	222	2.048	81.716	-28.248	1.00	249.77
	7535	O5	NAG	E	222	2.440	82.386	-27.023	1.00	249.77
	7536	C6	NAG	E	222	3.319	81.240	-28.926	1.00	249.77
	7537	O6	NAG	E	222	3.494	79.843	-28.749	1.00	249.77
	7538	C1	NAG	E	242	6.691	58.325	-21.511	1.00	184.18
55	7539	C2	NAG	E	242	6.772	58.888	-22.927	1.00	184.18
	7540	N2	NAG	E	242	7.616	60.057	-22.949	1.00	184.18
	7541	C7	NAG	E	242	8.669	60.081	-23.755	1.00	184.18
	7542	O7	NAG	E	242	8.972	59.137	-24.489	1.00	184.18
	7543	C8	NAG	E	242	9.523	61.338	-23.746	1.00	184.18
60	7544	C3	NAG	E	242	5.382	59.264	-23.429	1.00	184.18
	7545	O3	NAG	E	242	5.460	59.693	-24.778	1.00	184.18
	7546	C4	NAG	E	242	4.452	58.056	-23.332	1.00	184.18
	7547	O4	NAG	E	242	3.102	58.481	-23.616	1.00	184.18
	7548	C5	NAG	E	242	4.513	57.446	-21.911	1.00	184.18
65	7549	O5	NAG	E	242	5.874	57.166	-21.520	1.00	184.18
	7550	C6	NAG	E	242	3.835	56.114	-21.900	1.00	184.18
	7551	O6	NAG	E	242	2.768	56.046	-20.979	1.00	184.18
	7552	C1	NAG	E	243	2.525	57.919	-24.745	1.00	162.87
	7553	C2	NAG	E	243	0.990	57.891	-24.616	1.00	162.87
70	7554	N2	NAG	E	243	0.580	57.065	-23.493	1.00	162.87

7555	C7	NAG E	243	-0.334	57.510	-22.639	1.00	162.87
7556	O7	NAG E	243	-0.848	58.623	-22.738	1.00	162.87
7557	C8	NAG E	243	-0.729	56.592	-21.497	1.00	162.87
7558	C3	NAG E	243	0.393	57.321	-25.904	1.00	162.87
7559	O3	NAG E	243	-1.018	57.363	-25.842	1.00	162.87
7560	C4	NAG E	243	0.891	58.108	-27.133	1.00	162.87
7561	O4	NAG E	243	0.428	57.479	-28.366	1.00	162.87
7562	C5	NAG E	243	2.430	58.133	-27.118	1.00	162.87
7563	O5	NAG E	243	2.904	58.707	-25.885	1.00	162.87
7564	C6	NAG E	243	3.044	58.927	-28.250	1.00	162.87
7565	O6	NAG E	243	2.770	60.311	-28.097	1.00	162.87
7566	C1	MAN E	244	-0.169	58.185	-29.362	1.00	177.48
7567	C2	MAN E	244	-1.467	58.963	-29.047	1.00	177.48
7568	O2	MAN E	244	-1.159	60.326	-28.837	1.00	177.48
7569	C3	MAN E	244	-2.273	58.794	-30.382	1.00	177.48
7570	O3	MAN E	244	-3.531	59.444	-30.342	1.00	177.48
7571	C4	MAN E	244	-1.469	59.230	-31.646	1.00	177.48
7572	O4	MAN E	244	-2.267	59.074	-32.823	1.00	177.48
7573	C5	MAN E	244	-0.223	58.317	-31.725	1.00	177.48
7574	O5	MAN E	244	0.620	58.472	-30.547	1.00	177.48
7575	C6	MAN E	244	0.611	58.487	-33.000	1.00	177.48
7576	O6	MAN E	244	1.488	59.592	-32.913	1.00	177.48
7577	C1	NAG E	: 250	13.381	78.909	-13.725	1.00	249.71
7578	C2	NAG E	250	12.909	80.209	-13.049	1.00	249.71
7579	N2	NAG E	250	13.077	80.124	-11.608	1.00	249.71
7580	C7	NAG E	250	13.987	80.876	-10.993	1.00	249.71
7581	O7	NAG E	250	14.727	81.658	-11.592	1.00	249.71
7582	C8	NAG E	250	14.097	80.733	-9.481	1.00	249.71
7583	C3	NAG E	250	11.429	80.446	-13.387	1.00	249.71
7584	O3	NAG E	250	11.000	81.693	-12.858	1.00	249.71
7585	C4	NAG E	250	11.216	80.427	-14.906	1.00	249.71
7586	O4	NAG E	250	9.826	80.512	-15.194	1.00	249.71
7587	C5	NAG E	250	11.793	79.133	-15.504	1.00	249.71
7588	O5	NAG E	250	13.187	78.993	-15.143	1.00	249.71
7589	C6	NAG E	250	11.720	79.107	-17.018	1.00	249.71
7590	O6	NAG E	250	12.531	78.071	-17.553	1.00	249.71
7591	C1	NAG E	274	17.852	58.017	0.947	1.00	232.95
7592	C2	NAG E	274	17.034	57.505	2.065	1.00	232.95
7593	N2	NAG E	274	16.704	58.587	2.972	1.00	232.95
7594	C7	NAG E	274	15.587	58.533	3.690	1.00	232.95
7595	O7	NAG E	274	14.789	57.594	3.617	1.00	232.95
7596	C8	NAG E	274	15.307	59.699	4.627	1.00	232.95
7597	C3	NAG E	274	17.729	56.379	2.842	1.00	232.95
7598	O3	NAG E	274	16.822	55.816	3.780	1.00	232.95
7599	C4	NAG E	274	18.227	55.288	1.888	1.00	232.95
7600	O4	NAG E	274	18.999	54.339	2.613	1.00	232.95
7601	C5	NAG E	274	19.081	55.909	0.772	1.00	232.95
7602	O5	NAG E	274	18.329	56.933	0.083	1.00	232.95
7603	C6	NAG E	274	19.520	54.898	-0.274	1.00	232.95
7604	O6	NAG E	274	20.106	55.536	-1.399	1.00	232.95
7605	C1	NAG E	335	-12.841	75.891	-12.527	1.00	244.27
7606	C2	NAG E	335	-11.869	76.721	-11.656	1.00	244.27
7607	N2	NAG E	335	-12.291	76.605	-10.271	1.00	244.27
7608	C7	NAG E	335	-11.503	76.035	-9.365	1.00	244.27
7609	O7	NAG E	335	-10.386	75.589	-9.628	1.00	244.27
7610	C8	NAG E	335	-12.039	75.956	-7.947	1.00	244.27
7611	C3	NAG E	335	-11.803	78.214	-12.025	1.00	244.27
7612	O3	NAG E	335	-10.618	78.779	-11.480	1.00	244.27
7613	C4	NAG E	335	-11.806	78.418	-13.537	1.00	244.27
7614	O4	NAG E	335	-11.818	79.805	-13.844	1.00	244.27
7615	C5	NAG E	335	-13.044	77.739	-14.108	1.00	244.27
7616	O5	NAG E	335	-12.940	76.310	-13.913	1.00	244.27
7617	C6	NAG E	335	-13.184	77.982	-15.605	1.00	244.27
7618	O6	NAG E	335	-14.397	78.652	-15.913	1.00	244.27
7619	C1	NAG E	340	-14.368	66.477	8.751	1.00	249.77
7620	C2	NAG E	340	-13.779	65.349	9.574	1.00	249.77
7621	N2	NAG E	340	-13.415	64.233	8.721	1.00	249.77
7622	C7	NAG E	340	-12.195	63.711	8.818	1.00	249.77
7623	O7	NAG E	340	-11.344	64.132	9.612	1.00	249.77
7624	C8	NAG E	340	-11.863	62.550	7.900	1.00	249.77

	7625	C3	NAG E	340	-14.783	64.920	10.636	1.00	249.77
	7626	O3	NAG E	340	-14.195	63.909	11.453	1.00	249.77
	7627	C4	NAG E	340	-15.166	66.132	11.500	1.00	249.77
5	7628	O4	NAG E	340	-16.238	65.759	12.355	1.00	249.77
	7629	C5	NAG E	340	-15.575	67.356	10.636	1.00	249.77
	7630	O5	NAG E	340	-14.610	67.605	9.591	1.00	249.77
	7631	C6	NAG E	340	-15.666	68.648	11.433	1.00	249.77
10	7632	O6	NAG E	340	-15.300	69.781	10.659	1.00	249.77
	7633	C1	NAG E	366	-12.398	52.150	-11.858	1.00	131.22
	7634	C2	NAG E	366	-11.828	51.489	-13.095	1.00	131.22
	7635	N2	NAG E	366	-11.760	52.463	-14.162	1.00	131.22
15	7636	C7	NAG E	366	-10.652	53.170	-14.339	1.00	131.22
	7637	O7	NAG E	366	-9.658	53.028	-13.631	1.00	131.22
	7638	C8	NAG E	366	-10.642	54.189	-15.474	1.00	131.22
	7639	C3	NAG E	366	-12.712	50.337	-13.517	1.00	131.22
20	7640	O3	NAG E	366	-12.088	49.646	-14.588	1.00	131.22
	7641	C4	NAG E	366	-12.958	49.373	-12.351	1.00	131.22
	7642	O4	NAG E	366	-13.982	48.430	-12.735	1.00	131.22
	7643	C5	NAG E	366	-13.414	50.137	-11.096	1.00	131.22
25	7644	O5	NAG E	366	-12.496	51.204	-10.795	1.00	131.22
	7645	C6	NAG E	366	-13.478	49.261	-9.862	1.00	131.22
	7646	O6	NAG E	366	-13.939	49.998	-8.740	1.00	131.22
	7647	C1	NAG E	367	-13.682	47.077	-12.614	1.00	245.35
30	7648	C2	NAG E	367	-14.975	46.261	-12.520	1.00	245.35
	7649	N2	NAG E	367	-15.776	46.701	-11.394	1.00	245.35
	7650	C7	NAG E	367	-16.904	47.372	-11.610	1.00	245.35
	7651	O7	NAG E	367	-17.315	47.646	-12.739	1.00	245.35
35	7652	C8	NAG E	367	-17.698	47.808	-10.389	1.00	245.35
	7653	C3	NAG E	367	-14.620	44.778	-12.391	1.00	245.35
	7654	O3	NAG E	367	-15.804	43.995	-12.351	1.00	245.35
	7655	C4	NAG E	367	-13.757	44.354	-13.584	1.00	245.35
	7656	O4	NAG E	367	-13.340	43.005	-13.423	1.00	245.35
	7657	C5	NAG E	367	-12.529	45.270	-13.701	1.00	245.35
	7658	O5	NAG E	367	-12.935	46.662	-13.772	1.00	245.35
	7659	C6	NAG E	367	-11.710	44.973	-14.941	1.00	245.35
	7660	O6	NAG E	367	-11.792	46.031	-15.884	1.00	245.35

Table 6. Atomic coordinates of PhFcεRIα1-172, Form T2

ATOM NUMBER	ATOM TYPE	RESIDUE	#	X	Y	Z	OCC	B
1	CB	LYS C	4	16.063	45.227	50.293	1.00	240.56
2	CG	LYS C	4	17.178	44.372	49.692	1.00	240.56
3	CD	LYS C	4	18.081	43.766	50.766	1.00	240.56
4	CE	LYS C	4	19.152	42.864	50.151	1.00	240.56
5	NZ	LYS C	4	20.054	42.261	51.173	1.00	240.56
6	C	LYS C	4	14.440	44.631	48.479	1.00	248.46
7	O	LYS C	4	14.364	43.506	48.972	1.00	248.46
8	N	LYS C	4	14.039	46.614	49.935	1.00	248.46
9	CA	LYS C	4	15.077	45.783	49.257	1.00	248.46
10	N	PRO C	5	13.962	44.902	47.256	1.00	240.49
11	CD	PRO C	5	13.761	46.229	46.635	1.00	226.60
12	CA	PRO C	5	13.338	43.853	46.448	1.00	240.49
13	CB	PRO C	5	12.401	44.636	45.543	1.00	226.60
14	CG	PRO C	5	13.189	45.881	45.274	1.00	226.60
15	C	PRO C	5	14.379	43.053	45.660	1.00	240.49
16	O	PRO C	5	15.487	43.534	45.409	1.00	240.49
17	N	LYS C	6	14.022	41.831	45.280	1.00	200.38
18	CA	LYS C	6	14.932	40.986	44.518	1.00	200.38
19	CB	LYS C	6	15.670	40.017	45.446	1.00	249.33
20	CG	LYS C	6	16.701	39.153	44.729	1.00	249.33
21	CD	LYS C	6	17.530	38.312	45.692	1.00	249.33
22	CE	LYS C	6	18.564	37.480	44.943	1.00	249.33
23	NZ	LYS C	6	19.471	36.732	45.855	1.00	249.33
24	C	LYS C	6	14.168	40.207	43.449	1.00	200.38
25	O	LYS C	6	13.352	39.327	43.755	1.00	200.38
26	N	VAL C	7	14.451	40.538	42.190	1.00	184.84
27	CA	VAL C	7	13.799	39.902	41.052	1.00	184.84
28	CB	VAL C	7	14.155	40.623	39.744	1.00	175.84
29	CG1	VAL C	7	13.207	40.181	38.645	1.00	175.84
30	CG2	VAL C	7	14.108	42.134	39.944	1.00	175.84
31	C	VAL C	7	14.153	38.431	40.884	1.00	184.84
32	O	VAL C	7	15.316	38.073	40.746	1.00	184.84
33	N	SER C	8	13.132	37.584	40.887	1.00	212.94
34	CA	SER C	8	13.318	36.148	40.720	1.00	212.84
35	CB	SER C	8	12.487	35.385	41.758	1.00	203.15
36	OG	SER C	8	11.148	35.858	41.801	1.00	203.15
37	C	SER C	8	12.886	35.755	39.307	1.00	212.94
38	O	SER C	8	12.169	36.508	38.646	1.00	212.94
39	N	LEU C	9	13.330	34.593	38.834	1.00	249.13
40	CA	LEU C	9	12.855	34.137	37.495	1.00	249.13
41	CB	LEU C	9	14.150	34.163	36.540	1.00	143.92
42	CG	LEU C	9	14.916	35.465	36.269	1.00	143.92
43	CD1	LEU C	9	15.771	35.258	35.022	1.00	143.92
44	CD2	LEU C	9	13.966	36.637	36.063	1.00	143.92
45	C	LEU C	9	12.395	32.728	37.507	1.00	249.13
46	O	LEU C	9	12.617	31.964	38.445	1.00	249.13
47	N	ASN C	10	11.667	32.389	36.451	1.00	171.60
48	CA	ASN C	10	11.095	31.064	36.326	1.00	171.60
49	CB	ASN C	10	9.847	30.927	37.201	1.00	226.23
50	CG	ASN C	10	9.428	29.487	37.375	1.00	226.23
51	OD1	ASN C	10	10.163	28.684	37.948	1.00	226.23
52	ND2	ASN C	10	8.251	29.146	36.870	1.00	226.23
53	C	ASN C	10	10.724	30.744	34.882	1.00	171.60
54	O	ASN C	10	9.817	31.353	34.315	1.00	171.60
55	N	PRO C	11	11.452	29.806	34.238	1.00	202.18
56	CD	PRO C	11	11.153	29.449	32.850	1.00	161.79
57	CA	PRO C	11	12.551	28.981	34.761	1.00	202.18
58	CB	PRO C	11	13.028	28.248	33.517	1.00	161.79
59	CG	PRO C	11	11.770	28.086	32.742	1.00	161.79
60	C	PRO C	11	13.687	29.788	35.394	1.00	202.18
61	O	PRO C	11	13.753	31.010	35.265	1.00	202.18
62	N	PRO C	12	14.598	29.101	36.104	1.00	182.42
63	CD	PRO C	12	14.562	27.680	36.472	1.00	171.80
64	CA	PRO C	12	15.721	29.778	36.762	1.00	182.42
65	CB	PRO C	12	16.307	28.681	37.663	1.00	171.80

	136	CB	GLU	C	20	12.136	30.161	25.259	1.00	176.57
	137	CG	GLU	C	20	12.994	29.290	24.335	1.00	176.57
	138	CD	GLU	C	20	14.115	28.594	25.077	1.00	176.57
	139	OE1	GLU	C	20	14.898	29.282	25.777	1.00	176.57
5	140	OE2	GLU	C	20	14.217	27.356	24.959	1.00	176.57
	141	C	GLU	C	20	10.297	31.833	25.582	1.00	154.05
	142	O	GLU	C	20	10.532	33.032	25.419	1.00	154.05
	143	N	ASN	C	21	9.550	31.365	26.587	1.00	173.20
	144	CA	ASN	C	21	8.957	32.290	27.559	1.00	173.20
10	145	CB	ASN	C	21	7.446	32.074	27.682	1.00	249.69
	146	CG	ASN	C	21	6.794	31.675	26.378	1.00	249.69
	147	OD1	ASN	C	21	7.014	32.277	25.326	1.00	249.69
	148	ND2	ASN	C	21	5.961	30.647	26.472	1.00	249.69
	149	C	ASN	C	21	9.559	32.227	28.975	1.00	173.20
15	150	O	ASN	C	21	9.892	31.148	29.474	1.00	173.20
	151	N	VAL	C	22	9.661	33.393	29.617	1.00	186.44
	152	CA	VAL	C	22	10.209	33.508	30.964	1.00	186.44
	153	CB	VAL	C	22	11.664	34.016	30.926	1.00	163.28
	154	CG1	VAL	C	22	11.701	35.486	30.538	1.00	163.28
20	155	CG2	VAL	C	22	12.315	33.802	32.273	1.00	163.28
	156	C	VAL	C	22	9.379	34.489	31.797	1.00	186.44
	157	O	VAL	C	22	8.852	35.463	31.271	1.00	186.44
	158	N	THR	C	23	9.289	34.241	33.102	1.00	165.76
	159	CA	THR	C	23	8.512	35.092	34.014	1.00	165.76
25	160	CB	THR	C	23	7.425	34.263	34.728	1.00	249.09
	161	OG1	THR	C	23	6.671	33.521	33.760	1.00	249.09
	162	CG2	THR	C	23	6.492	35.177	35.511	1.00	249.09
	163	C	THR	C	23	9.348	35.780	35.098	1.00	165.76
	164	O	THR	C	23	10.061	35.119	35.850	1.00	165.76
30	165	N	LEU	C	24	9.239	37.099	35.195	1.00	173.95
	166	CA	LEU	C	24	9.990	37.842	36.206	1.00	173.95
	167	CB	LEU	C	24	10.661	39.079	35.589	1.00	128.36
	168	CG	LEU	C	24	11.163	39.097	34.140	1.00	128.36
	169	CD1	LEU	C	24	12.080	40.307	33.939	1.00	128.36
35	170	CD2	LEU	C	24	11.903	37.824	33.821	1.00	128.36
	171	C	LEU	C	24	9.089	38.297	37.365	1.00	173.95
	172	O	LEU	C	24	8.276	39.207	37.208	1.00	173.95
	173	N	THR	C	25	9.249	37.669	38.526	1.00	172.54
	174	CA	THR	C	25	8.463	37.995	39.717	1.00	172.54
40	175	CB	THR	C	25	8.096	36.712	40.504	1.00	195.25
	176	OG1	THR	C	25	7.369	35.824	39.645	1.00	195.25
	177	CG2	THR	C	25	7.244	37.045	41.724	1.00	195.25
	178	C	THR	C	25	9.253	38.923	40.636	1.00	172.54
	179	O	THR	C	25	10.427	38.681	40.895	1.00	172.54
45	180	N	CYS	C	26	8.610	39.978	41.130	1.00	199.84
	181	CA	CYS	C	26	9.269	40.937	42.025	1.00	199.84
	182	C	CYS	C	26	9.272	40.407	43.458	1.00	199.84
	183	O	CYS	C	26	8.303	39.775	43.889	1.00	199.84
	184	CB	CYS	C	26	8.556	42.292	41.955	1.00	211.93
50	185	SG	CYS	C	26	9.426	43.668	42.769	1.00	211.93
	186	N	ASN	C	27	10.358	40.673	44.186	1.00	249.36
	187	CA	ASN	C	27	10.531	40.203	45.564	1.00	249.36
	188	CB	ASN	C	27	11.176	41.291	46.437	1.00	249.69
	189	CG	ASN	C	27	11.614	40.764	47.804	1.00	249.69
55	190	OD1	ASN	C	27	12.279	39.728	47.907	1.00	249.69
	191	ND2	ASN	C	27	11.246	41.481	48.858	1.00	249.69
	192	C	ASN	C	27	9.245	39.705	46.225	1.00	249.36
	193	O	ASN	C	27	8.484	40.481	46.815	1.00	249.36
	194	N	GLY	C	28	9.029	38.395	46.116	1.00	249.69
60	195	CA	GLY	C	28	7.858	37.746	46.685	1.00	249.69
	196	C	GLY	C	28	7.872	36.313	46.199	1.00	249.69
	197	O	GLY	C	28	7.839	36.074	44.991	1.00	249.69
	198	N	ASN	C	29	7.927	35.361	47.129	1.00	249.69
	199	CA	ASN	C	29	7.980	33.942	46.771	1.00	249.69
65	200	CB	ASN	C	29	8.454	33.111	47.988	1.00	249.69
	201	CG	ASN	C	29	8.804	31.655	47.627	1.00	249.69
	202	OD1	ASN	C	29	8.854	31.278	46.450	1.00	249.69
	203	ND2	ASN	C	29	9.055	30.840	48.650	1.00	249.69
	204	C	ASN	C	29	6.655	33.386	46.224	1.00	249.69
70	205	O	ASN	C	29	6.633	32.784	45.140	1.00	249.69

	206	N	ASN	C	30	5.554	33.594	46.946	1.00	249.69
	207	CA	ASN	C	30	4.270	33.055	46.497	1.00	249.69
	208	CB	ASN	C	30	3.852	31.902	47.424	1.00	249.69
	209	CG	ASN	C	30	4.822	30.717	47.372	1.00	249.69
5	210	OD1	ASN	C	30	5.230	30.182	48.410	1.00	249.69
	211	ND2	ASN	C	30	5.186	30.299	46.163	1.00	249.69
	212	C	ASN	C	30	3.119	34.055	46.361	1.00	249.69
	213	O	ASN	C	30	2.662	34.325	45.248	1.00	249.69
	214	N	PHE	C	31	2.650	34.602	47.482	1.00	249.69
10	215	CA	PHE	C	31	1.531	35.546	47.446	1.00	249.52
	216	CB	PHE	C	31	0.361	35.003	48.290	1.00	249.52
	217	CG	PHE	C	31	-0.075	33.609	47.903	1.00	249.52
	218	CD1	PHE	C	31	0.636	32.498	48.348	1.00	249.52
	219	CD2	PHE	C	31	-1.176	33.411	47.071	1.00	249.52
15	220	CE1	PHE	C	31	0.261	31.211	47.966	1.00	249.52
	221	CE2	PHE	C	31	-1.557	32.128	46.684	1.00	249.52
	222	CZ	PHE	C	31	-0.838	31.026	47.132	1.00	249.69
	223	C	PHE	C	31	1.872	36.984	47.884	1.00	249.69
	224	O	PHE	C	31	2.350	37.22?	49.003	1.00	249.62
20	225	N	PHE	C	32	1.605	37.936	46.986	1.00	249.62
	226	CA	PHE	C	32	1.872	39.354	47.227	1.00	249.69
	227	CB	PHE	C	32	2.862	39.873	46.176	1.00	249.69
	228	CG	PHE	C	32	3.487	41.203	46.520	1.00	249.69
	229	CD1	PHE	C	32	4.351	41.325	47.611	1.00	249.69
25	230	CD2	PHE	C	32	3.224	42.334	45.741	1.00	249.69
	231	CE1	PHE	C	32	4.948	42.554	47.918	1.00	249.69
	232	CE2	PHE	C	32	3.814	43.566	46.039	1.00	249.69
	233	CZ	PHE	C	32	4.678	43.673	47.176	1.00	249.62
	234	C	PHE	C	32	0.569	40.161	46.738	1.00	249.62
30	235	O	PHE	C	32	-0.470	39.650	47.595	1.00	238.93
	236	N	GLU	C	33	0.636	41.424	47.631	1.00	238.93
	237	CA	GLU	C	33	-0.554	42.273	49.079	1.00	249.69
	238	CB	GLU	C	33	-0.811	42.705	49.339	1.00	249.69
	239	CG	GLU	C	33	-2.234	43.193	48.762	1.00	249.69
35	240	CD	GLU	C	33	-3.285	42.246	48.947	1.00	249.69
	241	OE1	GLU	C	33	-3.144	41.010	48.124	1.00	249.69
	242	OE2	GLU	C	33	-4.250	42.733	46.721	1.00	238.93
	243	C	GLU	C	33	-0.613	43.512	45.998	1.00	238.93
	244	O	GLU	C	33	-1.589	43.716	46.762	1.00	237.42
40	245	N	VAL	C	34	0.420	44.344	45.959	1.00	237.42
	246	CA	VAL	C	34	0.452	45.563	46.235	1.00	249.69
	247	CB	VAL	C	34	1.760	46.350	45.447	1.00	249.69
	248	CG1	VAL	C	34	1.775	47.644	47.726	1.00	249.69
	249	CG2	VAL	C	34	1.875	46.644	44.447	1.00	237.42
45	250	C	VAL	C	34	0.284	45.376	43.880	1.00	237.42
	251	O	VAL	C	34	0.665	44.351	43.812	1.00	249.64
	252	N	SER	C	35	-0.305	46.386	42.370	1.00	249.64
	253	CA	SER	C	35	-0.535	46.390	42.058	1.00	249.69
	254	CB	SER	C	35	-1.976	46.787	42.327	1.00	249.69
50	255	OG	SER	C	35	-2.186	48.165	41.729	1.00	249.64
	256	C	SER	C	35	0.403	47.409	40.504	1.00	249.64
	257	O	SER	C	35	0.418	47.573	42.573	1.00	249.69
	258	N	SER	C	36	1.171	48.101	42.112	1.00	249.69
	259	CA	SER	C	36	2.129	49.109	42.987	1.00	249.69
55	260	CB	SER	C	36	2.054	50.374	44.280	1.00	249.69
	261	OG	SER	C	36	2.599	50.160	42.130	1.00	249.69
	262	C	SER	C	36	3.555	48.551	43.142	1.00	249.69
	263	O	SER	C	36	4.261	48.626	40.999	1.00	198.99
	264	N	THR	C	37	3.961	47.977	40.863	1.00	198.99
60	265	CA	THR	C	37	5.286	47.408	40.697	1.00	176.65
	266	CB	THR	C	37	5.205	45.867	41.840	1.00	176.65
	267	OG1	THR	C	37	4.557	45.280	40.573	1.00	176.65
	268	CG2	THR	C	37	6.597	45.275	39.632	1.00	198.99
	269	C	THR	C	37	5.905	48.053	38.619	1.00	198.99
65	270	O	THR	C	37	5.232	48.246	39.723	1.00	249.69
	271	N	LYS	C	38	7.182	48.400	38.606	1.00	249.69
	272	CA	LYS	C	38	7.865	49.041	39.109	1.00	249.38
	273	CB	LYS	C	38	8.609	50.287	39.792	1.00	249.38
	274	CG	LYS	C	38	7.697	51.314	40.303	1.00	249.38
70	275	CD	LYS	C	38	8.467	52.537			

	276	CE	LYS	C	38	7.527	53.572	40.930	1.00	249.38
	277	NZ	LYS	C	38	8.240	54.792	41.414	1.00	249.38
	278	C	LYS	C	38	8.837	48.092	37.894	1.00	249.69
	279	O	LYS	C	38	9.473	47.247	38.519	1.00	249.69
5	280	N	TRP	C	39	8.933	48.221	36.576	1.00	205.23
	281	CA	TRP	C	39	9.837	47.391	35.790	1.00	205.23
	282	CB	TRP	C	39	9.052	46.417	34.916	1.00	163.48
	283	CG	TRP	C	39	8.273	45.376	35.653	1.00	163.48
	284	CD2	TRP	C	39	8.795	44.365	36.525	1.00	163.48
10	285	CE2	TRP	C	39	7.715	43.525	36.893	1.00	163.48
	286	CE3	TRP	C	39	10.069	44.083	37.032	1.00	163.48
	287	CD1	TRP	C	39	6.939	45.125	35.542	1.00	163.48
	288	NE1	TRP	C	39	6.591	44.013	36.278	1.00	163.48
	289	CZ2	TRP	C	39	7.866	42.419	37.737	1.00	163.48
15	290	CZ3	TRP	C	39	10.225	42.976	37.881	1.00	163.48
	291	CH2	TRP	C	39	9.125	42.162	38.220	1.00	163.48
	292	C	TRP	C	39	10.637	48.332	34.908	1.00	205.23
	293	O	TRP	C	39	10.076	49.233	34.280	1.00	205.23
	294	''	PHE	C	40	11.947	48.138	34.857	1.00	127.08
20	295	CA	PHE	C	40	12.800	49.016	34.034	1.00	127.08
	296	CB	PHE	C	40	13.686	49.895	34.930	1.00	249.69
	297	CG	PHE	C	40	12.922	50.766	35.900	1.00	249.69
	298	CD1	PHE	C	40	12.431	50.242	37.097	1.00	249.69
	299	CD2	PHE	C	40	12.724	52.121	35.630	1.00	249.69
25	300	CE1	PHE	C	40	11.762	51.055	38.010	1.00	249.69
	301	CE2	PHE	C	40	12.054	52.941	36.539	1.00	249.69
	302	CZ	PHE	C	40	11.574	52.408	37.731	1.00	249.69
	303	C	PHE	C	40	13.714	48.284	33.012	1.00	127.08
	304	O	PHE	C	40	14.938	48.204	33.191	1.00	127.08
30	305	N	HIS	C	41	13.118	47.801	31.936	1.00	117.94
	306	CA	HIS	C	41	13.846	47.101	30.884	1.00	117.94
	307	CB	HIS	C	41	12.846	46.566	29.848	1.00	198.34
	308	CG	HIS	C	41	13.482	45.817	28.723	1.00	198.34
	309	CD2	HIS	C	41	13.214	45.791	27.395	1.00	198.34
35	310	ND1	HIS	C	41	14.515	44.930	28.924	1.00	198.34
	311	CE1	HIS	C	41	14.856	44.390	27.769	1.00	198.34
	312	NE2	HIS	C	41	14.082	44.895	26.826	1.00	198.34
	313	C	HIS	C	41	14.863	48.015	30.192	1.00	117.94
	314	O	HIS	C	41	14.509	48.859	29.389	1.00	117.94
40	315	N	ASN	C	42	16.135	47.813	30.481	1.00	147.15
	316	CA	ASN	C	42	17.216	48.618	29.912	1.00	147.15
	317	CB	ASN	C	42	17.135	48.679	28.370	1.00	208.25
	318	CG	ASN	C	42	17.652	47.411	27.699	1.00	208.25
	319	OD1	ASN	C	42	17.253	46.309	28.074	1.00	208.25
45	320	ND2	ASN	C	42	18.527	47.562	26.702	1.00	208.25
	321	C	ASN	C	42	17.140	50.019	30.506	1.00	147.15
	322	O	ASN	C	42	17.627	50.986	29.917	1.00	147.15
	323	N	GLY	C	43	16.527	50.115	31.683	1.00	230.72
	324	CA	GLY	C	43	16.372	51.400	32.344	1.00	230.72
50	325	C	GLY	C	43	15.019	52.031	32.048	1.00	230.72
	326	O	GLY	C	43	14.369	52.590	32.933	1.00	230.72
	327	N	SER	C	44	14.596	51.837	30.790	1.00	208.53
	328	CA	SER	C	44	13.320	52.490	30.334	1.00	208.53
	329	CB	SER	C	44	13.133	52.231	28.83	1.00	178.10
55	330	OG	SER	C	44	14.168	52.830	28.070	1.00	178.10
	331	C	SER	C	44	12.146	51.881	31.079	1.00	208.53
	332	O	SER	C	44	11.961	50.670	31.066	1.00	208.53
	333	N	LEU	C	45	11.338	52.719	31.713	1.00	211.15
	334	CA	LEU	C	45	10.186	52.214	32.442	1.00	211.15
60	335	CB	LEU	C	45	9.346	53.372	32.985	1.00	239.89
	336	CG	LEU	C	45	8.132	52.948	33.821	1.00	239.89
	337	CD1	LEU	C	45	8.571	52.034	34.952	1.00	239.89
	338	CD2	LEU	C	45	7.433	54.178	34.368	1.00	239.89
	339	C	LEU	C	45	9.330	51.325	31.540	1.00	211.15
65	340	O	LEU	C	45	9.278	51.528	30.323	1.00	211.15
	341	N	SER	C	46	8.669	50.339	32.143	1.00	166.46
	342	CA	SER	C	46	7.826	49.404	31.400	1.00	166.46
	343	CB	SER	C	46	8.138	47.964	31.815	1.00	249.69
	344	OG	SER	C	46	7.394	47.032	31.043	1.00	249.69
70	345	C	SER	C	46	6.345	49.671	31.608	1.00	166.46

Line	Serial	Atom	Res	Chain	ResSeq	X	Y	Z	Occ	B
	346	O	SER	C	46	5.973	50.451	32.488	1.00	166.46
	347	N	GLU	C	47	5.512	48.996	30.813	1.00	202.45
	348	CA	GLU	C	47	4.064	49.168	30.864	1.00	202.45
	349	CB	GLU	C	47	3.485	49.010	29.458	1.00	249.69
5	350	CG	GLU	C	47	4.000	50.047	28.469	1.00	249.69
	351	CD	GLU	C	47	3.429	49.860	27.078	1.00	249.69
	352	OE1	GLU	C	47	3.693	48.805	26.462	1.00	249.69
	353	OE2	GLU	C	47	2.715	50.769	26.600	1.00	249.69
	354	C	GLU	C	47	3.296	48.271	31.832	1.00	202.45
10	355	O	GLU	C	47	2.108	48.506	32.090	1.00	202.45
	356	N	GLU	C	48	3.948	47.243	32.361	1.00	214.28
	357	CA	GLU	C	48	3.264	46.372	33.301	1.00	214.28
	358	CB	GLU	C	48	3.882	44.973	33.294	1.00	197.36
	359	CG	GLU	C	48	3.286	44.027	34.340	1.00	197.36
15	360	CD	GLU	C	48	1.825	43.715	34.097	1.00	197.36
	361	OE1	GLU	C	48	1.535	42.984	33.130	1.00	197.36
	362	OE2	GLU	C	48	0.964	44.203	34.866	1.00	197.36
	363	C	GLU	C	48	3.343	46.977	34.702	1.00	214.28
	364	O	GLU	C	48	4.236	47.788	34.995	1.00	214.28
20	365	N	THR	C	49	2.398	46.584	35.557	1.00	211.95
	366	CA	THR	C	49	2.335	47.069	36.932	1.00	211.95
	367	CB	THR	C	49	1.126	48.003	37.123	1.00	249.69
	368	OG1	THR	C	49	-0.069	47.327	36.706	1.00	249.69
	369	CG2	THR	C	49	1.305	49.278	36.301	1.00	249.69
25	370	C	THR	C	49	2.220	45.895	37.901	1.00	211.95
	371	O	THR	C	49	2.631	45.988	39.055	1.00	211.95
	372	N	ASN	C	50	1.650	44.797	37.421	1.00	207.90
	373	CA	ASN	C	50	1.502	43.601	38.234	1.00	207.90
	374	CB	ASN	C	50	0.856	42.486	37.403	1.00	210.82
30	375	CG	ASN	C	50	0.443	41.295	38.245	1.00	210.82
	376	OD1	ASN	C	50	0.925	41.126	39.365	1.00	210.82
	377	ND2	ASN	C	50	-0.437	40.456	37.705	1.00	210.82
	378	C	ASN	C	50	2.914	43.187	38.670	1.00	207.90
	379	O	ASN	C	50	3.888	43.479	37.978	1.00	207.90
35	380	N	SER	C	51	3.036	42.509	39.808	1.00	249.50
	381	CA	SER	C	51	4.352	42.086	40.286	1.00	249.50
	382	CB	SER	C	51	4.260	41.569	41.728	1.00	249.69
	383	OG	SER	C	51	3.632	40.295	41.780	1.00	249.69
	384	C	SER	C	51	4.994	41.012	39.395	1.00	249.50
40	385	O	SER	C	51	6.196	40.775	39.483	1.00	249.50
	386	N	SER	C	52	4.195	40.367	38.544	1.00	228.11
	387	CA	SER	C	52	4.705	39.328	37.645	1.00	228.11
	388	CB	SER	C	52	3.867	38.049	37.741	1.00	168.18
	389	OG	SER	C	52	3.908	37.491	39.042	1.00	168.18
45	390	C	SER	C	52	4.726	39.783	36.194	1.00	228.11
	391	O	SER	C	52	3.692	39.843	35.528	1.00	228.11
	392	N	LEU	C	53	5.919	40.096	35.708	1.00	153.71
	393	CA	LEU	C	53	6.111	40.542	34.332	1.00	153.71
	394	CB	LEU	C	53	7.219	41.594	34.278	1.00	123.91
50	395	CG	LEU	C	53	7.891	41.882	32.939	1.00	123.91
	396	CD1	LEU	C	53	6.841	42.018	31.823	1.00	123.91
	397	CD2	LEU	C	53	8.744	43.157	33.084	1.00	123.91
	398	C	LEU	C	53	6.476	39.373	33.439	1.00	153.71
	399	O	LEU	C	53	7.604	38.887	33.461	1.00	153.71
55	400	N	ASN	C	54	5.514	38.918	32.655	1.00	221.05
	401	CA	ASN	C	54	5.772	37.804	31.773	1.00	221.05
	402	CB	ASN	C	54	4.474	37.081	31.431	1.00	192.59
	403	CG	ASN	C	54	3.924	36.312	32.601	1.00	192.59
	404	OD1	ASN	C	54	4.626	35.511	33.211	1.00	192.59
60	405	ND2	ASN	C	54	2.661	36.548	32.922	1.00	192.59
	406	C	ASN	C	54	6.477	38.221	30.497	1.00	221.05
	407	O	ASN	C	54	6.451	39.391	30.098	1.00	221.05
	408	N	ILE	C	55	7.116	37.234	29.873	1.00	249.69
	409	CA	ILE	C	55	7.850	37.402	28.624	1.00	249.69
65	410	CB	ILE	C	55	9.374	37.380	28.869	1.00	131.97
	411	CG2	ILE	C	55	10.103	36.988	27.599	1.00	131.97
	412	CG1	ILE	C	55	9.822	38.756	29.380	1.00	131.97
	413	CD1	ILE	C	55	11.301	38.863	29.665	1.00	131.97
	414	C	ILE	C	55	7.468	36.235	27.720	1.00	249.69
70	415	O	ILE	C	55	7.742	35.080	28.048	1.00	249.69

	416	N	VAL	C	56	6.829	36.531	26.595	1.00	201.86
	417	CA	VAL	C	56	6.422	35.474	25.687	1.00	201.86
	418	CB	VAL	C	56	5.043	35.759	25.089	1.00	231.54
	419	CG1	VAL	C	56	4.431	34.468	24.565	1.00	231.54
5	420	CG2	VAL	C	56	4.144	36.385	26.138	1.00	231.54
	421	C	VAL	C	56	7.454	35.345	24.578	1.00	201.86
	422	O	VAL	C	56	8.595	35.775	24.747	1.00	201.86
	423	N	ASN	C	57	7.056	34.758	23.451	1.00	157.94
	424	CA	ASN	C	57	7.953	34.542	22.310	1.00	157.94
10	425	CB	ASN	C	57	7.179	34.657	20.994	1.00	249.57
	426	CG	ASN	C	57	6.212	33.499	20.793	1.00	249.57
	427	OD1	ASN	C	57	6.593	32.333	20.911	1.00	249.57
	428	ND2	ASN	C	57	4.958	33.812	20.488	1.00	249.57
	429	C	ASN	C	57	9.147	35.472	22.324	1.00	157.94
15	430	O	ASN	C	57	9.103	36.592	21.825	1.00	157.94
	431	N	ALA	C	58	10.213	34.960	22.924	1.00	146.95
	432	CA	ALA	C	58	11.477	35.658	23.112	1.00	146.95
	433	CB	ALA	C	58	12.467	34.717	23.796	1.00	132.39
	434	C	ALA	C	58	12.122	36.270	21.878	1.00	146.95
20	435	O	ALA	C	58	12.657	35.566	21.014	1.00	146.95
	436	N	LYS	C	59	12.087	37.596	21.816	1.00	135.91
	437	CA	LYS	C	59	12.680	38.350	20.710	1.00	135.91
	438	CB	LYS	C	59	11.742	39.483	20.270	1.00	248.43
	439	CG	LYS	C	59	10.375	39.002	19.795	1.00	248.43
25	440	CD	LYS	C	59	?.???	40.157	19.482	1.00	248.43
	441	CE	LYS	C	59	8.053	39.641	19.094	1.00	248.43
	442	NZ	LYS	C	59	7.100	40.738	18.771	1.00	248.43
	443	C	LYS	C	59	13.986	38.928	21.228	1.00	135.91
	444	O	LYS	C	59	14.052	39.415	22.354	1.00	135.91
30	445	N	PHE	C	60	15.020	38.866	20.406	1.00	130.99
	446	CA	PHE	C	60	16.330	39.375	20.784	1.00	130.99
	447	CB	PHE	C	60	17.171	39.581	19.523	1.00	226.68
	448	CG	PHE	C	60	17.469	38.309	18.781	1.00	226.68
	449	CD1	PHE	C	60	17.704	38.327	17.410	1.00	226.68
35	450	CD2	PHE	C	60	17.535	37.093	19.458	1.00	226.68
	451	CE1	PHE	C	60	17.998	37.156	16.724	1.00	226.68
	452	CE2	PHE	C	60	17.829	35.919	18.782	1.00	226.68
	453	CZ	PHE	C	60	18.061	35.951	17.411	1.00	226.68
	454	C	PHE	C	60	16.296	40.672	21.597	1.00	130.99
40	455	O	PHE	C	60	17.171	40.914	22.439	1.00	130.99
	456	N	GLU	C	61	15.289	41.507	21.338	1.00	229.15
	457	CA	GLU	C	61	15.136	42.789	22.028	1.00	229.15
	458	CB	GLU	C	61	14.021	43.603	21.363	1.00	236.43
	459	CG	GLU	C	61	14.258	43.926	19.878	1.00	236.43
45	460	CD	GLU	C	61	14.424	42.686	19.003	1.00	236.43
	461	OE1	GLU	C	61	13.554	41.786	19.062	1.00	236.43
	462	OE2	GLU	C	61	15.423	42.616	18.250	1.00	236.43
	463	C	GLU	C	61	14.832	42.608	23.508	1.00	229.15
	464	O	GLU	C	61	15.107	43.491	24.316	1.00	229.15
50	465	N	ASP	C	62	14.260	41.456	23.849	1.00	169.19
	466	CA	ASP	C	62	13.926	41.142	25.233	1.00	169.19
	467	CB	ASP	C	62	13.066	39.884	25.316	1.00	219.70
	468	CG	ASP	C	62	11.857	39.951	24.419	1.00	219.70
	469	OD1	ASP	C	62	11.324	41.064	24.225	1.00	219.70
55	470	OD2	ASP	C	62	11.430	38.891	23.919	1.00	219.70
	471	C	ASP	C	62	15.184	40.932	26.066	1.00	169.19
	472	O	ASP	C	62	15.152	41.049	27.289	1.00	169.19
	473	N	SER	C	63	16.289	40.608	25.400	1.00	159.66
	474	CA	SER	C	63	17.564	40.400	26.084	1.00	159.66
60	475	CB	SER	C	63	18.659	39.965	25.089	1.00	141.40
	476	OG	SER	C	63	18.325	38.774	24.394	1.00	141.40
	477	C	SER	C	63	17.962	41.730	26.714	1.00	159.66
	478	O	SER	C	63	18.006	42.746	26.029	1.00	159.66
	479	N	GLY	C	64	18.242	41.730	28.009	1.00	163.83
65	480	CA	GLY	C	64	18.620	42.974	28.641	1.00	163.83
	481	C	GLY	C	64	18.666	42.973	30.154	1.00	163.83
	482	O	GLY	C	64	18.652	41.917	30.792	1.00	163.83
	483	N	GLU	C	65	18.719	44.181	30.713	1.00	155.20
	484	CA	GLU	C	65	18.792	44.422	32.152	1.00	155.20
70	485	CB	GLU	C	65	19.859	45.482	32.390	1.00	246.28

486	CG	GLU	C	65	19.972	45.990	33.800	1.00	246.28
487	CD	GLU	C	65	20.739	47.294	33.859	1.00	246.28
488	OE1	GLU	C	65	20.270	48.276	33.250	1.00	246.28
489	OE2	GLU	C	65	21.806	47.341	34.506	1.00	246.28
490	C	GLU	C	65	17.444	44.883	32.727	1.00	155.20
491	O	GLU	C	65	16.907	45.897	32.306	1.00	155.20
492	N	TYR	C	66	16.899	44.149	33.692	1.00	218.21
493	CA	TYR	C	66	15.614	44.507	34.299	1.00	218.21
494	CB	TYR	C	66	14.600	43.380	34.131	1.00	195.34
495	CG	TYR	C	66	14.195	43.050	32.722	1.00	195.34
496	CD1	TYR	C	66	15.027	42.319	31.889	1.00	195.34
497	CE1	TYR	C	66	14.607	41.929	30.619	1.00	195.34
498	CD2	TYR	C	66	12.934	43.398	32.250	1.00	195.34
499	CE2	TYR	C	66	12.505	43.016	30.985	1.00	195.34
500	CZ	TYR	C	66	13.342	42.277	30.175	1.00	195.34
501	OH	TYR	C	66	12.896	41.868	28.938	1.00	195.34
502	C	TYR	C	66	15.691	44.815	35.795	1.00	218.21
503	O	TYR	C	66	16.721	44.584	36.431	1.00	218.21
504	N	LYS	C	67	14.577	45.311	36.350	1.00	178.65
505	CA	LYS	C	67	14.467	45.652	37.782	1.00	178.65
506	CB	LYS	C	67	15.471	46.748	38.152	1.00	172.69
507	CG	LYS	C	67	15.399	47.981	37.275	1.00	172.69
508	CD	LYS	C	67	16.474	48.976	37.663	1.00	172.69
509	CE	LYS	C	67	16.722	50.003	36.565	1.00	172.69
510	NZ	LYS	C	67	17.749	51.022	36.952	1.00	172.69
511	C	LYS	C	67	13.078	46.103	38.229	1.00	178.65
512	O	LYS	C	67	12.289	46.623	37.437	1.00	178.65
513	N	CYS	C	68	12.794	45.898	39.512	1.00	193.02
514	CA	CYS	C	68	11.523	46.307	40.083	1.00	193.02
515	C	CYS	C	68	11.724	47.110	41.369	1.00	193.02
516	O	CYS	C	68	12.709	46.929	42.091	1.00	193.02
517	CB	CYS	C	68	10.604	45.104	40.336	1.00	142.23
518	SG	CYS	C	68	11.079	43.935	41.620	1.00	142.23
519	N	GLN	C	69	10.780	48.008	41.636	1.00	226.79
520	CA	GLN	C	69	10.806	48.882	42.802	1.00	226.79
521	CB	GLN	C	69	11.511	50.191	42.437	1.00	248.82
522	CG	GLN	C	69	11.193	51.363	43.344	1.00	248.82
523	CD	GLN	C	69	11.804	52.664	42.851	1.00	248.82
524	OE1	GLN	C	69	11.623	53.050	41.694	1.00	248.82
525	NE2	GLN	C	69	12.526	53.352	43.730	1.00	248.82
526	C	GLN	C	69	9.370	49.163	43.221	1.00	226.79
527	O	GLN	C	69	8.470	49.208	42.382	1.00	226.79
528	N	HIS	C	70	9.149	49.349	44.515	1.00	241.71
529	CA	HIS	C	70	7.806	49.635	45.003	1.00	241.71
530	CB	HIS	C	70	7.524	48.852	46.292	1.00	246.85
531	CG	HIS	C	70	7.366	47.378	46.075	1.00	246.85
532	CD2	HIS	C	70	7.971	46.319	46.666	1.00	246.85
533	ND1	HIS	C	70	6.487	46.852	45.155	1.00	246.85
534	CE1	HIS	C	70	6.56	45.530	45.184	1.00	246.85
535	NE2	HIS	C	70	7.448	45.184	46.094	1.00	246.85
536	C	HIS	C	70	7.601	51.127	45.236	1.00	241.71
537	O	HIS	C	70	8.435	51.946	44.851	1.00	241.71
538	N	GLN	C	71	6.485	51.470	45.872	1.00	248.91
539	CA	GLN	C	71	6.139	52.861	46.161	1.00	248.91
540	CB	GLN	C	71	4.804	52.897	46.835	1.00	249.69
541	CG	GLN	C	71	4.049	54.235	46.919	1.00	249.69
542	CD	GLN	C	71	3.630	54.682	45.519	1.00	249.69
543	OE1	GLN	C	71	3.071	53.904	44.741	1.00	249.69
544	NE2	GLN	C	71	3.889	55.949	45.201	1.00	249.69
545	C	GLN	C	71	7.243	53.579	46.956	1.00	248.91
546	O	GLN	C	71	7.670	54.680	46.599	1.00	248.91
547	N	GLN	C	72	7.705	52.942	48.026	1.00	236.85
548	CA	GLN	C	72	8.741	53.519	48.875	1.00	236.85
549	CB	GLN	C	72	8.117	53.962	50.201	1.00	249.69
550	CG	GLN	C	72	9.064	54.624	51.198	1.00	249.69
551	CD	GLN	C	72	8.391	54.885	52.545	1.00	249.69
552	OE1	GLN	C	72	7.360	55.560	52.617	1.00	249.69
553	NE2	GLN	C	72	8.973	54.348	53.617	1.00	249.69
554	C	GLN	C	72	9.860	52.501	49.127	1.00	236.85
555	O	GLN	C	72	10.188	52.188	50.274	1.00	236.85

Line	Serial	Atom	Res	Chain	ResNum	X	Y	Z	Occ	B
	556	N	VAL	C	73	10.435	51.975	48.050	1.00	249.69
	557	CA	VAL	C	73	11.519	51.001	48.163	1.00	249.69
	558	CB	VAL	C	73	11.016	49.546	47.988	1.00	190.27
	559	CG1	VAL	C	73	12.100	48.583	48.424	1.00	190.27
5	560	CG2	VAL	C	73	9.740	49.315	48.789	1.00	190.27
	561	C	VAL	C	73	12.547	51.280	47.077	1.00	249.69
	562	O	VAL	C	73	12.195	51.074	45.966	1.00	249.69
	563	N	ASN	C	74	13.819	51.080	47.397	1.00	225.53
	564	CA	ASN	C	74	14.877	51.314	46.426	1.00	225.53
10	565	CB	ASN	C	74	16.220	51.480	47.153	1.00	240.44
	566	CG	ASN	C	74	16.174	52.577	48.221	1.00	240.44
	567	OD1	ASN	C	74	15.597	53.643	47.999	1.00	240.44
	568	ND2	ASN	C	74	16.786	52.316	49.374	1.00	240.44
	569	C	ASN	C	74	14.929	50.162	45.407	1.00	225.53
15	570	O	ASN	C	74	14.963	48.987	45.778	1.00	225.53
	571	N	GLU	C	75	14.918	50.516	44.123	1.00	249.69
	572	CA	GLU	C	75	14.943	49.543	43.030	1.00	249.69
	573	CB	GLU	C	75	15.262	50.260	41.708	1.00	249.60
	574	CG	GLU	C	75	16.260	51.104	41.834	1.00	249.60
20	575	CD	GLU	C	75	16.362	52.238	40.567	1.00	249.60
	576	OE1	GLU	C	75	15.308	52.660	40.046	1.00	249.60
	577	OE2	GLU	C	75	17.493	52.480	40.096	1.00	249.60
	578	C	GLU	C	75	15.886	48.356	43.233	1.00	249.69
	579	O	GLU	C	75	16.998	48.508	43.733	1.00	249.69
25	580	N	SER	C	76	15.421	47.175	42.830	1.00	230.56
	581	CA	SER	C	76	16.178	45.932	42.968	1.00	230.56
	582	CB	SER	C	76	15.307	44.734	42.596	1.00	187.63
	583	OG	SER	C	76	15.123	44.661	41.190	1.00	187.63
	584	C	SER	C	76	17.435	45.877	42.115	1.00	230.56
30	585	O	SER	C	76	17.565	46.600	41.124	1.00	230.56
	586	N	GLU	C	77	18.356	45.002	42.510	1.00	249.20
	587	CA	GLU	C	77	19.602	44.825	41.778	1.00	249.20
	588	CB	GLU	C	77	20.531	43.861	42.527	1.00	249.69
	589	CG	GLU	C	77	21.030	44.390	43.870	1.00	249.69
35	590	CD	GLU	C	77	21.895	45.639	43.734	1.00	249.69
	591	OE1	GLU	C	77	22.002	46.187	42.611	1.00	249.69
	592	OE2	GLU	C	77	22.468	46.078	44.755	1.00	249.69
	593	C	GLU	C	77	19.257	44.256	40.410	1.00	249.20
	594	O	GLU	C	77	18.786	43.124	40.304	1.00	249.20
40	595	N	PRO	C	78	19.492	45.042	39.346	1.00	211.01
	596	CD	PRO	C	78	20.275	46.292	39.342	1.00	171.69
	597	CA	PRO	C	78	19.193	44.608	37.977	1.00	211.01
	598	CB	PRO	C	78	20.023	45.581	37.127	1.00	171.69
	599	CG	PRO	C	78	20.054	46.826	37.951	1.00	171.69
45	600	C	PRO	C	78	19.580	43.155	37.720	1.00	211.01
	601	O	PRO	C	78	20.416	42.597	38.420	1.00	211.01
	602	N	VAL	C	79	18.950	42.537	36.728	1.00	200.35
	603	CA	VAL	C	79	19.282	41.166	36.344	1.00	200.35
	604	CB	VAL	C	79	18.203	40.146	36.754	1.00	129.43
50	605	CG1	VAL	C	79	18.471	38.805	36.090	1.00	129.43
	606	CG2	VAL	C	79	18.208	39.966	38.259	1.00	129.43
	607	C	VAL	C	79	19.371	41.203	34.835	1.00	200.35
	608	O	VAL	C	79	18.589	41.902	34.191	1.00	200.35
	609	N	TYR	C	80	20.324	40.476	34.262	1.00	130.20
55	610	CA	TYR	C	80	20.458	40.495	32.817	1.00	130.20
	611	CB	TYR	C	80	21.910	40.686	32.410	1.00	206.89
	612	CG	TYR	C	80	22.046	41.126	30.971	1.00	206.89
	613	CD1	TYR	C	80	21.927	42.471	30.618	1.00	206.89
	614	CE1	TYR	C	80	22.011	42.880	29.290	1.00	206.89
60	615	CD2	TYR	C	80	22.254	40.199	29.954	1.00	206.89
	616	CE2	TYR	C	80	22.341	40.598	28.621	1.00	206.89
	617	CZ	TYR	C	80	22.217	41.939	28.299	1.00	206.89
	618	OH	TYR	C	80	22.299	42.339	26.988	1.00	206.89
	619	C	TYR	C	80	19.928	39.237	32.170	1.00	130.20
65	620	O	TYR	C	80	20.195	38.133	32.638	1.00	130.20
	621	N	LEU	C	81	19.172	39.406	31.093	1.00	124.74
	622	CA	LEU	C	81	18.624	38.266	30.390	1.00	124.74
	623	CB	LEU	C	81	17.103	38.367	30.285	1.00	90.50
	624	CG	LEU	C	81	16.470	37.260	29.428	1.00	90.50
70	625	CD1	LEU	C	81	16.710	35.944	30.122	1.00	90.50

	626	CD2	LEU	C	81	14.994	37.467	29.222	1.00	90.50
	627	C	LEU	C	81	19.216	38.222	28.998	1.00	124.74
	628	O	LEU	C	81	19.179	39.232	28.300	1.00	124.74
	629	N	GLU	C	82	19.771	37.075	28.595	1.00	106.68
5	630	CA	GLU	C	82	20.322	36.967	27.253	1.00	106.68
	631	CB	GLU	C	82	21.797	36.601	27.305	1.00	249.60
	632	CG	GLU	C	82	22.564	37.080	26.079	1.00	249.60
	633	CD	GLU	C	82	24.041	36.748	26.143	1.00	249.60
	634	OE1	GLU	C	82	24.609	36.761	27.257	1.00	249.60
10	635	OE2	GLU	C	82	24.637	36.489	25.075	1.00	249.60
	636	C	GLU	C	82	19.546	35.917	26.454	1.00	106.68
	637	O	GLU	C	82	19.224	34.834	26.994	1.00	106.68
	638	N	VAL	C	83	19.234	36.244	25.186	1.00	145.59
	639	CA	VAL	C	83	18.513	35.318	24.292	1.00	145.59
15	640	CB	VAL	C	83	17.270	35.943	23.679	1.00	134.02
	641	CG1	VAL	C	83	16.562	34.914	22.796	1.00	134.02
	642	CG2	VAL	C	83	16.343	36.429	24.781	1.00	134.02
	643	C	VAL	C	83	19.417	34.835	23.164	1.00	145.59
	644	O	VAL	C	83	20.212	35.603	22.600	1.00	145.59
20	645	N	PHE	C	84	19.259	33.562	22.822	1.00	150.61
	646	CA	PHE	C	84	20.117	32.945	21.833	1.00	150.61
	647	CB	PHE	C	84	21.072	31.978	22.515	1.00	134.04
	648	CG	PHE	C	84	21.985	32.603	23.516	1.00	134.04
	649	CD1	PHE	C	84	21.566	32.852	24.818	1.00	134.04
25	650	CD2	PHE	C	84	23.282	32.918	23.158	1.00	134.04
	651	CE1	PHE	C	84	22.433	33.403	25.743	1.00	134.04
	652	CE2	PHE	C	84	24.151	33.468	24.078	1.00	134.04
	653	CZ	PHE	C	84	23.729	33.712	25.370	1.00	134.04
	654	C	PHE	C	84	19.487	32.151	20.719	1.00	150.61
30	655	O	PHE	C	84	18.363	31.654	20.842	1.00	176.12
	656	N	SER	C	85	20.276	31.999	19.653	1.00	176.12
	657	CA	SER	C	85	19.898	31.208	18.491	1.00	176.12
	658	CB	SER	C	85	19.635	32.073	17.269	1.00	141.64
	659	OG	SER	C	85	19.275	31.250	16.175	1.00	141.64
35	660	C	SER	C	85	21.092	30.334	18.214	1.00	176.12
	661	O	SER	C	85	22.171	30.838	17.876	1.00	176.12
	662	N	ASP	C	86	20.900	29.030	18.377	1.00	126.17
	663	CA	ASP	C	86	21.976	28.062	18.156	1.00	126.17
	664	CB	ASP	C	86	23.135	28.325	19.122	1.00	148.28
40	665	CG	ASP	C	86	24.477	28.085	18.490	1.00	148.28
	666	OD1	ASP	C	86	24.674	26.995	17.898	1.00	148.28
	667	OD2	ASP	C	86	25.329	28.999	18.587	1.00	148.28
	668	C	ASP	C	86	21.448	26.656	18.392	1.00	126.17
	669	O	ASP	C	86	20.356	26.480	18.922	1.00	126.17
45	670	N	TRP	C	87	22.220	25.650	18.003	1.00	154.85
	671	CA	TRP	C	87	21.780	24.277	18.204	1.00	154.85
	672	CB	TRP	C	87	22.714	23.312	17.473	1.00	249.47
	673	CG	TRP	C	87	22.275	23.058	16.067	1.00	249.47
	674	CD2	TRP	C	87	22.713	23.754	14.895	1.00	249.47
50	675	CE2	TRP	C	87	22.000	23.217	13.798	1.00	249.47
	676	CE3	TRP	C	87	23.645	24.782	14.661	1.00	249.47
	677	CD1	TRP	C	87	21.335	22.152	15.650	1.00	249.47
	678	NE1	TRP	C	87	21.165	22.243	14.290	1.00	249.47
	679	CZ2	TRP	C	87	22.184	23.670	12.489	1.00	249.47
55	680	CZ3	TRP	C	87	23.828	25.232	13.361	1.00	249.47
	681	CH2	TRP	C	87	23.098	24.675	12.291	1.00	249.47
	682	C	TRP	C	87	21.715	23.947	19.683	1.00	154.85
	683	O	TRP	C	87	20.676	23.513	20.170	1.00	154.85
	684	N	LEU	C	88	22.820	24.160	20.394	1.00	160.72
60	685	CA	LEU	C	88	22.851	23.888	21.820	1.00	160.72
	686	CB	LEU	C	88	23.811	22.726	22.122	1.00	161.67
	687	CG	LEU	C	88	23.421	21.360	21.543	1.00	161.67
	688	CD1	LEU	C	88	24.392	20.299	22.027	1.00	161.67
	689	CD2	LEU	C	88	22.005	21.001	21.965	1.00	161.67
65	690	C	LEU	C	88	23.251	25.124	22.623	1.00	160.72
	691	O	LEU	C	88	24.103	25.909	22.192	1.00	160.72
	692	N	LEU	C	89	22.613	25.306	23.780	1.00	139.08
	693	CA	LEU	C	89	22.929	26.426	24.654	1.00	139.08
	694	CB	LEU	C	89	21.801	27.440	24.663	1.00	166.24
70	695	CG	LEU	C	89	22.043	28.607	25.629	1.00	166.24

	696	CD1	LEU	C	89	23.405	29.250	25.356	1.00	166.24
	697	CD2	LEU	C	89	20.917	29.623	25.492	1.00	166.24
	698	C	LEU	C	89	23.123	25.891	26.057	1.00	139.08
	699	O	LEU	C	89	22.297	25.098	26.533	1.00	139.08
5	700	N	LEU	C	90	24.212	26.304	26.715	1.00	149.33
	701	CA	LEU	C	90	24.490	25.844	28.077	1.00	149.33
	702	CB	LEU	C	90	25.993	25.806	28.323	1.00	143.04
	703	CG	LEU	C	90	26.370	25.474	29.765	1.00	143.04
	704	CD1	LEU	C	90	25.808	24.104	30.144	1.00	143.04
10	705	CD2	LEU	C	90	27.884	25.509	29.938	1.00	143.04
	706	C	LEU	C	90	23.834	26.755	29.106	1.00	149.33
	707	O	LEU	C	90	24.213	27.914	29.243	1.00	149.33
	708	N	GLN	C	91	22.861	26.226	29.839	1.00	125.14
	709	CA	GLN	C	91	22.166	27.026	30.825	1.00	125.14
15	710	CB	GLN	C	91	20.656	26.784	30.745	1.00	164.13
	711	CG	GLN	C	91	20.043	27.113	29.398	1.00	164.13
	712	CD	GLN	C	91	18.552	26.873	29.373	1.00	164.13
	713	OE1	GLN	C	91	18.078	25.769	29.661	1.00	164.13
	714	NE2	GLN	C	91	17.799	27.910	29.035	1.00	164.13
20	715	C	GLN	C	91	22.633	26.746	32.238	1.00	125.14
	716	O	GLN	C	91	22.832	25.583	32.625	1.00	125.14
	717	N	ALA	C	92	22.787	27.820	33.014	1.00	120.03
	718	CA	ALA	C	92	23.217	27.706	34.404	1.00	120.03
	719	CB	ALA	C	92	24.586	28.363	34.567	1.00	230.41
25	720	C	ALA	C	92	22.204	28.360	35.331	1.00	120.03
	721	O	ALA	C	92	21.618	29.392	34.993	1.00	120.03
	722	N	SER	C	93	22.009	27.738	36.490	1.00	162.82
	723	CA	SER	C	93	21.091	28.244	37.499	1.00	162.82
	724	CB	SER	C	93	21.158	27.396	38.784	1.00	102.92
30	725	OG	SER	C	93	22.476	27.269	39.270	1.00	102.92
	726	C	SER	C	93	21.472	29.682	37.798	1.00	162.82
	727	O	SER	C	93	20.699	30.618	37.567	1.00	162.82
	728	N	ALA	C	94	22.679	29.849	38.313	1.00	108.42
	729	CA	ALA	C	94	23.224	31.174	38.620	1.00	108.42
35	730	CB	ALA	C	94	23.252	31.403	40.121	1.00	218.96
	731	C	ALA	C	94	24.643	31.150	38.051	1.00	108.42
	732	O	ALA	C	94	25.237	30.083	37.932	1.00	108.42
	733	N	GLU	C	95	25.180	32.303	37.678	1.00	153.28
	734	CA	GLU	C	95	26.518	32.317	37.122	1.00	153.28
40	735	CB	GLU	C	95	26.615	33.364	36.025	1.00	202.07
	736	CG	GLU	C	95	25.708	33.060	34.858	1.00	202.07
	737	CD	GLU	C	95	25.982	33.949	33.677	1.00	202.07
	738	OE1	GLU	C	95	25.257	33.821	32.668	1.00	202.07
	739	OE2	GLU	C	95	26.925	34.772	33.751	1.00	202.07
45	740	C	GLU	C	95	27.586	32.559	38.176	1.00	153.28
	741	O	GLU	C	95	28.757	32.209	37.973	1.00	153.28
	742	N	VAL	C	96	27.180	33.151	39.302	1.00	129.17
	743	CA	VAL	C	96	28.105	33.428	40.407	1.00	129.17
	744	CB	VAL	C	96	28.289	34.930	40.613	1.00	121.01
50	745	CG1	VAL	C	96	29.526	35.175	41.441	1.00	121.01
	746	CG2	VAL	C	96	28.379	35.630	39.273	1.00	121.01
	747	C	VAL	C	96	27.548	32.826	41.694	1.00	129.17
	748	O	VAL	C	96	26.380	33.012	42.009	1.00	129.17
	749	N	VAL	C	97	28.383	32.123	42.449	1.00	144.84
55	750	CA	VAL	C	97	27.885	31.495	43.658	1.00	144.84
	751	CB	VAL	C	97	27.584	30.011	43.391	1.00	123.55
	752	CG1	VAL	C	97	26.631	29.492	44.443	1.00	123.55
	753	CG2	VAL	C	97	27.013	29.816	42.007	1.00	123.55
	754	C	VAL	C	97	28.756	31.574	44.921	1.00	144.84
60	755	O	VAL	C	97	29.987	31.649	44.847	1.00	144.84
	756	N	MET	C	98	28.083	31.537	46.073	1.00	143.10
	757	CA	MET	C	98	28.713	31.568	47.396	1.00	143.10
	758	CB	MET	C	98	27.725	32.094	48.440	1.00	249.69
	759	CG	MET	C	98	27.288	33.530	48.256	1.00	249.69
65	760	SD	MET	C	98	28.558	34.688	48.776	1.00	249.69
	761	CE	MET	C	98	28.400	34.595	50.561	1.00	249.69
	762	C	MET	C	98	29.093	30.140	47.792	1.00	143.10
	763	O	MET	C	98	28.224	29.260	47.820	1.00	143.10
	764	N	GLU	C	99	30.366	29.905	48.115	1.00	134.64
70	765	CA	GLU	C	99	30.817	28.560	48.495	1.00	134.64

766	CB	GLU	C	99	32.113	28.640	49.296	1.00	249.69
767	CG	GLU	C	99	32.854	27.373	49.225	1.00	249.69
768	CD	GLU	C	99	34.077	27.361	50.242	1.00	249.69
769	OE1	GLU	C	99	34.676	28.433	50.488	1.00	249.69
770	OE2	GLU	C	99	34.370	26.275	50.787	1.00	249.69
771	C	GLU	C	99	29.760	27.848	49.328	1.00	134.64
772	O	GLU	C	99	29.307	28.382	50.333	1.00	134.64
773	N	GLY	C	100	29.348	26.660	48.899	1.00	174.64
774	CA	GLY	C	100	28.349	25.925	49.654	1.00	174.64
775	C	GLY	C	100	26.950	25.885	49.070	1.00	174.64
776	O	GLY	C	100	26.164	25.012	49.424	1.00	174.64
777	N	GLN	C	101	26.630	26.825	48.185	1.00	145.91
778	CA	GLN	C	101	25.309	26.876	47.562	1.00	145.91
779	CB	GLN	C	101	25.060	28.258	46.960	1.00	202.42
780	CG	GLN	C	101	24.842	29.331	47.995	1.00	202.42
781	CD	GLN	C	101	23.913	28.865	49.091	1.00	202.42
782	OE1	GLN	C	101	24.266	27.997	49.893	1.00	202.42
783	NE2	GLN	C	101	22.712	29.428	49.123	1.00	202.42
784	C	GLN	C	101	25.106	25.805	46.487	1.00	145.91
785	O	GLN	C	101	26.031	25.063	46.149	1.00	145.91
786	N	PRO	C	102	23.886	25.701	45.939	1.00	126.29
787	CD	PRO	C	102	22.626	26.310	46.410	1.00	226.98
788	CA	PRO	C	102	23.621	24.698	44.908	1.00	126.29
789	CB	PRO	C	102	22.151	24.385	45.124	1.00	226.98
790	CG	PRO	C	102	21.598	25.737	45.443	1.00	226.98
791	C	PRO	C	102	23.911	25.213	43.497	1.00	126.29
792	O	PRO	C	102	23.787	26.412	43.199	1.00	126.29
793	N	LEU	C	103	24.286	24.291	42.620	1.00	131.06
794	CA	LEU	C	103	24.592	24.644	41.240	1.00	131.06
795	CB	LEU	C	103	26.086	24.692	41.058	1.00	130.31
796	CG	LEU	C	103	26.385	25.294	39.703	1.00	130.31
797	CD1	LEU	C	103	25.983	26.756	39.788	1.00	130.31
798	CD2	LEU	C	103	27.857	25.143	39.332	1.00	130.31
799	C	LEU	C	103	24.020	23.658	40.214	1.00	131.06
800	O	LEU	C	103	24.265	22.458	40.297	1.00	131.06
801	N	PHE	C	104	23.267	24.151	39.239	1.00	115.91
802	CA	PHE	C	104	22.698	23.265	38.229	1.00	115.91
803	CB	PHE	C	104	21.177	23.174	38.354	1.00	184.63
804	CG	PHE	C	104	20.701	22.781	39.706	1.00	184.63
805	CD1	PHE	C	104	20.673	23.704	40.748	1.00	184.63
806	CD2	PHE	C	104	20.284	21.483	39.950	1.00	184.63
807	CE1	PHE	C	104	20.232	23.335	42.025	1.00	184.63
808	CE2	PHE	C	104	19.841	21.104	41.225	1.00	184.63
809	CZ	PHE	C	104	19.815	22.034	42.264	1.00	184.63
810	C	PHE	C	104	23.026	23.754	36.826	1.00	115.91
811	O	PHE	C	104	22.731	24.898	36.464	1.00	115.91
812	N	LEU	C	105	23.636	22.890	36.025	1.00	135.47
813	CA	LEU	C	105	23.955	23.247	34.643	1.00	135.47
814	CB	LEU	C	105	25.417	23.009	34.331	1.00	111.96
815	CG	LEU	C	105	26.347	23.800	35.242	1.00	111.96
816	CD1	LEU	C	105	27.796	23.589	34.767	1.00	111.96
817	CD2	LEU	C	105	25.961	25.269	35.233	1.00	111.96
818	C	LEU	C	105	23.101	22.381	33.740	1.00	135.47
819	O	LEU	C	105	22.734	21.264	34.094	1.00	135.47
820	N	ARG	C	106	22.782	22.888	32.564	1.00	142.54
821	CA	ARG	C	106	21.928	22.134	31.679	1.00	142.54
822	CB	ARG	C	106	20.500	22.619	31.876	1.00	187.32
823	CG	ARG	C	106	19.479	21.927	31.044	1.00	187.32
824	CD	ARG	C	106	18.129	22.598	31.190	1.00	187.32
825	NE	ARG	C	106	17.177	22.007	30.262	1.00	187.32
826	CZ	ARG	C	106	16.158	22.658	29.719	1.00	187.32
827	NH1	ARG	C	106	15.956	23.937	30.020	1.00	187.32
828	NH2	ARG	C	106	15.359	22.032	28.858	1.00	187.32
829	C	ARG	C	106	22.347	22.297	30.232	1.00	142.54
830	O	ARG	C	106	22.485	23.424	29.750	1.00	142.54
831	N	CYS	C	107	22.580	21.177	29.547	1.00	145.66
832	CA	CYS	C	107	22.950	21.221	28.129	1.00	145.66
833	C	CYS	C	107	21.612	21.282	27.439	1.00	145.66
834	O	CYS	C	107	20.923	20.257	27.350	1.00	145.66
835	CB	CYS	C	107	23.679	19.945	27.717	1.00	147.17

	836	SG	CYS	C	107	24.521	20.003	26.086	1.00	147.17
	837	N	HIS	C	108	21.242	22.477	26.975	1.00	187.51
	838	CA	HIS	C	108	19.945	22.697	26.334	1.00	187.51
	839	CB	HIS	C	108	19.369	24.051	26.763	1.00	249.50
5	840	CG	HIS	C	108	17.934	24.251	26.389	1.00	249.50
	841	CD2	HIS	C	108	17.311	25.271	25.756	1.00	249.50
	842	ND1	HIS	C	108	16.945	23.348	26.724	1.00	249.50
	843	CE1	HIS	C	108	15.777	23.808	26.317	1.00	249.50
	844	NE2	HIS	C	108	15.969	24.974	25.727	1.00	249.50
10	845	C	HIS	C	108	19.929	22.622	24.824	1.00	187.51
	846	O	HIS	C	108	20.677	23.334	24.148	1.00	187.51
	847	N	GLY	C	109	19.049	21.765	24.310	1.00	207.18
	848	CA	GLY	C	109	18.916	21.601	22.879	1.00	207.18
	849	C	GLY	C	109	17.989	22.668	22.337	1.00	207.18
15	850	O	GLY	C	109	17.304	23.341	23.106	1.00	207.18
	851	N	TRP	C	110	17.976	22.837	21.017	1.00	133.19
	852	CA	TRP	C	110	17.119	23.828	20.384	1.00	133.19
	853	CB	TRP	C	110	17.724	24.269	19.044	1.00	164.64
	854	CG	TRP	C	110	16.806	25.128	18.221	1.00	164.64
20	855	CD2	TRP	C	110	16.829	26.561	18.110	1.00	164.64
	856	CE2	TRP	C	110	15.742	26.928	17.286	1.00	164.64
	857	CE3	TRP	C	110	17.659	27.566	18.625	1.00	164.64
	858	CD1	TRP	C	110	15.753	24.710	17.479	1.00	164.64
	859	NE1	TRP	C	110	15.103	25.780	16.917	1.00	164.64
25	860	CZ2	TRP	C	110	15.460	28.261	16.964	1.00	164.64
	861	CZ3	TRP	C	110	17.380	28.901	18.301	1.00	164.64
	862	CH2	TRP	C	110	16.285	29.231	17.474	1.00	164.64
	863	C	TRP	C	110	15.711	23.243	20.194	1.00	133.19
	864	O	TRP	C	110	15.535	22.018	20.064	1.00	133.19
30	865	N	ARG	C	111	14.709	24.124	20.194	1.00	142.65
	866	CA	ARG	C	111	13.309	23.711	20.051	1.00	142.65
	867	CB	ARG	C	111	13.020	23.259	18.618	1.00	249.69
	868	CG	ARG	C	111	12.569	24.383	17.699	1.00	249.69
	869	CD	ARG	C	111	11.976	23.832	16.409	1.00	249.69
35	870	NE	ARG	C	111	10.799	24.593	16.004	1.00	249.69
	871	CZ	ARG	C	111	9.704	24.725	16.755	1.00	249.69
	872	NH1	ARG	C	111	9.634	24.144	17.952	1.00	249.69
	873	NH2	ARG	C	111	8.674	25.440	16.311	1.00	249.69
	874	C	ARG	C	111	12.979	22.588	21.013	1.00	142.65
40	875	O	ARG	C	111	12.125	21.759	20.747	1.00	142.65
	876	N	ASN	C	112	13.675	22.582	22.137	1.00	230.43
	877	CA	ASN	C	112	13.477	21.574	23.156	1.00	230.43
	878	CB	ASN	C	112	12.133	21.797	23.858	1.00	249.69
	879	CG	ASN	C	112	12.030	21.045	25.178	1.00	249.69
45	880	OD1	ASN	C	112	12.829	20.147	25.466	1.00	249.69
	881	ND2	ASN	C	112	11.036	21.404	25.983	1.00	249.69
	882	C	ASN	C	112	13.531	20.163	22.573	1.00	230.43
	883	O	ASN	C	112	12.862	19.257	23.075	1.00	230.43
	884	N	TRP	C	113	14.310	19.970	21.511	1.00	206.47
50	885	CA	TRP	C	113	14.426	18.637	20.916	1.00	206.47
	886	CB	TRP	C	113	15.220	18.665	19.611	1.00	233.56
	887	CG	TRP	C	113	14.430	19.060	18.428	1.00	233.56
	888	CD2	TRP	C	113	14.905	19.800	17.309	1.00	233.56
	889	CE2	TRP	C	113	13.832	19.895	16.392	1.00	233.56
55	890	CE3	TRP	C	113	16.129	20.395	16.990	1.00	233.56
	891	CD1	TRP	C	113	13.132	18.740	18.158	1.00	233.56
	892	NE1	TRP	C	113	12.764	19.239	16.937	1.00	233.56
	893	CZ2	TRP	C	113	13.952	20.566	15.166	1.00	233.56
	894	CZ3	TRP	C	113	16.253	21.061	15.772	1.00	233.56
60	895	CH2	TRP	C	113	15.165	21.139	14.873	1.00	233.56
	896	C	TRP	C	113	15.137	17.714	21.887	1.00	206.47
	897	O	TRP	C	113	15.328	18.062	23.050	1.00	206.47
	898	N	ASP	C	114	15.535	16.540	21.408	1.00	249.46
	899	CA	ASP	C	114	16.242	15.589	22.256	1.00	249.46
65	900	CB	ASP	C	114	15.542	14.218	22.229	1.00	249.69
	901	CG	ASP	C	114	14.352	14.137	23.189	1.00	249.69
	902	OD1	ASP	C	114	14.546	14.363	24.407	1.00	249.69
	903	OD2	ASP	C	114	13.227	13.838	22.729	1.00	249.69
	904	C	ASP	C	114	17.704	15.447	21.834	1.00	249.46
70	905	O	ASP	C	114	18.008	15.291	20.643	1.00	249.46

	906	N	VAL	C	115	18.602	15.512	22.818	1.00	150.51
	907	CA	VAL	C	115	20.027	15.388	22.545	1.00	150.51
	908	CB	VAL	C	115	20.831	16.572	23.147	1.00	133.46
	909	CG1	VAL	C	115	22.243	16.592	22.569	1.00	133.46
5	910	CG2	VAL	C	115	20.140	17.884	22.859	1.00	133.46
	911	C	VAL	C	115	20.559	14.078	23.135	1.00	150.51
	912	O	VAL	C	115	20.153	13.669	24.225	1.00	150.51
	913	N	TYR	C	116	21.468	13.432	22.404	1.00	198.57
	914	CA	TYR	C	116	22.066	12.170	22.826	1.00	198.57
10	915	CB	TYR	C	116	21.673	11.070	21.847	1.00	249.69
	916	CG	TYR	C	116	20.185	10.787	21.832	1.00	249.69
	917	CD1	TYR	C	116	19.350	11.339	20.856	1.00	249.69
	918	CE1	TYR	C	116	17.974	11.099	20.866	1.00	249.69
	919	CD2	TYR	C	116	19.608	9.987	22.816	1.00	249.69
15	920	CE2	TYR	C	116	18.241	9.741	22.838	1.00	249.69
	921	CZ	TYR	C	116	17.429	10.296	21.865	1.00	249.69
	922	OH	TYR	C	116	16.075	10.047	21.894	1.00	249.69
	923	C	TYR	C	116	23.582	12.257	22.914	1.00	198.57
	924	O	TYR	C	116	24.174	13.239	22.455	1.00	198.57
20	925	N	LYS	C	117	24.198	11.230	23.500	1.00	159.55
	926	CA	LYS	C	117	25.660	11.186	23.661	1.00	159.55
	927	CB	LYS	C	117	26.357	10.893	22.320	1.00	249.69
	928	CG	LYS	C	117	26.455	9.408	21.969	1.00	249.69
	929	CD	LYS	C	117	27.543	9.165	20.910	1.00	249.69
25	930	CE	LYS	C	117	28.915	9.642	21.399	1.00	249.69
	931	NZ	LYS	C	117	30.027	9.430	20.424	1.00	249.69
	932	C	LYS	C	117	26.242	12.486	24.245	1.00	159.55
	933	O	LYS	C	117	27.200	13.081	23.698	1.00	159.55
	934	N	VAL	C	118	25.675	12.904	25.371	1.00	141.55
30	935	CA	VAL	C	118	26.095	14.127	26.016	1.00	141.55
	936	CB	VAL	C	118	24.919	14.737	26.790	1.00	150.57
	937	CG1	VAL	C	118	25.416	15.626	27.908	1.00	150.57
	938	CG2	VAL	C	118	24.067	15.543	25.830	1.00	150.57
	939	C	VAL	C	118	27.305	14.028	26.927	1.00	141.55
35	940	O	VAL	C	118	27.466	13.067	27.672	1.00	141.55
	941	N	ILE	C	119	28.140	15.062	26.850	1.00	119.98
	942	CA	ILE	C	119	29.358	15.192	27.640	1.00	119.98
	943	CB	ILE	C	119	30.578	14.818	26.826	1.00	122.95
	944	CG2	ILE	C	119	31.814	14.861	27.700	1.00	122.95
40	945	CG1	ILE	C	119	30.368	13.438	26.214	1.00	122.95
	946	CD1	ILE	C	119	31.187	13.228	24.988	1.00	122.95
	947	C	ILE	C	119	29.528	16.649	28.029	1.00	119.98
	948	O	ILE	C	119	29.454	17.518	27.179	1.00	119.98
	949	N	TYR	C	120	29.744	16.919	29.310	1.00	136.43
45	950	CA	TYR	C	120	29.962	18.289	29.759	1.00	136.43
	951	CB	TYR	C	120	29.334	18.542	31.119	1.00	134.07
	952	CG	TYR	C	120	27.833	18.525	31.107	1.00	134.07
	953	CD1	TYR	C	120	27.125	17.332	31.234	1.00	134.07
	954	CE1	TYR	C	120	25.733	17.310	31.200	1.00	134.07
50	955	CD2	TYR	C	120	27.113	19.704	30.949	1.00	134.07
	956	CE2	TYR	C	120	25.721	19.705	30.912	1.00	134.07
	957	CZ	TYR	C	120	25.037	18.507	31.037	1.00	134.07
	958	OH	TYR	C	120	23.658	18.523	30.988	1.00	134.07
	959	C	TYR	C	120	31.455	18.459	29.877	1.00	136.43
55	960	O	TYR	C	120	32.171	17.497	30.131	1.00	136.43
	961	N	TYR	C	121	31.935	19.674	29.682	1.00	132.15
	962	CA	TYR	C	121	33.366	19.916	29.782	1.00	132.15
	963	CB	TYR	C	121	33.991	20.177	28.405	1.00	142.37
	964	CG	TYR	C	121	34.032	19.017	27.437	1.00	142.37
60	965	CD1	TYR	C	121	32.863	18.383	27.007	1.00	142.37
	966	CE1	TYR	C	121	32.889	17.388	26.038	1.00	142.37
	967	CD2	TYR	C	121	35.237	18.620	26.879	1.00	142.37
	968	CE2	TYR	C	121	35.284	17.616	25.900	1.00	142.37
	969	CZ	TYR	C	121	34.098	17.005	25.481	1.00	142.37
65	970	OH	TYR	C	121	34.141	16.024	24.499	1.00	142.37
	971	C	TYR	C	121	33.668	21.119	30.667	1.00	132.15
	972	O	TYR	C	121	33.025	22.159	30.543	1.00	132.15
	973	N	LYS	C	122	34.650	20.977	31.554	1.00	126.92
	974	CA	LYS	C	122	35.056	22.076	32.413	1.00	126.92
70	975	CB	LYS	C	122	34.793	21.754	33.878	1.00	206.28

976	CG	LYS	C	122	35.177	22.888	34.807	1.00	206.28
977	CD	LYS	C	122	35.209	22.420	36.238	1.00	206.28
978	CE	LYS	C	122	35.768	23.480	37.149	1.00	206.28
979	NZ	LYS	C	122	35.923	22.930	38.515	1.00	206.28
980	C	LYS	C	122	36.544	22.299	32.193	1.00	126.92
981	O	LYS	C	122	37.349	21.420	32.461	1.00	126.92
982	N	ASP	C	123	36.902	23.477	31.699	1.00	135.65
983	CA	ASP	C	123	38.294	23.827	31.435	1.00	135.65
984	CB	ASP	C	123	39.093	23.949	32.740	1.00	170.94
985	CG	ASP	C	123	38.763	25.212	33.507	1.00	170.94
986	OD1	ASP	C	123	38.780	26.308	32.904	1.00	170.94
987	OD2	ASP	C	123	38.496	25.117	34.721	1.00	170.94
988	C	ASP	C	123	38.987	22.847	30.509	1.00	135.65
989	O	ASP	C	123	40.082	22.372	30.818	1.00	135.65
990	N	GLY	C	124	38.345	22.547	29.378	1.00	178.68
991	CA	GLY	C	124	38.917	21.638	28.395	1.00	178.68
992	C	GLY	C	124	38.936	20.152	28.718	1.00	178.68
993	O	GLY	C	124	39.295	19.336	27.879	1.00	178.68
994	N	GLU	C	125	38.539	19.797	29.929	1.00	128.18
995	CA	GLU	C	125	38.536	18.407	30.368	1.00	128.18
996	CB	GLU	C	125	38.963	18.324	31.847	1.00	249.69
997	CG	GLU	C	125	40.422	18.660	32.115	1.00	249.69
998	CD	GLU	C	125	41.355	17.552	31.693	1.00	249.69
999	OE1	GLU	C	125	41.251	16.453	32.273	1.00	249.69
1000	OE2	GLU	C	125	42.189	17.777	30.786	1.00	249.69
1001	C	GLU	C	125	37.176	17.749	30.215	1.00	128.18
1002	O	GLU	C	125	36.149	18.395	30.403	1.00	128.18
1003	N	ALA	C	126	37.165	16.468	29.866	1.00	114.67
1004	CA	ALA	C	126	35.904	15.742	29.753	1.00	114.67
1005	CB	ALA	C	126	36.156	14.376	29.162	1.00	125.78
1006	C	ALA	C	126	35.397	15.622	31.195	1.00	114.67
1007	O	ALA	C	126	36.190	15.374	32.099	1.00	114.67
1008	N	LEU	C	127	34.101	15.788	31.437	1.00	136.95
1009	CA	LEU	C	127	33.633	15.718	32.816	1.00	136.95
1010	CB	LEU	C	127	33.090	17.062	33.235	1.00	112.43
1011	CG	LEU	C	127	33.259	17.216	34.734	1.00	112.43
1012	CD1	LEU	C	127	34.725	17.020	35.093	1.00	112.43
1013	CD2	LEU	C	127	32.768	18.588	35.170	1.00	112.43
1014	C	LEU	C	127	32.612	14.648	33.156	1.00	136.95
1015	O	LEU	C	127	32.870	13.803	34.019	1.00	136.95
1016	N	LYS	C	128	31.444	14.696	32.518	1.00	111.10
1017	CA	LYS	C	128	30.397	13.689	32.750	1.00	111.10
1018	CB	LYS	C	128	29.228	14.302	33.525	1.00	196.03
1019	CG	LYS	C	128	29.586	14.833	34.905	1.00	196.03
1020	CD	LYS	C	128	29.864	13.714	35.892	1.00	196.03
1021	CE	LYS	C	128	30.150	14.277	37.285	1.00	196.03
1022	NZ	LYS	C	128	30.192	13.214	38.329	1.00	196.03
1023	C	LYS	C	128	29.929	13.215	31.379	1.00	111.10
1024	O	LYS	C	128	30.196	13.874	30.360	1.00	111.10
1025	N	TYR	C	129	29.243	12.078	31.339	1.00	147.54
1026	CA	TYR	C	129	28.753	11.567	30.058	1.00	147.54
1027	CB	TYR	C	129	29.834	10.755	29.363	1.00	149.35
1028	CG	TYR	C	129	29.282	9.856	28.292	1.00	149.35
1029	CD1	TYR	C	129	29.066	10.331	27.005	1.00	149.35
1030	CE1	TYR	C	129	28.507	9.509	26.029	1.00	149.35
1031	CD2	TYR	C	129	28.929	8.534	28.584	1.00	149.35
1032	CE2	TYR	C	129	28.371	7.707	27.619	1.00	149.35
1033	CZ	TYR	C	129	28.161	8.194	26.340	1.00	149.35
1034	OH	TYR	C	129	27.613	7.363	25.373	1.00	149.35
1035	C	TYR	C	129	27.500	10.704	30.177	1.00	147.54
1036	O	TYR	C	129	27.384	9.893	31.098	1.00	147.54
1037	N	TRP	C	130	26.571	10.876	29.231	1.00	199.38
1038	CA	TRP	C	130	25.323	10.109	29.216	1.00	199.38
1039	CB	TRP	C	130	24.219	10.809	30.022	1.00	218.46
1040	CG	TRP	C	130	24.599	11.335	31.370	1.00	218.46
1041	CD2	TRP	C	130	24.246	10.782	32.632	1.00	218.46
1042	CE2	TRP	C	130	24.770	11.627	33.631	1.00	218.46
1043	CE3	TRP	C	130	23.517	9.648	33.029	1.00	218.46
1044	CD1	TRP	C	130	25.325	12.465	31.639	1.00	218.46
1045	NE1	TRP	C	130	25.431	12.652	32.992	1.00	218.46

	1046	CZ2	TRP	C	130	24.605	11.381	34.996	1.00	218.46
	1047	CZ3	TRP	C	130	23.349	9.398	34.390	1.00	218.46
	1048	CH2	TRP	C	130	23.895	10.258	35.357	1.00	218.46
	1049	C	TRP	C	130	24.794	9.910	27.794	1.00	199.38
5	1050	O	TRP	C	130	25.272	10.526	26.839	1.00	199.38
	1051	N	TYR	C	131	23.787	9.053	27.671	1.00	229.56
	1052	CA	TYR	C	131	23.148	8.778	26.386	1.00	229.56
	1053	CB	TYR	C	131	22.591	7.356	26.372	1.00	246.37
	1054	CG	TYR	C	131	22.180	6.894	24.998	1.00	246.37
10	1055	CD1	TYR	C	131	23.142	6.593	24.031	1.00	246.37
	1056	CE1	TYR	C	131	22.771	6.206	22.748	1.00	246.37
	1057	CD2	TYR	C	131	20.834	6.795	24.647	1.00	246.37
	1058	CE2	TYR	C	131	20.454	6.411	23.370	1.00	246.37
	1059	CZ	TYR	C	131	21.422	6.120	22.425	1.00	246.37
15	1060	OH	TYR	C	131	21.037	5.759	21.152	1.00	246.37
	1061	C	TYR	C	131	22.003	9.783	26.290	1.00	229.56
	1062	O	TYR	C	131	22.194	10.887	25.767	1.00	229.56
	1063	N	GLU	C	132	20.814	9.387	26.766	1.00	249.69
	1064	CA	GLU	C	132	19.674	10.303	26.812	1.00	249.69
20	1065	CB	GLU	C	132	18.455	9.632	27.444	1.00	249.69
	1066	CG	GLU	C	132	17.670	8.696	26.529	1.00	249.69
	1067	CD	GLU	C	132	16.251	9.186	26.293	1.00	249.69
	1068	OE1	GLU	C	132	15.815	10.108	27.021	1.00	249.69
	1069	OE2	GLU	C	132	15.566	8.651	25.388	1.00	249.69
25	1070	C	GLU	C	132	20.299	11.278	27.798	1.00	249.69
	1071	O	GLU	C	132	20.759	10.849	28.865	1.00	249.69
	1072	N	ASN	C	133	20.318	12.573	27.483	1.00	172.36
	1073	CA	ASN	C	133	21.034	13.476	28.374	1.00	172.36
	1074	CB	ASN	C	133	21.319	14.844	27.675	1.00	175.23
30	1075	CG	ASN	C	133	20.166	15.840	27.735	1.00	175.23
	1076	OD1	ASN	C	133	18.999	15.492	27.529	1.00	175.23
	1077	ND2	ASN	C	133	20.506	17.113	27.974	1.00	175.23
	1078	C	ASN	C	133	20.565	13.626	29.815	1.00	172.36
	1079	O	ASN	C	133	19.680	12.906	30.290	1.00	172.36
35	1080	N	HIS	C	134	21.238	14.521	30.522	1.00	165.75
	1081	CA	HIS	C	134	20.960	14.757	31.918	1.00	165.75
	1082	CB	HIS	C	134	21.912	13.910	32.756	1.00	249.69
	1083	CG	HIS	C	134	21.588	13.916	34.223	1.00	249.69
	1084	CD2	HIS	C	134	22.305	14.372	35.277	1.00	249.69
40	1085	ND1	HIS	C	134	20.407	13.441	34.715	1.00	249.69
	1086	CE1	HIS	C	134	20.390	13.599	36.041	1.00	249.69
	1087	NE2	HIS	C	134	21.526	14.161	36.397	1.00	249.69
	1088	C	HIS	C	134	21.166	16.233	32.200	1.00	165.75
	1089	O	HIS	C	134	21.223	17.050	31.285	1.00	165.75
45	1090	N	ASN	C	135	21.278	16.572	33.470	1.00	159.28
	1091	CA	ASN	C	135	21.467	17.948	33.879	1.00	159.28
	1092	CB	ASN	C	135	20.111	18.596	34.178	1.00	249.51
	1093	CG	ASN	C	135	19.266	18.779	32.923	1.00	249.51
	1094	OD1	ASN	C	135	19.783	19.248	31.903	1.00	249.51
50	1095	ND2	ASN	C	135	17.974	18.439	32.990	1.00	249.51
	1096	C	ASN	C	135	22.374	18.001	35.116	1.00	159.28
	1097	O	ASN	C	135	21.887	18.08C	36.253	1.00	159.28
	1098	N	ILE	C	136	23.692	17.946	34.884	1.00	134.89
	1099	CA	ILE	C	136	24.734	17.989	35.934	1.00	134.89
55	1100	CB	ILE	C	136	26.090	18.399	35.318	1.00	169.29
	1101	CG2	ILE	C	136	25.962	19.723	34.593	1.00	169.29
	1102	CG1	ILE	C	136	27.139	18.510	36.407	1.00	169.29
	1103	CD1	ILE	C	136	28.472	18.980	35.884	1.00	169.29
	1104	C	ILE	C	136	24.408	18.906	37.123	1.00	134.89
60	1105	O	ILE	C	136	24.498	20.125	37.049	1.00	134.89
	1106	N	SER	C	137	24.055	18.280	38.232	1.00	137.39
	1107	CA	SER	C	137	23.678	19.000	39.422	1.00	137.39
	1108	CB	SER	C	137	22.367	18.437	39.940	1.00	121.23
	1109	OG	SER	C	137	22.076	18.966	41.222	1.00	121.23
65	1110	C	SER	C	137	24.687	19.025	40.566	1.00	137.39
	1111	O	SER	C	137	25.458	18.081	40.775	1.00	137.39
	1112	N	ILE	C	138	24.647	20.113	41.331	1.00	121.18
	1113	CA	ILE	C	138	25.539	20.309	42.478	1.00	121.18
	1114	CB	ILE	C	138	26.683	21.238	42.109	1.00	97.12
70	1115	CG2	ILE	C	138	27.385	21.749	43.358	1.00	97.12

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	1116	CG1	ILE	C	138	27.646	20.502	41.187	1.00	97.12
	1117	CD1	ILE	C	138	28.637	21.411	40.528	1.00	97.12
	1118	C	ILE	C	138	24.814	20.886	43.697	1.00	121.18
	1119	O	ILE	C	138	24.212	21.966	43.651	1.00	121.18
5	1120	N	THR	C	139	24.890	20.145	44.796	1.00	175.86
	1121	CA	THR	C	139	24.253	20.532	46.042	1.00	175.86
	1122	CB	THR	C	139	24.065	19.297	46.929	1.00	224.21
	1123	OG1	THR	C	139	25.324	18.622	47.063	1.00	224.21
	1124	CG2	THR	C	139	23.061	18.341	46.298	1.00	224.21
10	1125	C	THR	C	139	25.144	21.539	46.745	1.00	175.86
	1126	O	THR	C	139	24.927	22.746	46.654	1.00	175.86
	1127	N	ASN	C	140	26.149	21.024	47.447	1.00	196.19
	1128	CA	ASN	C	140	27.111	21.852	48.165	1.00	196.19
	1129	CB	ASN	C	140	27.710	21.053	49.330	1.00	249.69
15	1130	CG	ASN	C	140	28.741	21.837	50.109	1.00	249.69
	1131	OD1	ASN	C	140	29.656	22.417	49.523	1.00	249.69
	1132	ND2	ASN	C	140	28.610	21.845	51.432	1.00	196.19
	1133	C	ASN	C	140	28.184	22.213	47.146	1.00	196.19
	1134	O	ASN	C	140	28.799	21.327	46.560	1.00	134.37
20	1135	N	ALA	C	141	28.400	23.507	46.932	1.00	134.37
	1136	CA	ALA	C	141	29.383	23.954	45.949	1.00	79.03
	1137	CB	ALA	C	141	28.834	25.131	45.148	1.00	134.37
	1138	C	ALA	C	141	30.763	24.317	46.507	1.00	134.37
	1139	O	ALA	C	141	30.896	25.112	47.452	1.00	119.18
25	1140	N	THR	C	142	31.793	23.724	45.898	1.00	119.18
	1141	CA	THR	C	142	33.183	23.954	46.281	1.00	209.05
	1142	CB	THR	C	142	34.057	22.720	46.002	1.00	209.05
	1143	OG1	THR	C	142	33.458	21.553	46.578	1.00	209.05
	1144	CG2	THR	C	142	35.431	22.907	46.602	1.00	119.18
30	1145	C	THR	C	142	33.691	25.093	45.416	1.00	119.18
	1146	O	THR	C	142	33.128	25.381	44.356	1.00	145.21
	1147	N	VAL	C	143	34.752	25.741	45.865	1.00	145.21
	1148	CA	VAL	C	143	35.299	26.836	45.096	1.00	137.97
	1149	CB	VAL	C	143	36.295	27.672	45.910	1.00	137.97
35	1150	CG1	VAL	C	143	37.596	26.915	46.096	1.00	137.97
	1151	CG2	VAL	C	143	36.549	28.993	45.202	1.00	145.21
	1152	C	VAL	C	143	36.023	26.287	43.879	1.00	145.21
	1153	O	VAL	C	143	36.183	26.981	42.881	1.00	198.77
	1154	N	GLU	C	144	36.469	25.040	43.956	1.00	198.77
40	1155	CA	GLU	C	144	37.176	24.445	42.833	1.00	249.69
	1156	CB	GLU	C	144	37.858	23.142	43.241	1.00	249.69
	1157	CG	GLU	C	144	38.885	23.312	44.330	1.00	249.69
	1158	CD	GLU	C	144	38.447	22.661	45.624	1.00	249.69
	1159	OE1	GLU	C	144	38.251	21.428	45.621	1.00	249.69
45	1160	OE2	GLU	C	144	38.293	23.377	46.639	1.00	198.77
	1161	C	GLU	C	144	36.217	24.179	41.694	1.00	198.77
	1162	O	GLU	C	144	36.656	23.892	40.581	1.00	130.51
	1163	N	ASP	C	145	34.912	24.274	41.969	1.00	130.51
	1164	CA	ASP	C	145	33.904	24.049	40.930	1.00	171.03
50	1165	CB	ASP	C	145	32.523	23.868	41.555	1.00	171.03
	1166	CG	ASP	C	145	32.326	22.490	42.136	1.00	171.03
	1167	OD1	ASP	C	145	32.478	21.503	41.380	1.00	171.03
	1168	OD2	ASP	C	145	32.011	22.392	43.340	1.00	130.51
	1169	C	ASP	C	145	33.863	25.213	39.839	1.00	130.51
55	1170	O	ASP	C	145	33.299	25.086	38.851	1.00	126.39
	1171	N	SER	C	146	34.461	26.342	40.327	1.00	126.39
	1172	CA	SER	C	146	34.505	27.546	39.491	1.00	126.60
	1173	CB	SER	C	146	35.120	28.723	40.270	1.00	126.60
	1174	OG	SER	C	146	34.403	29.041	41.449	1.00	126.39
60	1175	C	SER	C	146	35.343	27.301	38.244	1.00	126.39
	1176	O	SER	C	146	36.478	26.850	38.351	1.00	222.43
	1177	N	GLY	C	147	34.798	27.614	37.072	1.00	222.43
	1178	CA	GLY	C	147	35.550	27.410	35.846	1.00	222.43
	1179	C	GLY	C	147	34.769	27.771	34.607	1.00	222.43
65	1180	O	GLY	C	147	33.801	28.520	34.682	1.00	128.05
	1181	N	THR	C	148	35.187	27.236	33.463	1.00	128.05
	1182	CA	THR	C	148	34.508	27.506	32.186	1.00	134.31
	1183	CB	THR	C	148	35.474	28.253	31.201	1.00	134.31
	1184	OG1	THR	C	148	36.046	27.326	30.281	1.00	134.31
70	1185	CG2	THR	C	148	36.609	28.943	31.973		

	1186	C	THR	C	148	33.949	26.223	31.538	1.00	128.05
	1187	O	THR	C	148	34.679	25.363	31.076	1.00	128.05
	1188	N	TYR	C	149	32.634	26.114	31.517	1.00	106.87
	1189	CA	TYR	C	149	31.975	24.945	30.975	1.00	106.87
5	1190	CB	TYR	C	149	30.819	24.510	31.905	1.00	100.05
	1191	CG	TYR	C	149	31.204	24.226	33.336	1.00	100.05
	1192	CD1	TYR	C	149	31.489	25.254	34.210	1.00	100.05
	1193	CE1	TYR	C	149	31.799	24.992	35.538	1.00	100.05
	1194	CD2	TYR	C	149	31.247	22.922	33.816	1.00	100.05
10	1195	CE2	TYR	C	149	31.557	22.643	35.125	1.00	100.05
	1196	CZ	TYR	C	149	31.829	23.676	35.993	1.00	100.05
	1197	OH	TYR	C	149	32.111	23.390	37.325	1.00	100.05
	1198	C	TYR	C	149	31.404	25.100	29.567	1.00	106.87
	1199	O	TYR	C	149	31.228	26.210	29.077	1.00	106.87
15	1200	N	TYR	C	150	31.105	23.953	28.946	1.00	107.82
	1201	CA	TYR	C	150	30.490	23.838	27.614	1.00	107.82
	1202	CB	TYR	C	150	31.451	24.307	26.499	1.00	160.56
	1203	CG	TYR	C	150	32.523	23.336	26.058	1.00	160.56
	1204	CD1	TYR	C	150	32.201	22.195	25.317	1.00	160.56
20	1205	CE1	TYR	C	150	33.199	21.307	24.872	1.00	160.56
	1206	CD2	TYR	C	150	33.576	23.576	26.351	1.00	160.56
	1207	CE2	TYR	C	150	34.880	22.698	25.912	1.00	160.56
	1208	CZ	TYR	C	150	34.533	21.564	25.169	1.00	160.56
	1209	OH	TYR	C	150	35.507	20.693	24.719	1.00	160.56
25	1210	C	TYR	C	150	30.111	22.370	27.462	1.00	107.82
	1211	O	TYR	C	150	30.700	21.521	28.119	1.00	107.82
	1212	N	CYS	C	151	29.112	22.074	26.641	1.00	88.46
	1213	CA	CYS	C	151	28.711	20.694	26.450	1.00	88.46
	1214	C	CYS	C	151	28.660	20.293	24.976	1.00	88.46
30	1215	O	CYS	C	151	28.585	21.155	24.103	1.00	88.46
	1216	CB	CYS	C	151	27.359	20.425	27.087	1.00	149.34
	1217	SG	CYS	C	151	25.995	21.380	26.366	1.00	149.34
	1218	N	THR	C	152	28.711	18.981	24.715	1.00	145.00
	1219	CA	THR	C	152	28.675	18.446	23.358	1.00	145.00
35	1220	CB	THR	C	152	30.034	17.838	22.951	1.00	154.69
	1221	OG1	THR	C	152	30.213	16.582	23.614	1.00	154.69
	1222	CG2	THR	C	152	31.182	18.762	23.334	1.00	154.69
	1223	C	THR	C	152	27.631	17.343	23.278	1.00	145.00
	1224	O	THR	C	152	27.420	16.609	24.240	1.00	145.00
40	1225	N	GLY	C	153	26.988	17.213	22.125	1.00	161.71
	1226	CA	GLY	C	153	25.980	16.180	21.982	1.00	161.71
	1227	C	GLY	C	153	25.515	15.979	20.558	1.00	161.71
	1228	O	GLY	C	153	25.830	16.783	19.670	1.00	161.71
	1229	N	LYS	C	154	24.759	14.905	20.345	1.00	155.18
45	1230	CA	LYS	C	154	24.249	14.582	19.022	1.00	155.18
	1231	CB	LYS	C	154	24.531	13.110	18.710	1.00	249.69
	1232	CG	LYS	C	154	24.159	12.677	17.303	1.00	249.69
	1233	CD	LYS	C	154	24.540	11.227	17.071	1.00	249.69
	1234	CE	LYS	C	154	24.106	10.749	15.692	1.00	249.69
50	1235	NZ	LYS	C	154	24.460	9.317	15.459	1.00	249.69
	1236	C	LYS	C	154	22.748	14.876	18.895	1.00	155.18
	1237	O	LYS	C	154	21.927	14.291	19.599	1.00	155.18
	1238	N	VAL	C	155	22.410	15.798	17.993	1.00	207.77
	1239	CA	VAL	C	155	21.031	16.198	17.727	1.00	207.77
55	1240	CB	VAL	C	155	20.918	17.729	17.614	1.00	240.62
	1241	CG1	VAL	C	155	19.500	18.129	17.274	1.00	240.62
	1242	CG2	VAL	C	155	21.336	18.369	18.918	1.00	240.62
	1243	C	VAL	C	155	20.663	15.572	16.392	1.00	207.77
	1244	O	VAL	C	155	21.387	15.758	15.410	1.00	207.77
60	1245	N	TRP	C	156	19.536	14.860	16.343	1.00	218.56
	1246	CA	TRP	C	156	19.108	14.172	15.113	1.00	218.56
	1247	CB	TRP	C	156	19.013	15.124	13.897	1.00	249.69
	1248	CG	TRP	C	156	17.915	16.165	13.921	1.00	249.69
	1249	CD2	TRP	C	156	16.500	15.936	13.835	1.00	249.69
65	1250	CE2	TRP	C	156	15.869	17.203	13.878	1.00	249.69
	1251	CE3	TRP	C	156	15.705	14.788	13.725	1.00	249.69
	1252	CD1	TRP	C	156	18.077	17.523	14.010	1.00	249.69
	1253	NE1	TRP	C	156	16.854	18.152	13.983	1.00	249.69
	1254	CZ2	TRP	C	156	14.481	17.354	13.816	1.00	249.69
70	1255	CZ3	TRP	C	156	14.324	14.939	13.660	1.00	249.69

	1256	CH2	TRP	C	156	13.728	16.214	13.709	1.00	249.69
	1257	C	TRP	C	156	20.213	13.163	14.835	1.00	218.56
	1258	O	TRP	C	156	20.243	12.080	15.416	1.00	218.56
	1259	N	GLN	C	157	21.130	13.548	13.949	1.00	165.87
5	1260	CA	GLN	C	157	22.264	12.707	13.578	1.00	165.87
	1261	CB	GLN	C	157	21.918	11.902	12.321	1.00	216.87
	1262	CG	GLN	C	157	20.967	10.737	12.583	1.00	216.87
	1263	CD	GLN	C	157	21.564	9.669	13.496	1.00	216.87
	1264	OE1	GLN	C	157	22.561	9.032	13.154	1.00	216.87
10	1265	NE2	GLN	C	157	20.951	9.468	14.661	1.00	216.87
	1266	C	GLN	C	157	23.592	13.461	13.378	1.00	165.87
	1267	O	GLN	C	157	24.495	12.979	12.705	1.00	165.87
	1268	N	LEU	C	158	23.706	14.648	13.960	1.00	219.11
	1269	CA	LEU	C	158	24.940	15.419	13.858	1.00	219.11
15	1270	CB	LEU	C	158	24.767	16.628	12.929	1.00	248.45
	1271	CG	LEU	C	158	24.766	16.392	11.415	1.00	248.45
	1272	CD1	LEU	C	158	25.460	17.580	10.748	1.00	248.45
	1273	CD2	LEU	C	158	25.498	15.110	11.054	1.00	248.45
	1274	C	LEU	C	158	25.415	15.892	15.230	1.00	219.11
20	1275	O	LEU	C	158	24.619	16.116	16.136	1.00	219.11
	1276	N	ASP	C	159	26.724	16.040	15.374	1.00	202.98
	1277	CA	ASP	C	159	27.314	16.485	16.629	1.00	202.98
	1278	CB	ASP	C	159	28.746	15.957	16.757	1.00	249.69
	1279	CG	ASP	C	159	28.834	14.458	16.563	1.00	249.69
25	1280	OD1	ASP	C	159	28.215	13.718	17.356	1.00	249.69
	1281	OD2	ASP	C	159	29.522	14.017	15.616	1.00	249.69
	1282	C	ASP	C	159	27.341	18.007	16.704	1.00	202.98
	1283	O	ASP	C	159	27.474	18.690	15.682	1.00	202.98
	1284	N	TYR	C	160	27.209	18.541	17.915	1.00	193.11
30	1285	CA	TYR	C	160	27.246	19.988	18.104	1.00	193.11
	1286	CB	TYR	C	160	25.852	20.584	18.043	1.00	187.38
	1287	CG	TYR	C	160	25.114	20.253	16.778	1.00	187.38
	1288	CD1	TYR	C	160	24.305	19.113	16.702	1.00	187.38
	1289	CE1	TYR	C	160	23.579	18.813	15.553	1.00	187.38
35	1290	CD2	TYR	C	160	25.195	21.087	15.665	1.00	187.38
	1291	CE2	TYR	C	160	24.479	20.796	14.504	1.00	187.38
	1292	CZ	TYR	C	160	23.666	19.657	14.458	1.00	187.38
	1293	OH	TYR	C	160	22.920	19.374	13.337	1.00	187.38
	1294	C	TYR	C	160	27.895	20.388	19.413	1.00	193.11
40	1295	O	TYR	C	160	27.769	19.705	20.429	1.00	193.11
	1296	N	GLU	C	161	28.585	21.519	19.360	1.00	171.02
	1297	CA	GLU	C	161	29.296	22.064	20.494	1.00	171.02
	1298	CB	GLU	C	161	30.740	22.358	20.052	1.00	238.76
	1299	CG	GLU	C	161	31.660	22.975	21.085	1.00	238.76
45	1300	CD	GLU	C	161	33.121	22.878	20.671	1.00	238.76
	1301	OE1	GLU	C	161	33.948	23.655	21.196	1.00	238.76
	1302	OE2	GLU	C	161	33.445	22.015	19.827	1.00	238.76
	1303	C	GLU	C	161	28.560	23.321	20.952	1.00	171.02
	1304	O	GLU	C	161	28.044	24.068	20.135	1.00	171.02
50	1305	N	SER	C	162	28.500	23.533	22.263	1.00	160.21
	1306	CA	SER	C	162	27.820	24.693	22.840	1.00	160.21
	1307	CB	SER	C	162	27.182	24.308	24.174	1.00	143.02
	1308	OG	SER	C	162	28.169	23.903	25.109	1.00	143.02
	1309	C	SER	C	162	28.767	25.856	23.078	1.00	160.21
55	1310	O	SER	C	162	29.978	25.678	23.147	1.00	160.21
	1311	N	GLU	C	163	28.211	27.053	23.200	1.00	142.78
	1312	CA	GLU	C	163	29.043	28.207	23.471	1.00	142.78
	1313	CB	GLU	C	163	28.195	29.492	23.498	1.00	247.65
	1314	CG	GLU	C	163	27.742	30.009	22.130	1.00	247.65
60	1315	CD	GLU	C	163	28.870	30.651	21.331	1.00	247.65
	1316	OE1	GLU	C	163	29.506	31.604	21.841	1.00	247.65
	1317	OE2	GLU	C	163	29.114	30.207	20.189	1.00	247.65
	1318	C	GLU	C	163	29.632	27.931	24.857	1.00	142.78
	1319	O	GLU	C	163	28.995	27.254	25.666	1.00	142.78
65	1320	N	PRO	C	164	30.843	28.429	25.144	1.00	104.76
	1321	CD	PRO	C	164	31.762	29.158	24.241	1.00	198.66
	1322	CA	PRO	C	164	31.481	28.209	26.442	1.00	104.76
	1323	CB	PRO	C	164	32.947	28.445	26.144	1.00	198.66
	1324	CG	PRO	C	164	32.874	29.581	25.180	1.00	198.66
70	1325	C	PRO	C	164	30.943	29.170	27.501	1.00	104.76

	1326	O	PRO	C	164	30.623	30.318	27.189	1.00	104.76
	1327	N	LEU	C	165	30.872	28.719	28.751	1.00	150.81
	1328	CA	LEU	C	165	30.352	29.562	29.820	1.00	150.81
	1329	CB	LEU	C	165	28.962	29.067	30.202	1.00	114.56
5	1330	CG	LEU	C	165	28.295	29.843	31.329	1.00	114.56
	1331	CD1	LEU	C	165	28.627	31.336	31.179	1.00	114.56
	1332	CD2	LEU	C	165	26.778	29.596	31.296	1.00	114.56
	1333	C	LEU	C	165	31.213	29.644	31.065	1.00	150.81
	1334	O	LEU	C	165	31.648	28.620	31.589	1.00	150.81
	1335	N	ASN	C	166	31.445	30.864	31.538	1.00	123.03
10	1336	CA	ASN	C	166	32.247	31.058	32.744	1.00	123.03
	1337	CB	ASN	C	166	32.969	32.409	32.716	1.00	146.40
	1338	CG	ASN	C	166	34.388	32.314	32.177	1.00	146.40
	1339	OD1	ASN	C	166	35.031	31.273	32.254	1.00	146.40
	1340	ND2	ASN	C	166	34.888	33.429	31.660	1.00	146.40
15	1341	C	ASN	C	166	31.402	30.985	34.019	1.00	123.03
	1342	O	ASN	C	166	30.257	31.409	34.022	1.00	123.03
	1343	N	ILE	C	167	31.976	30.458	35.103	1.00	149.03
	1344	CA	ILE	C	167	31.266	30.330	36.374	1.00	149.03
20	1345	CB	ILE	C	167	30.670	28.946	36.551	1.00	98.22
	1346	CG2	ILE	C	167	30.085	28.799	37.947	1.00	98.22
	1347	CG1	ILE	C	167	29.610	28.707	35.473	1.00	98.22
	1348	CD1	ILE	C	-167	29.025	27.336	35.526	1.00	98.22
	1349	C	ILE	C	167	32.178	30.592	37.548	1.00	149.03
25	1350	O	ILE	C	167	33.233	29.983	37.667	1.00	149.03
	1351	N	THR	C	168	31.755	31.471	38.440	1.00	107.43
	1352	CA	THR	C	168	32.586	31.792	39.591	1.00	107.43
	1353	CB	THR	C	168	33.120	33.225	39.487	1.00	120.91
	1354	OG1	THR	C	168	33.823	33.372	38.246	1.00	120.91
30	1355	CG2	THR	C	168	34.054	33.526	40.633	1.00	120.91
	1356	C	THR	C	168	31.955	31.603	40.965	1.00	107.43
	1357	O	THR	C	168	30.943	32.192	41.312	1.00	107.43
	1358	N	VAL	C	169	32.594	30.761	41.750	1.00	107.46
	1359	CA	VAL	C	169	32.152	30.470	43.092	1.00	107.46
35	1360	CB	VAL	C	169	32.206	28.935	43.374	1.00	105.06
	1361	CG1	VAL	C	169	32.281	28.657	44.853	1.00	105.06
	1362	CG2	VAL	C	169	30.966	28.269	42.794	1.00	105.06
	1363	C	VAL	C	169	33.083	31.217	44.025	1.00	107.46
	1364	O	VAL	C	169	34.266	30.874	44.135	1.00	107.46
40	1365	N	ILE	C	170	32.548	32.248	44.677	1.00	143.55
	1366	CA	ILE	C	170	33.320	33.068	45.614	1.00	143.55
	1367	CB	ILE	C	170	32.910	34.549	45.488	1.00	150.86
	1368	CG2	ILE	C	170	32.957	34.967	44.028	1.00	150.86
	1369	CG1	ILE	C	170	31.487	34.741	46.000	1.00	150.86
45	1370	CD1	ILE	C	170	31.020	36.188	45.961	1.00	150.86
	1371	C	ILE	C	170	33.102	32.586	47.056	1.00	143.55
	1372	O	ILE	C	170	32.173	31.824	47.309	1.00	143.55
	1373	N	LYS	C	171	33.939	33.028	47.994	1.00	170.19
	1374	CA	LYS	C	171	33.795	32.588	49.379	1.00	170.19
50	1375	CB	LYS	C	171	35.038	31.812	49.790	1.00	247.79
	1376	CG	LYS	C	171	36.307	32.611	49.598	1.00	247.79
	1377	CD	LYS	C	171	37.503	31.712	49.375	1.00	247.79
	1378	CE	LYS	C	171	37.723	30.756	50.537	1.00	247.79
	1379	NZ	LYS	C	171	38.942	29.921	50.335	1.00	247.79
55	1380	C	LYS	C	171	33.539	33.715	50.378	1.00	170.19
	1381	O	LYS	C	171	33.540	33.498	51.596	1.00	170.19
	1382	C1	NAG	C	221	5.113	30.265	25.361	1.00	249.69
	1383	C2	NAG	C	221	5.275	28.765	25.132	1.00	249.69
	1384	N2	NAG	C	221	6.660	28.481	24.798	1.00	249.69
60	1385	C7	NAG	C	221	7.164	27.267	25.015	1.00	249.69
	1386	O7	NAG	C	221	6.500	26.331	25.485	1.00	249.69
	1387	C8	NAG	C	221	8.624	27.050	24.648	1.00	249.69
	1388	C3	NAG	C	221	4.349	28.288	24.010	1.00	249.69
	1389	O3	NAG	C	221	4.386	26.868	23.925	1.00	249.69
65	1390	C4	NAG	C	221	2.899	28.741	24.228	1.00	249.69
	1391	O4	NAG	C	221	2.183	28.474	23.002	1.00	249.69
	1392	C5	NAG	C	221	2.851	30.255	24.559	1.00	249.69
	1393	O5	NAG	C	221	3.741	30.568	25.655	1.00	249.69
	1394	C6	NAG	C	221	1.472	30.743	24.975	1.00	249.69
70	1395	O6	NAG	C	221	0.977	30.009	26.087	1.00	249.69

	1396	C1	NAG C	222	0.788	28.434	23.006	1.00	249.69
	1397	C2	NAG C	222	0.312	27.230	22.166	1.00	249.69
	1398	N2	NAG C	222	0.806	25.988	22.749	1.00	249.69
	1399	C7	NAG C	222	-0.041	25.044	23.166	1.00	249.69
5	1400	O7	NAG C	222	-1.270	25.153	23.088	1.00	249.69
	1401	C8	NAG C	222	0.570	23.783	23.761	1.00	249.69
	1402	C3	NAG C	222	0.819	27.382	20.711	1.00	249.69
	1403	O3	NAG C	222	0.285	26.347	19.894	1.00	249.69
	1404	C4	NAG C	222	0.422	28.755	20.130	1.00	249.69
10	1405	O4	NAG C	222	1.038	28.935	18.860	1.00	249.69
	1406	C5	NAG C	222	0.860	29.881	21.083	1.00	249.69
	1407	O5	NAG C	222	0.308	29.658	22.408	1.00	249.69
	1408	C6	NAG C	222	0.423	31.266	20.635	1.00	249.69
	1409	O6	NAG C	222	1.512	32.185	20.656	1.00	249.69
15	1410	C1	NAG C	242	18.968	46.404	25.932	1.00	249.69
	1411	C2	NAG C	242	18.118	46.230	24.662	1.00	249.69
	1412	N2	NAG C	242	16.700	46.211	24.968	1.00	249.69
	1413	C7	NAG C	242	15.905	47.139	24.446	1.00	249.69
	1414	O7	NAG C	242	16.318	48.033	23.707	1.00	249.69
20	1415	C8	NAG C	242	14.433	47.071	24.794	1.00	249.69
	1416	C3	NAG C	242	18.532	44.931	23.964	1.00	249.69
	1417	O3	NAG C	242	17.775	44.760	22.773	1.00	249.69
	1418	C4	NAG C	242	20.036	44.983	23.636	1.00	249.69
	1419	O4	NAG C	242	20.457	43.699	23.125	1.00	249.69
25	1420	C5	NAG C	242	20.872	45.340	24.894	1.00	249.69
	1421	O5	NAG C	242	20.352	46.526	25.559	1.00	249.69
	1422	C6	NAG C	242	22.318	45.643	24.539	1.00	249.69
	1423	O6	NAG C	242	23.194	44.624	24.998	1.00	249.69
	1424	C1	NAG C	243	21.000	43.678	21.849	1.00	249.69
30	1425	C2	NAG C	243	21.827	42.403	21.660	1.00	249.69
	1426	N2	NAG C	243	22.908	42.331	22.621	1.00	249.69
	1427	C7	NAG C	243	23.110	41.201	23.298	1.00	249.69
	1428	O7	NAG C	243	22.404	40.193	23.157	1.00	249.69
	1429	C8	NAG C	243	24.264	41.186	24.287	1.00	249.69
35	1430	C3	NAG C	243	22.382	42.377	20.246	1.00	249.69
	1431	O3	NAG C	243	23.150	41.195	20.045	1.00	249.69
	1432	C4	NAG C	243	21.223	42.406	19.276	1.00	249.69
	1433	O4	NAG C	243	21.794	42.333	17.983	1.00	249.69
	1434	C5	NAG C	243	20.366	43.682	19.518	1.00	249.69
40	1435	O5	NAG C	243	19.915	43.690	20.906	1.00	249.69
	1436	C6	NAG C	243	19.112	43.738	18.662	1.00	249.69
	1437	O6	NAG C	243	18.229	42.666	18.966	1.00	249.69
	1438	C1	MAN C	244	21.150	41.717	16.941	1.00	247.75
	1439	C2	MAN C	244	21.485	42.608	15.841	1.00	247.75
45	1440	O2	MAN C	244	22.880	42.966	15.943	1.00	247.75
	1441	C3	MAN C	244	21.041	42.012	14.541	1.00	247.75
	1442	O3	MAN C	244	21.229	42.927	13.482	1.00	247.75
	1443	C4	MAN C	244	21.699	40.671	14.305	1.00	247.75
	1444	O4	MAN C	244	21.301	40.157	13.050	1.00	247.75
50	1445	C5	MAN C	244	21.269	39.743	15.442	1.00	247.75
	1446	O5	MAN C	244	21.734	40.330	16.721	1.00	247.75
	1447	C6	MAN C	244	21.705	38.271	15.255	1.00	247.75
	1448	O6	MAN C	244	23.038	38.030	15.676	1.00	247.75
	1449	C1	NAG C	250	0.024	39.200	37.140	1.00	249.69
55	1450	C2	NAG C	250	-0.633	37.995	37.P14	1.00	249.69
	1451	N2	NAG C	250	-0.363	38.033	39.271	1.00	249.69
	1452	C7	NAG C	250	-1.342	38.313	40.126	1.00	249.69
	1453	O7	NAG C	250	-2.500	38.550	39.764	1.00	249.69
	1454	C8	NAG C	250	-0.985	38.336	41.607	1.00	249.69
60	1455	C3	NAG C	250	-0.084	36.691	37.242	1.00	249.69
	1456	O3	NAG C	250	-0.751	35.573	37.814	1.00	249.69
	1457	C4	NAG C	250	-0.273	36.691	35.716	1.00	249.69
	1458	O4	NAG C	250	0.355	35.542	35.160	1.00	249.69
	1459	C5	NAG C	250	0.338	37.973	35.105	1.00	249.69
65	1460	O5	NAG C	250	-0.235	39.149	35.731	1.00	249.69
	1461	C6	NAG C	250	0.100	38.106	33.606	1.00	249.69
	1462	O6	NAG C	250	0.341	39.435	33.163	1.00	249.69
	1463	C1	NAG C	274	17.463	53.378	50.102	1.00	249.69
	1464	C2	NAG C	274	18.624	52.801	50.945	1.00	249.69
70	1465	N2	NAG C	274	18.123	51.805	51.883	1.00	249.69

	1466	C7	NAG C	274	18.919	50.834	52.330	1.00	249.69
	1467	O7	NAG C	274	20.099	50.723	51.992	1.00	249.69
	1468	C8	NAG C	274	18.316	49.836	53.303	1.00	249.69
	1469	C3	NAG C	274	19.337	53.945	51.704	1.00	249.69
5	1470	O3	NAG C	274	20.487	53.442	52.377	1.00	249.69
	1471	C4	NAG C	274	19.755	55.062	50.730	1.00	249.69
	1472	O4	NAG C	274	20.286	56.164	51.457	1.00	249.69
	1473	C5	NAG C	274	18.548	55.520	49.899	1.00	249.69
	1474	O5	NAG C	274	17.957	54.391	49.203	1.00	249.69
10	1475	C6	NAG C	274	18.929	56.550	48.849	1.00	249.69
	1476	O6	NAG C	274	17.844	56.817	47.970	1.00	249.69
	1477	C1	NAG C	335	16.958	19.435	32.669	1.00	249.69
	1478	C2	NAG C	335	15.937	19.674	33.820	1.00	249.69
	1479	N2	NAG C	335	16.535	19.244	35.073	1.00	249.69
15	1480	C7	NAG C	335	16.783	20.124	36.042	1.00	249.69
	1481	O7	NAG C	335	16.517	21.327	35.947	1.00	249.69
	1482	C8	NAG C	335	17.416	19.588	37.314	1.00	249.69
	1483	C3	NAG C	335	14.586	18.951	33.638	1.00	249.69
	1484	O3	NAG C	335	13.605	19.572	34.457	1.00	249.69
20	1485	C4	NAG C	335	14.117	18.995	32.190	1.00	249.69
	1486	O4	NAG C	335	12.912	18.250	32.042	1.00	249.69
	1487	C5	NAG C	335	15.219	18.405	31.318	1.00	249.69
	1488	O5	NAG C	335	16.370	19.273	31.353	1.00	249.69
	1489	C6	NAG C	335	14.799	18.275	29.862	1.00	249.69
25	1490	O6	NAG C	335	14.956	16.942	29.398	1.00	249.69
	1491	C1	NAG C	340	29.647	21.246	52.250	1.00	249.46
	1492	C2	NAG C	340	30.433	22.313	53.032	1.00	249.46
	1493	N2	NAG C	340	30.974	23.304	52.117	1.00	249.46
	1494	C7	NAG C	340	30.836	24.605	52.373	1.00	249.46
30	1495	O7	NAG C	340	30.269	25.044	53.381	1.00	249.46
	1496	C8	NAG C	340	31.425	25.569	51.356	1.00	249.46
	1497	C3	NAG C	340	31.568	21.625	53.818	1.00	249.46
	1498	O3	NAG C	340	32.255	22.575	54.628	1.00	249.46
	1499	C4	NAG C	340	30.996	20.503	54.702	1.00	249.46
35	1500	O4	NAG C	340	32.063	19.789	55.308	1.00	249.46
	1501	C5	NAG C	340	30.136	19.545	53.853	1.00	249.46
	1502	O5	NAG C	340	29.101	20.280	53.154	1.00	249.46
	1503	C6	NAG C	340	29.442	18.463	54.660	1.00	249.46
	1504	O6	NAG C	340	28.518	17.737	53.851	1.00	249.46
40	1505	C1	NAG C	366	36.171	33.414	30.999	1.00	209.37
	1506	C2	NAG C	366	36.136	34.345	29.797	1.00	209.37
	1507	N2	NAG C	366	35.092	33.912	28.886	1.00	209.37
	1508	C7	NAG C	366	33.862	34.405	28.999	1.00	209.37
	1509	O7	NAG C	366	33.555	35.244	29.848	1.00	209.37
45	1510	C8	NAG C	366	32.813	33.903	28.017	1.00	209.37
	1511	C3	NAG C	366	37.487	34.322	29.088	1.00	209.37
	1512	O3	NAG C	366	37.518	35.319	28.073	1.00	209.37
	1513	C4	NAG C	366	38.646	34.557	30.067	1.00	209.37
	1514	O4	NAG C	366	39.884	34.256	29.386	1.00	209.37
50	1515	C5	NAG C	366	38.505	33.652	31.302	1.00	209.37
	1516	O5	NAG C	366	37.207	33.813	31.891	1.00	209.37
	1517	C6	NAG C	366	39.518	33.935	32.390	1.00	209.37
	1518	O6	NAG C	366	39.449	32.957	33.413	1.00	209.37
	1519	C1	NAG C	367	40.870	35.232	29.397	1.00	249.69
55	1520	C2	NAG C	367	42.234	34.596	29.111	1.00	249.69
	1521	N2	NAG C	367	42.528	33.546	30.070	1.00	249.69
	1522	C7	NAG C	367	42.583	32.277	29.668	1.00	249.69
	1523	O7	NAG C	367	42.394	31.931	28.498	1.00	249.69
	1524	C8	NAG C	367	42.895	31.227	30.725	1.00	249.69
60	1525	C3	NAG C	367	43.292	35.695	29.166	1.00	249.69
	1526	O3	NAG C	367	44.574	35.149	28.892	1.00	249.69
	1527	C4	NAG C	367	42.950	36.779	28.132	1.00	249.69
	1528	O4	NAG C	367	43.876	37.854	28.245	1.00	249.69
	1529	C5	NAG C	367	41.511	37.296	28.348	1.00	249.69
65	1530	O5	NAG C	367	40.568	36.196	28.373	1.00	249.69
	1531	C6	NAG C	367	41.060	38.236	27.251	1.00	249.69
	1532	O6	NAG C	367	40.020	37.661	26.474	1.00	249.69
	1533	CB	LYS A	4	3.684	19.933	14.932	1.00	249.69
	1534	CG	LYS A	4	2.729	21.022	14.456	1.00	249.69
70	1535	CD	LYS A	4	2.217	21.880	15.610	1.00	249.69

	1536	CE	LYS	A	4.	1.292	22.987	15.108	1.00	249.69
	1537	NZ	LYS	A	4	0.762	23.841	16.212	1.00	249.69
	1538	C	LYS	A	4	5.030	20.019	12.832	1.00	249.22
	1539	O	LYS	A	4	5.450	21.116	13.205	1.00	249.22
5	1540	N	LYS	A	4	5.205	18.061	14.356	1.00	249.22
	1541	CA	LYS	A	4	4.291	19.100	13.797	1.00	249.22
	1542	N	PRO	A	5	5.213	19.581	11.582	1.00	249.41
	1543	CD	PRO	A	5	4.979	18.215	11.068	1.00	133.18
	1544	CA	PRO	A	5	5.912	20.398	10.589	1.00	249.41
10	1545	CB	PRO	A	5	6.459	19.360	9.606	1.00	133.18
	1546	CG	PRO	A	5	5.376	18.335	9.599	1.00	133.18
	1547	C	PRO	A	5	4.969	21.407	9.927	1.00	249.41
	1548	O	PRO	A	5	3.754	21.219	9.927	1.00	249.41
	1549	N	LYS	A	6	5.529	22.477	9.377	1.00	196.60
15	1550	CA	LYS	A	6	4.724	23.489	8.709	1.00	196.60
	1551	CB	LYS	A	6	4.429	24.652	9.660	1.00	249.69
	1552	CG	LYS	A	6	3.524	25.719	9.050	1.00	249.69
	1553	CD	LYS	A	6	3.113	26.783	10.067	1.00	249.69
	1554	CE	LYS	A	6	2.180	27.812	9.436	1.00	249.69
20	1555	NZ	LYS	A	6	1.664	28.800	10.424	1.00	249.69
	1556	C	LYS	A	6	5.433	24.000	7.458	1.00	196.60
	1557	O	LYS	A	6	6.478	24.664	7.539	1.00	196.60
	1558	N	VAL	A	7	4.850	23.695	6.304	1.00	192.34
	1559	CA	VAL	A	7	5.416	24.094	5.029	1.00	192.34
25	1560	CB	VAL	A	7	4.656	23.429	3.870	1.00	160.27
	1561	CG1	VAL	A	7	5.470	23.549	2.587	1.00	160.27
	1562	CG2	VAL	A	7	4.363	21.983	4.195	1.00	160.27
	1563	C	VAL	A	7	5.403	25.607	4.807	1.00	192.34
	1564	O	VAL	A	7	4.350	26.253	4.868	1.00	192.34
30	1565	N	SER	A	8	6.582	26.165	4.544	1.00	184.23
	1566	CA	SER	A	8	6.726	27.594	4.284	1.00	184.23
	1567	CB	SER	A	8	7.897	28.148	5.099	1.00	230.08
	1568	OG	SER	A	8	9.063	27.354	4.945	1.00	230.08
	1569	C	SER	A	8	6.978	27.814	2.789	1.00	184.23
35	1570	O	SER	A	8	7.389	26.889	2.087	1.00	184.23
	1571	N	LEU	A	9	6.726	29.025	2.297	1.00	167.11
	1572	CA	LEU	A	9	6.948	29.312	0.880	1.00	167.11
	1573	CB	LEU	A	9	5.626	29.535	0.147	1.00	178.21
	1574	CG	LEU	A	9	4.541	28.451	0.105	1.00	178.21
40	1575	CD1	LEU	A	9	3.549	28.821	-0.980	1.00	178.21
	1576	CD2	LEU	A	9	5.128	27.083	-0.188	1.00	178.21
	1577	C	LEU	A	9	7.817	30.533	0.666	1.00	167.11
	1578	O	LEU	A	9	7.946	31.373	1.552	1.00	167.11
	1579	N	ASN	A	10	8.405	30.629	-0.522	1.00	147.32
45	1580	CA	ASN	A	10	9.260	31.769	-0.855	1.00	147.32
	1581	CB	ASN	A	10	10.634	31.610	-0.219	1.00	249.69
	1582	CG	ASN	A	10	11.421	32.902	-0.234	1.00	249.69
	1583	OD1	ASN	A	10	11.028	33.886	0.395	1.00	249.69
	1584	ND2	ASN	A	10	12.534	32.911	-0.959	1.00	249.69
50	1585	C	ASN	A	10	9.396	31.902	-2.374	1.00	147.32
	1586	O	ASN	A	10	10.037	31.073	-3.022	1.00	147.32
	1587	N	PRO	A	11	8.851	32.979	-2.953	1.00	237.62
	1588	CD	PRO	A	11	8.944	33.177	-4.413	1.00	161.80
	1589	CA	PRO	A	11	8.057	34.058	-2.348	1.00	237.62
55	1590	CB	PRO	A	11	7.554	34.834	-3.552	1.00	161.80
	1591	CG	PRO	A	11	8.646	34.638	-4.548	1.00	161.80
	1592	C	PRO	A	11	6.921	33.599	-1.438	1.00	237.62
	1593	O	PRO	A	11	6.554	32.428	-1.435	1.00	237.62
	1594	N	PRO	A	12	6.338	34.529	-0.662	1.00	147.54
60	1595	CD	PRO	A	12	6.781	35.905	-0.441	1.00	140.19
	1596	CA	PRO	A	12	5.229	34.189	0.236	1.00	147.54
	1597	CB	PRO	A	12	5.107	35.433	1.112	1.00	140.19
	1598	CG	PRO	A	12	6.465	36.081	1.016	1.00	140.19
	1599	C	PRO	A	12	3.967	33.943	-0.572	1.00	147.54
65	1600	O	PRO	A	12	3.063	33.202	-0.148	1.00	147.54
	1601	N	TRP	A	13	3.929	34.576	-1.744	1.00	165.94
	1602	CA	TRP	A	13	2.824	34.492	-2.698	1.00	165.94
	1603	CB	TRP	A	13	3.247	35.209	-3.968	1.00	139.27
	1604	CG	TRP	A	13	3.825	36.552	-3.699	1.00	139.27
70	1605	CD2	TRP	A	13	3.455	37.438	-2.648	1.00	139.27

	1606	CE2	TRP	A	13	4.233	38.603	-2.790	1.00	139.27
	1607	CE3	TRP	A	13	2.546	37.363	-1.594	1.00	139.27
	1608	CD1	TRP	A	13	4.784	37.201	-4.428	1.00	139.27
	1609	NE1·	TRP	A	13	5.035	38.438	-3.891	1.00	139.27
5	1610	CZ2	TRP	A	13	4.122	39.682	-1.917	1.00	139.27
	1611	CZ3	TRP	A	13	2.433	38.434	-0.731	1.00	139.27
	1612	CH2	TRP	A	13	3.218	39.577	-0.892	1.00	139.27
	1613	C	TRP	A	13	2.428	33.061	-3.048	1.00	165.94
	1614	O	TRP	A	13	3.219	32.342	-3.663	1.00	165.94
10	1615	N	ASN	A	14	1.213	32.652	-2.689	1.00	109.00
	1616	CA	ASN	A	14	0.782	31.293	-2.990	1.00	109.00
	1617	CB	ASN	A	14	0.167	30.660	-1.746	1.00	167.27
	1618	CG	ASN	A	14	-1.091	31.352	-1.312	1.00	167.27
	1619	OD1	ASN	A	14	-1.088	32.556	-1.050	1.00	167.27
15	1620	ND2	ASN	A	14	-2.188	30.596	-1.234	1.00	167.27
	1621	C	ASN	A	14	-0.200	31.224	-4.164	1.00	109.00
	1622	O	ASN	A	14	-0.981	30.275	-4.295	1.00	109.00
	1623	N	ARG	A	15	-0.153	32.255	-5.006	1.00	160.32
	1624	CA	ARG	A	15	-0.977	32.384	-6.220	1.00	160.32
20	1625	CB	ARG	A	15	-2.094	33.426	-6.042	1.00	119.95
	1626	CG	ARG	A	15	-2.974	33.286	-4.790	1.00	119.95
	1627	CD	ARG	A	15	-4.127	34.296	-4.834	1.00	119.95
	1628	NE	ARG	A	15	-5.205	33.881	-5.737	1.00	119.95
	1629	CZ	ARG	A	15	-5.920	34.709	-6.500	1.00	119.95
25	1630	NH1	ARG	A	15	-5.674	36.015	-6.492	1.00	119.95
	1631	NH2	ARG	A	15	-6.894	34.239	-7.267	1.00	119.95
	1632	C	ARG	A	15	0.012	32.914	-7.260	1.00	160.32
	1633	O	ARG	A	15	0.338	34.098	-7.259	1.00	160.32
	1634	N	ILE	A	16	0.490	32.054	-8.148	1.00	135.68
30	1635	CA	ILE	A	16	1.479	32.491	-9.124	1.00	135.68
	1636	CB	ILE	A	16	2.803	31.783	-8.904	1.00	134.22
	1637	CG2	ILE	A	16	3.532	32.401	-7.704	1.00	134.22
	1638	CG1	ILE	A	16	2.534	30.272	-8.762	1.00	134.22
	1639	CD1	ILE	A	16	3.763	29.404	-8.762	1.00	134.22
35	1640	C	ILE	A	16	1.141	32.283	-10.581	1.00	135.68
	1641	O	ILE	A	16	0.358	31.408	-10.938	1.00	135.68
	1642	N	PHE	A	17	1.774	33.090	-11.425	1.00	145.71
	1643	CA	PHE	A	17	1.589	33.015	-12.870	1.00	145.71
	1644	CB	PHE	A	17	2.211	34.246	-13.547	1.00	146.10
40	1645	CG	PHE	A	17	1.276	35.401	-13.687	1.00	146.10
	1646	CD1	PHE	A	17	1.752	36.702	-13.601	1.00	146.10
	1647	CD2	PHE	A	17	-0.067	35.195	-13.957	1.00	146.10
	1648	CE1	PHE	A	17	0.901	37.798	-13.781	1.00	146.10
	1649	CE2	PHE	A	17	-0.927	36.273	-14.142	1.00	146.10
45	1650	CZ	PHE	A	17	-0.437	37.586	-14.054	1.00	146.10
	1651	C	PHE	A	17	2.240	31.744	-13.417	1.00	145.71
	1652	O	PHE	A	17	2.882	30.991	-12.692	1.00	145.71
	1653	N	LYS	A	18	2.074	31.534	-14.713	1.00	190.00
	1654	CA	LYS	A	18	2.625	30.380	-15.402	1.00	190.00
50	1655	CB	LYS	A	18	1.798	30.115	-16.669	1.00	249.19
	1656	CG	LYS	A	18	2.212	28.904	-17.483	1.00	249.19
	1657	CD	LYS	A	18	1.206	28.655	-18.601	1.00	249.19
	1658	CE	LYS	A	18	1.619	27.498	-19.493	1.00	249.19
	1659	NZ	LYS	A	18	2.837	27.814	-20.292	1.00	249.19
55	1660	C	LYS	A	18	4.101	30.602	-15.765	1.00	190.00
	1661	O	LYS	A	18	4.472	31.613	-16.368	1.00	190.00
	1662	N	GLY	A	19	4.945	29.648	-15.390	1.00	217.86
	1663	CA	GLY	A	19	6.356	29.759	-15.698	1.00	217.86
	1664	C	GLY	A	19	7.219	30.324	-14.582	1.00	217.86
60	1665	O	GLY	A	19	8.449	30.261	-14.675	1.00	217.86
	1666	N	GLU	A	20	6.593	30.874	-13.537	1.00	170.23
	1667	CA	GLU	A	20	7.330	31.452	-12.399	1.00	170.23
	1668	CB	GLU	A	20	6.435	32.409	-11.611	1.00	186.84
	1669	CG	GLU	A	20	5.663	33.418	-12.440	1.00	186.84
65	1670	CD	GLU	A	20	4.890	34.410	-11.578	1.00	186.84
	1671	OE1	GLU	A	20	4.121	33.972	-10.688	1.00	186.84
	1672	OE2	GLU	A	20	5.053	35.633	-11.793	1.00	186.84
	1673	C	GLU	A	20	7.823	30.341	-11.456	1.00	170.23
	1674	O	GLU	A	20	7.274	29.232	-11.466	1.00	170.23
70	1675	N	ASN	A	21	8.838	30.634	-10.636	1.00	187.01

No.	Serial	Atom	Res	Ch	Seq	X	Y	Z	Occ	B
		ASN	A	21	9.372	29.622	-9.707	1.00	187.01	
	1676	CA	ASN	A	21	10.888	29.456	-9.859	1.00	249.69
	1677	CB	ASN	A	21	11.371	29.621	-11.291	1.00	249.69
	1678	CG	ASN	A	21	10.828	29.039	-12.233	1.00	249.69
	1679	OD1	ASN	A	21	12.423	30.420	-11.435	1.00	249.69
5	1680	ND2	ASN	A	21	9.087	29.907	-8.230	1.00	187.01
	1681	C	ASN	A	21	9.136	31.054	-7.786	1.00	187.01
	1682	O	ASN	A	21	8.816	28.842	-7.477	1.00	223.09
	1683	N	VAL	A	22	8.516	28.936	-6.050	1.00	223.09
	1684	CA	VAL	A	22	6.995	28.809	-5.785	1.00	159.07
10	1685	CB	VAL	A	22	6.530	27.388	-6.039	1.00	159.07
	1686	CG1	VAL	A	22	6.680	29.212	-4.363	1.00	159.07
	1687	CG2	VAL	A	22	9.228	27.825	-5 280	1.00	223.09
	1688	C	VAL	A	22	9.418	26.731	-5.801	1.00	223.09
	1689	O	VAL	A	22	9.600	28.102	-4.033	1.00	162.43
15	1690	N	THR	A	23	10.307	27.125	-3.197	1.00	162.43
	1691	CA	THR	A	23	11.677	27.680	-2.758	1.00	218.62
	1692	CB	THR	A	23	12.384	28.165	-3.905	1.00	218.62
	1693	OG1	THR	A	23	12.498	26.594	-2.071	1.00	218.62
	1694	CG2	THR	A	23	9.549	26.715	-1.924	1.00	162.43
20	1695	C	THR	A	23	9.185	27.571	-1.114	1.00	162.43
	1696	O	THR	A	23	9.337	25.410	-1.736	1.00	159.52
	1697	N	LEU	A	24	8.635	24.916	-0.549	1.00	159.52
	1698	CA	LEU	A	24	7.593	23.860	-0.923	1.00	128.43
	1699	CB	LEU	A	24	6.845	23.919	-2.252	1.00	128.43
25	1700	CG	LEU	A	24	5.664	22.963	-2.175	1.00	128.43
	1701	CD1	LEU	A	24	6.352	25.322	-2.557	1.00	128.43
	1702	CD2	LEU	A	24	9.600	24.299	0.464	1.00	159.52
	1703	C	LEU	A	24	10.111	23.201	0.247	1.00	159.52
	1704	O	LEU	A	24	9.827	24.999	1.574	1.00	201.17
30	1705	N	THR	A	25	10.722	24.533	2.637	1.00	201.17
	1706	CA	THR	A	25	11.524	25.712	3.227	1.00	221.92
	1707	CB	THR	A	25	12.249	26.363	2.178	1.00	221.92
	1708	OG1	THR	A	25	12.501	25.225	4.293	1.00	221.92
	1709	CG2	THR	A	25	9.919	23.875	3.767	1.00	201.17
35	1710	C	THR	A	25	8.912	24.429	4.215	1.00	201.17
	1711	O	THR	A	25	10.363	22.707	4.232	1.00	178.89
	1712	N	CYS	A	26	9.668	21.995	5.311	1.00	178.89
	1713	CA	CYS	A	26	10.061	22.556	6.672	1.00	178.89
	1714	C	CYS	A	26	11.220	22.904	6.885	1.00	178.89
40	1715	O	CYS	A	26	9.989	20.504	5.257	1.00	171.78
	1716	CB	CYS	A	26	8.970	19.467	6.366	1.00	171.78
	1717	SG	CYS	A	26	9.095	22.623	7.589	1.00	234.74
	1718	N	ASN	A	27	9.307	23.180	8.929	1.00	234.74
	1719	CA	ASN	A	27	8.591	22.337	9.987	1.00	249.69
45	1720	CB	ASN	A	27	8.555	23.020	11.351	1.00	249.69
	1721	CG	ASN	A	27	8.194	24.193	11.463	1.00	249.69
	1722	OD1	ASN	A	27	8.928	22.284	12.395	1.00	249.69
	1723	ND2	ASN	A	27	10.772	23.362	9.323	1.00	234.74
	1724	C	ASN	A	27	11.425	22.453	9.832	1.00	234.74
50	1725	O	ASN	A	27	11.267	24.569	9.076	1.00	249.69
	1726	N	GLY	A	28	12.641	24.927	9.380	1.00	249.69
	1727	CA	GLY	A	28	12.886	26.299	8.768	1.00	249.69
	1728	C	GLY	A	28	12.749	26.475	7.551	1.00	249.69
	1729	O	GLY	A	28	13.240	27.275	9.600	1.00	249.69
55	1730	N	ASN	A	29	13.468	28.641	9.124	1.00	249.69
	1731	CA	ASN	A	29	13.452	29.617	10.321	1.00	249.69
	1732	CB	ASN	A	29	13.401	31.093	9.896	1.00	249.69
	1733	CG	ASN	A	29	13.221	31.413	8.716	1.00	249.69
	1734	OD1	ASN	A	29	13.548	31.993	10.868	1.00	249.69
60	1735	ND2	ASN	A	29	14.761	28.813	8.314	1.00	249.69
	1736	C	ASN	A	29	14.726	29.331	7.190	1.00	249.69
	1737	O	ASN	A	30	15.890	28.365	8.861	1.00	249.69
	1738	N	ASN	A	30	17.157	28.533	8.158	1.00	249.69
	1739	CA	ASN	A	30	18.002	29.581	8.895	1.00	249.69
65	1740	CB	ASN	A	30	17.349	30.959	8.911	1.00	249.69
	1741	CG	ASN	A	30	17.266	31.607	9.960	1.00	249.69
	1742	OD1	ASN	A	30	16.888	31.416	7.744	1.00	249.69
	1743	ND2	ASN	A	30	17.985	27.267	7.919	1.00	249.69
	1744	C	ASN	A	30	18.147	26.838	6.774	1.00	249.69
70	1745	O	ASN	A	30					

	1746	N	PHE	A	31	18.512	26.668	8.987	1.00	249.69
	1747	CA	PHE	A	31	19.345	25.474	8.836	1.00	249.69
	1748	CB	PHE	A	31	20.748	25.733	9.416	1.00	249.69
	1749	CG	PHE	A	31	21.429	26.957	8.841	1.00	249.69
5	1750	CD1	PHE	A	31	21.106	28.234	9.300	1.00	249.69
	1751	CD2	PHE	A	31	22.372	26.835	7.822	1.00	249.69
	1752	CE1	PHE	A	31	21.706	29.372	8.749	1.00	249.69
	1753	CE2	PHE	A	31	22.978	27.971	7.263	1.00	249.69
	1754	CZ	PHE	A	31	22.644	29.238	7.730	1.00	249.69
10	1755	C	PHE	A	31	18.752	24.200	9.450	1.00	249.69
	1756	O	PHE	A	31	18.444	24.144	10.647	1.00	249.69
	1757	N	PHE	A	32	18.608	23.175	8.608	1.00	249.69
	1758	CA	PHE	A	32	18.052	21.879	9.017	1.00	249.69
	1759	CB	PHE	A	32	16.789	21.579	8.201	1.00	249.69
15	1760	CG	PHE	A	32	15.943	20.469	8.766	1.00	249.69
	1761	CD1	PHE	A	32	15.293	20.621	9.991	1.00	249.69
	1762	CD2	PHE	A	32	15.785	19.274	8.064	1.00	249.69
	1763	CE1	PHE	A	32	14.496	19.598	10.509	1.00	249.69
	1764	CE2	PHE	A	32	14.990	18.245	8.573	1.00	249.69
20	1765	CZ	PHE	A	32	14.345	18.408	9.798	1.00	249.69
	1766	C	PHE	A	32	19.088	20.757	8.821	1.00	249.69
	1767	O	PHE	A	32	20.125	20.964	8.170	1.00	231.29
	1768	N	GLU	A	33	18.798	19.569	9.358	1.00	231.29
	1769	CA	GLU	A	33	19.741	18.455	9.270	1.00	249.69
25	1770	CB	GLU	A	33	20.145	18.036	10.688	1.00	249.69
	1771	CG	GLU	A	33	21.430	17.234	10.751	1.00	249.69
	1772	CD	GLU	A	33	22.544	17.870	9.925	1.00	249.69
	1773	OE1	GLU	A	33	22.781	19.095	10.061	1.00	249.69
	1774	OE2	GLU	A	33	23.193	17.142	9.140	1.00	231.29
30	1775	C	GLU	A	33	19.334	17.212	8.477	1.00	231.29
	1776	O	GLU	A	33	20.088	16.746	7.624	1.00	249.69
	1777	N	VAL	A	34	18.156	16.671	8.765	1.00	249.69
	1778	CA	VAL	A	34	17.677	15.462	8.096	1.00	206.86
	1779	CB	VAL	A	34	16.288	15.045	8.664	1.00	206.86
35	1780	CG1	VAL	A	34	15.809	13.765	8.012	1.00	206.86
	1781	CG2	VAL	A	34	16.382	14.858	10.166	1.00	249.69
	1782	C	VAL	A	34	17.599	15.536	6.560	1.00	249.69
	1783	O	VAL	A	34	17.381	16.608	5.977	1.00	249.69
	1784	N	SER	A	35	17.793	14.378	5.920	1.00	249.69
40	1785	CA	SER	A	35	17.744	14.245	4.458	1.00	177.13
	1786	CB	SER	A	35	18.968	13.478	3.941	1.00	177.13
	1787	OG	SER	A	35	18.874	12.099	4.268	1.00	249.69
	1788	C	SER	A	35	16.483	13.467	4.082	1.00	249.69
	1789	O	SER	A	35	16.208	13.245	2.902	1.00	238.60
45	1790	N	SER	A	36	15.739	13.038	5.100	1.00	238.60
	1791	CA	SER	A	36	14.506	12.290	4.902	1.00	249.69
	1792	CB	SER	A	36	14.437	11.091	5.862	1.00	249.69
	1793	OG	SER	A	36	14.205	11.498	7.203	1.00	238.60
	1794	C	SER	A	36	13.298	13.200	5.121	1.00	238.60
50	1795	O	SER	A	36	12.807	13.368	6.238	1.00	223.58
	1796	N	THR	A	37	12.835	13.795	4.030	1.00	223.58
	1797	CA	THR	A	37	11.686	14.678	4.061	1.00	216.59
	1798	CB	THR	A	37	12.108	16.135	3.751	1.00	216.59
	1799	OG1	THR	A	37	13.071	16.572	4.723	1.00	216.59
55	1800	CG2	THR	A	37	10.904	17.061	3.786	1.00	223.58
	1801	C	THR	A	37	10.706	14.165	3.004	1.00	223.58
	1802	O	THR	A	37	11.104	13.773	1.901	1.00	249.69
	1803	N	LYS	A	38	9.425	14.148	3.349	1.00	249.69
	1804	CA	LYS	A	38	8.410	13.655	2.430	1.00	249.69
60	1805	CB	LYS	A	38	7.490	12.670	3.166	1.00	249.69
	1806	CG	LYS	A	38	8.232	11.473	3.770	1.00	249.69
	1807	CD	LYS	A	38	7.296	10.511	4.515	1.00	249.69
	1808	CE	LYS	A	38	8.060	9.293	5.053	1.00	249.69
	1809	NZ	LYS	A	38	7.181	8.326	5.770	1.00	249.69
65	1810	C	LYS	A	38	7.588	14.782	1.806	1.00	249.69
	1811	O	LYS	A	38	7.301	15.793	2.456	1.00	201.19
	1812	N	TRP	A	39	7.229	14.611	0.536	1.00	201.19
	1813	CA	TRP	A	39	6.425	15.604	-0.171	1.00	173.49
	1814	CB	TRP	A	39	7.256	16.294	-1.250	1.00	173.49
70	1815	CG	TRP	A	39	8.384	17.170	-0.741	1.00	173.49

	1816	CD2	TRP A	39	8.282	18.328	0.122	1.00	173.49
	1817	CE2	TRP A	39	9.574	18.892	0.223	1.00	173.49
	1818	CE3	TRP A	39	7.223	18.950	0.812	1.00	173.49
	1819	CD1	TRP A	39	9.703	17.079	-1.099	1.00	173.49
5	1820	NE1	TRP A	39	10.418	18.112	-0.528	1.00	173.49
	1821	CZ2	TRP A	39	9.836	20.031	0.972	1.00	173.49
	1822	CZ3	TRP A	39	7.489	20.083	1.554	1.00	173.49
	1823	CH2	TRP A	39	8.785	20.611	1.629	1.00	173.49
	1824	C	TRP A	39	5.263	14.870	-0.821	1.00	201.19
10	1825	O	TRP A	39	5.473	13.844	-1.463	1.00	201.19
	1826	N	PHE A	40	4.045	15.385	-0.655	1.00	233.06
	1827	CA	PHE A	40	2.875	14.733	-1.231	1.00	233.06
	1828	CB	PHE A	40	1.983	14.154	-0.122	1.00	249.42
	1829	CG	PHE A	40	2.671	13.151	0.775	1.00	249.42
15	1830	CD1	PHE A	40	3.484	13.580	1.820	1.00	249.42
	1831	CD2	PHE A	40	2.482	11.778	0.592	1.00	249.42
	1832	CE1	PHE A	40	4.098	12.658	2.674	1.00	249.42
	1833	CE2	PHE A	40	3.089	10.854	1.435	1.00	249.42
	1834	CZ	PHE A	40	3.899	11.294	2.479	1.00	249.42
20	1835	C	PHE A	40	2.023	15.621	-2.139	1.00	233.06
	1836	O	PHE A	40	0.945	16.063	-1.744	1.00	233.06
	1837	N	HIS A	41	2.506	15.858	-3.358	1.00	146.58
	1838	CA	HIS A	41	1.787	16.676	-4.340	1.00	146.58
	1839	CB	HIS A	41	2.663	16.905	-5.569	1.00	196.00
25	1840	CG	HIS A	41	2.012	17.747	-6.619	1.00	196.00
	1841	CD2	HIS A	41	2.035	17.661	-7.971	1.00	196.00
	1842	ND1	HIS A	41	1.259	18.864	-6.322	1.00	196.00
	1843	CE1	HIS A	41	0.849	19.429	-7.441	1.00	196.00
	1844	NE2	HIS A	41	1.308	18.719	-8.457	1.00	196.00
30	1845	C	HIS A	41	0.459	16.041	-4.776	1.00	146.58
	1846	O	HIS A	41	0.458	15.095	-5.564	1.00	146.58
	1847	N	ASN A	42	-0.660	16.586	-4.280	1.00	208.40
	1848	CA	ASN A	42	-2.004	16.067	-4.570	1.00	208.40
	1849	CB	ASN A	42	-2.229	15.933	-6.087	1.00	249.69
35	1850	CG	ASN A	42	-2.538	17.270	-6.763	1.00	249.69
	1851	OD1	ASN A	42	-1.824	18.251	-6.553	1.00	249.69
	1852	ND2	ASN A	42	-3.591	17.305	-7.583	1.00	249.69
	1853	C	ASN A	42	-2.173	14.703	-3.887	1.00	208.40
	1854	O	ASN A	42	-2.981	13.871	-4.302	1.00	208.40
40	1855	N	GLY A	43	-1.401	14.499	-2.824	1.00	249.69
	1856	CA	GLY A	43	-1.445	13.248	-2.092	1.00	249.69
	1857	C	GLY A	43	-0.354	12.288	-2.555	1.00	249.69
	1858	O	GLY A	43	0.302	11.620	-1.744	1.00	249.69
	1859	N	SER A	44	-0.158	12.222	-3.870	1.00	243.81
45	4860	CA	SER A	44	0.845	11.350	-4.481	1.00	243.81
	1861	CB	SER A	44	0.812	11.493	-6.004	1.00	249.09
	1862	OG	SER A	44	-0.450	11.141	-6.535	1.00	249.69
	1863	C	SER A	44	2.250	11.676	-4.002	1.00	243.81
	1864	O	SER A	44	2.714	12.806	-4.162	1.00	243.81
50	1865	N	LEU A	45	2.936	10.687	-3.437	1.00	249.69
	1866	CA	LEU A	45	4.294	10.912	-2.958	1.00	249.69
	1867	CB	LEU A	45	4.913	9.605	-2.458	1.00	240.25
	1868	CG	LEU A	45	6.324	9.745	-1.879	1.00	240.25
	1869	CD1	LEU A	45	6.328	10.787	-0.773	1.00	240.25
55	1870	CD2	LEU A	45	6.798	8.405	-1.351	1.00	240.25
	1871	C	LEU A	45	5.160	11.512	-4.070	1.00	249.69
	1872	O	LEU A	45	4.939	11.248	-5.256	1.00	249.69
	1873	N	SER A	46	6.136	12.329	-3.675	1.00	216.07
	1874	CA	SER A	46	7.028	12.988	-4.621	1.00	216.07
60	1875	CB	SER A	46	7.156	14.473	-4.270	1.00	249.69
	1876	OG	SER A	46	7.934	15.159	-5.237	1.00	249.69
	1877	C	SER A	46	8.409	12.344	-4.645	1.00	216.07
	1878	O	SER A	46	8.733	11.515	-3.795	1.00	216.07
	1879	N	GLU A	47	9.223	12.753	-5.616	1.00	204.74
65	1880	CA	GLU A	47	10.572	12.214	-5.797	1.00	204.74
	1881	CB	GLU A	47	10.901	12.162	-7.289	1.00	249.69
	1882	CG	GLU A	47	9.973	11.256	-8.078	1.00	249.69
	1883	CD	GLU A	47	10.299	11.239	-9.554	1.00	249.69
	1884	OE1	GLU A	47	10.185	12.307	-10.203	1.00	249.69
70	1885	OE2	GLU A	47	10.673	10.158	-10.066	1.00	249.69

1886	C	GLU	A	47	11.702	12.933	-5.059	1.00	204.74
1887	O	GLU	A	47	12.819	12.424	-4.995	1.00	204.74
1888	N	GLU	A	48	11.429	14.113	-4.512	1.00	206.77
1889	CA	GLU	A	48	12.459	14.833	-3.780	1.00	206.77
1890	CB	GLU	A	48	12.206	16.344	-3.812	1.00	249.43
1891	CG	GLU	A	48	13.200	17.159	-2.982	1.00	249.43
1892	CD	GLU	A	48	14.627	17.087	-3.507	1.00	249.43
1893	OE1	GLU	A	48	14.902	17.685	-4.569	1.00	249.43
1894	OE2	GLU	A	48	15.472	16.431	-2.859	1.00	249.43
1895	C	GLU	A	48	12.492	14.344	-2.335	1.00	206.77
1896	O	GLU	A	48	11.500	13.825	-1.811	1.00	206.77
1897	N	THR	A	49	13.648	14.506	-1.702	1.00	249.69
1898	CA	THR	A	49	13.844	14.085	-0.324	1.00	249.69
1899	CB	THR	A	49	14.806	12.890	-0.252	1.00	249.53
1900	OG1	THR	A	49	16.030	13.218	-0.928	1.00	249.53
1901	CG2	THR	A	49	14.174	11.671	-0.909	1.00	249.53
1902	C	THR	A	49	14.417	15.232	0.500	1.00	249.69
1903	O	THR	A	49	14.224	15.294	1.716	1.00	249.69
1904	N	ASN	A	50	15.128	16.136	-0.166	1.00	249.69
1905	CA	ASN	A	50	15.710	17.294	0.504	1.00	249.69
1906	CB	ASN	A	50	16.438	18.174	-0.519	1.00	232.42
1907	CG	ASN	A	50	17.276	19.254	0.134	1.00	232.42
1908	OD1	ASN	A	50	17.063	19.590	1.301	1.00	232.42
1909	ND2	ASN	A	50	18.219	19.813	-0.615	1.00	232.42
1910	C	ASN	A	50	14.552	18.073	1.142	1.00	249.69
1911	O	ASN	A	50	13.423	18.003	0.658	1.00	249.69
1912	N	SER	A	51	14.817	18.808	2.217	1.00	181.87
1913	CA	SER	A	51	13.759	19.568	2.873	1.00	181.87
1914	CB	SER	A	51	14.240	20.110	4.220	1.00	249.47
1915	OG	SER	A	51	15.152	21.181	4.047	1.00	249.47
1916	C	SER	A	51	13.249	20.725	2.016	1.00	181.87
1917	O	SER	A	51	12.180	21.269	2.293	1.00	181.87
1918	N	SER	A	52	14.007	21.104	0.984	1.00	193.91
1919	CA	SER	A	52	13.606	22.199	0.087	1.00	193.91
1920	C8	SER	A	52	14.735	23.217	-0.086	1.00	144.08
1921	OG	SER	A	52	15.064	23.831	1.139	1.00	144.08
1922	C	SER	A	52	13.196	21.706	-1.297	1.00	193.91
1923	O	SER	A	52	14.045	21.367	-2.126	1.00	193.91
1924	N	LEU	A	53	11.890	21.680	-1.539	1.00	177.42
1925	CA	LEU	A	53	11.346	21.239	-2.817	1.00	177.42
1926	CB	LEU	A	53	10.034	20.488	-2.595	1.00	145.45
1927	CG	LEU	A	53	9.082	20.340	-3.785	1.00	145.45
1928	CD1	LEU	A	53	9.821	19.891	-5.043	1.00	145.45
1929	CD2	LEU	A	53	7.997	19.343	-3.401	1.00	145.45
1930	C	LEU	A	53	11.108	22.423	-3.737	1.00	177.42
1931	O	LEU	A	53	10.143	23.168	-3.574	1.00	177.42
1932	N	ASN	A	54	11.991	22.591	-4.709	1.00	220.39
1933	CA	ASN	A	54	11.845	23.692	-5.635	1.00	220.39
1934	CB	ASN	A	54	13.187	24.045	-6.254	1.00	193.36
1935	CG	ASN	A	54	14.109	24.677	-5.264	1.00	193.36
1936	OD1	ASN	A	54	13.746	25.644	-4.602	1.00	193.36
1937	ND2	ASN	A	54	15.311	24.140	-5.145	1.00	193.36
1938	C	ASN	A	54	10.834	23.415	-6.729	1.00	220.39
1939	O	ASN	A	54	10.486	22.267	-7.009	1.00	220.39
1940	N	ILE	A	55	10.362	24.496	-7.333	1.00	206.48
1941	CA	ILE	A	55	9.393	24.451	-8.415	1.00	206.48
1942	CB	ILE	A	55	7.984	24.867	-7.921	1.00	168.43
1943	CG2	ILE	A	55	7.135	25.353	-9.080	1.00	168.43
1944	CG1	ILE	A	55	7.316	23.696	-7.206	1.00	168.43
1945	CD1	ILE	A	55	5.920	24.004	-6.681	1.00	168.43
1946	C	ILE	A	55	9.877	25.442	-9.459	1.00	206.48
1947	O	ILE	A	55	9.979	26.641	-9.190	1.00	206.48
1948	N	VAL	A	56	10.194	24.943	-10.646	1.00	242.77
1949	CA	VAL	A	56	10.667	25.821	-11.700	1.00	242.77
1950	CB	VAL	A	56	11.790	25.165	-12.499	1.00	249.69
1951	CG1	VAL	A	56	12.589	26.233	-13.240	1.00	249.69
1952	CG2	VAL	A	56	12.687	24.377	-11.562	1.00	249.69
1953	C	VAL	A	56	9.511	26.168	-12.624	1.00	242.77
1954	O	VAL	A	56	8.354	26.060	-12.225	1.00	242.77
1955	N	ASN	A	57	9.822	26.580	-13.853	1.00	177.18

	Serial	Atom	Res	Chain	Res#	X	Y	Z	Occ	B
	1956	CA	ASN	A	57	8.804	26.971	-14.835	1.00	177.18
	1957	CB	ASN	A	57	9.265	26.619	-16.250	1.00	249.69
	1958	CG	ASN	A	57	10.430	27.489	-16.705	1.00	249.69
	1959	OD1	ASN	A	57	10.372	28.721	-16.617	1.00	249.69
5	1960	ND2	ASN	A	57	11.494	26.853	-17.187	1.00	249.69
	1961	C	ASN	A	57	7.436	26.374	-14.547	1.00	177.18
	1962	O	ASN	A	57	7.105	25.264	-14.964	1.00	177.18
	1963	N	ALA	A	58	6.661	27.166	-13.816	1.00	241.59
	1964	CA	ALA	A	58	5.322	26.838	-13.362	1.00	241.59
10	1965	CB	ALA	A	58	4.739	28.038	-12.623	1.00	177.10
	1966	C	ALA	A	58	4.339	26.363	-14.416	1.00	241.59
	1967	O	ALA	A	58	3.857	27.134	-15.237	1.00	241.59
	1968	N	LYS	A	59	4.031	25.077	-14.363	1.00	126.26
	1969	CA	LYS	A	59	3.078	24.446	-15.277	1.00	126.26
15	1970	CB	LYS	A	59	3.820	23.088	-15.761	1.00	249.69
	1971	CG	LYS	A	59	4.959	23.183	-16.494	1.00	249.69
	1972	CD	LYS	A	59	5.515	21.808	-16.859	1.00	249.69
	1973	CE	LYS	A	59	6.883	21.939	-17.528	1.00	249.69
	1974	NZ	LYS	A	59	7.458	20.619	-17.910	1.00	249.69
20	1975	C	LYS	A	59	1.790	24.246	-14.486	1.00	126.26
	1976	O	LYS	A	59	1.810	23.891	-13.311	1.00	126.26
	1977	N	PHE	A	60	0.672	24.490	-15.139	1.00	178.77
	1978	CA	PHE	A	60	-0.622	24.356	-14.497	1.00	178.77
	1979	CB	PHE	A	60	-1.715	24.325	-15.570	1.00	238.68
25	1980	CG	PHE	A	60	-1.824	25.601	-16.362	1.00	238.68
	1981	CD1	PHE	A	60	-2.296	25.585	-17.670	1.00	238.68
	1982	CD2	PHE	A	60	-1.468	26.820	-15.794	1.00	238.68
	1983	CE1	PHE	A	60	-2.411	26.758	-18.400	1.00	238.68
	1984	CE2	PHE	A	60	-1.580	28.002	-16.515	1.00	238.68
30	1985	CZ	PHE	A	60	-2.053	27.969	-17.821	1.00	238.68
	1986	C	PHE	A	60	-0.746	23.132	-13.592	1.00	178.77
	1987	O	PHE	A	60	-1.468	23.162	-12.588	1.00	178.77
	1988	N	GLU	A	61	-0.040	22.063	-13.948	1.00	249.03
	1989	CA	GLU	A	61	-0.076	20.822	-13.181	1.00	249.03
35	1990	CB	GLU	A	61	0.665	19.719	-13.945	1.00	249.30
	1991	CG	GLU	A	61	0.091	19.402	-15.330	1.00	249.30
	1992	CD	GLU	A	61	0.076	20.605	-16.264	1.00	249.30
	1993	OE1	GLU	A	61	1.132	21.254	-16.436	1.00	249.30
	1994	OE2	GLU	A	61	-0.997	20.895	-16.833	1.00	249.30
40	1995	C	GLU	A	61	0.537	20.991	-11.792	1.00	249.03
	1996	O	GLU	A	61	0.222	20.236	-10.870	1.00	249.03
	1997	N	ASP	A	62	1.412	21.984	-11.648	1.00	157.91
	1998	CA	ASP	A	62	2.062	22.251	-10.372	1.00	157.91
	1999	CB	ASP	A	62	3.191	23.264	-10.539	1.00	172.18
45	2000	CG	ASP	A	62	4.167	22.856	-11.598	1.00	172.18
	2001	OD1	ASP	A	62	4.368	21.633	-11.779	1.00	172.18
	2002	OD2	ASP	A	62	4.743	23.753	-12.244	1.00	172.18
	2003	C	ASP	A	62	1.058	22.795	-9.366	1.00	157.91
	2004	O	ASP	A	62	1.266	22.700	-8.159	1.00	157.91
50	2005	N	SER	A	63	-0.026	23.384	-9.864	1.00	191.12
	2006	CA	SER	A	63	-1.061	23.933	-8.991	1.00	191.12
	2007	CB	SER	A	63	-2.179	24.576	-9.822	1.00	203.60
	2008	OG	SER	A	63	-1.685	25.593	-10.671	1.00	203.60
	2009	C	SER	A	63	-1.634	22.778	-8.186	1.00	191.12
55	2010	O	SER	A	63	-2.040	21.773	-8.753	1.00	191.12
	2011	N	GLY	A	64	-1.662	22.907	-6.870	1.00	195.42
	2012	CA	GLY	A	64	-2.199	21.821	-6.087	1.00	195.42
	2013	C	GLY	A	64	-1.967	21.897	-4.596	1.00	195.42
	2014	O	GLY	A	64	-1.583	22.940	-4.069	1.00	195.42
60	2015	N	GLU	A	65	-2.199	20.765	-3.933	1.00	249.69
	2016	CA	GLU	A	65	-2.064	20.613	-2.484	1.00	249.69
	2017	CB	GLU	A	65	-3.302	19.876	-1.969	1.00	246.11
	2018	CG	GLU	A	65	-3.277	19.481	-0.514	1.00	246.11
	2019	CD	GLU	A	65	-4.310	18.417	-0.207	1.00	246.11
65	2020	OE1	GLU	A	65	-4.201	17.309	-0.778	1.00	246.11
	2021	OE2	GLU	A	65	-5.230	18.684	0.597	1.00	246.11
	2022	C	GLU	A	65	-0.790	19.844	-2.112	1.00	249.69
	2023	O	GLU	A	65	-0.613	18.711	-2.540	1.00	249.69
	2024	N	TYR	A	66	0.083	20.456	-1.308	1.00	196.27
70	2025	CA	TYR	A	66	1.334	19.818	-0.890	1.00	196.27

	2026	CB	TYR	A	66	2.534	20.641	-1.324	1.00	181.47
	2027	CG	TYR	A	66	2.737	20.798	-2.807	1.00	181.47
	2028	CD1	TYR	A	66	1.966	21.687	-3.549	1.00	181.47
	2029	CE1	TYR	A	66	2.227	21.911	-4.896	1.00	181.47
5	2030	CD2	TYR	A	66	3.769	20.122	-3.454	1.00	181.47
	2031	CE2	TYR	A	66	4.040	20.332	-4.800	1.00	181.47
	2032	CZ	TYR	A	66	3.268	21.230	-5.513	1.00	181.47
	2033	OH	TYR	A	66	3.561	21.460	-6.838	1.00	181.47
	2034	C	TYR	A	66	1.462	19.616	0.622	1.00	196.27
10	2035	O	TYR	A	66	0.665	20.149	1.402	1.00	196.27
	2036	N	LYS	A	67	2.493	18.862	1.021	1.00	214.47
	2037	CA	LYS	A	67	2.778	18.572	2.435	1.00	214.47
	2038	CB	LYS	A	67	1.630	17.783	3.059	1.00	179.29
	2039	CG	LYS	A	67	1.262	16.527	2.300	1.00	179.29
15	2040	CD	LYS	A	67	0.071	15.859	2.955	1.00	179.29
	2041	CE	LYS	A	67	-0.626	14.887	2.008	1.00	179.29
	2042	NZ	LYS	A	67	-1.808	14.194	2.632	1.00	179.29
	2043	C	LYS	A	67	4.077	17.799	2.681	1.00	214.47
	2044	O	LYS	A	67	4.546	17.060	1.826	1.00	214.47
20	2045	N	CYS	A	68	4.644	17.981	3.869	1.00	202.66
	2046	CA	CYS	A	68	5.865	17.291	4.259	1.00	202.66
	2047	C	CYS	A	68	5.713	16.618	5.621	1.00	202.66
	2048	O	CYS	A	68	4.961	17.075	6.483	1.00	202.66
	2049	CB	CYS	A	68	7.067	18.245	4.273	1.00	195.74
25	2050	SG	CYS	A	68	7.101	19.551	5.556	1.00	195.74
	2051	N	GLN	A	69	6.439	15.519	5.797	1.00	233.18
	2052	CA	GLN	A	69	6.420	14.730	7.024	1.00	233.18
	2053	CB	GLN	A	69	5.367	13.631	6.896	1.00	249.69
	2054	CG	GLN	A	69	5.562	12.460	7.835	1.00	249.69
30	2055	CD	GLN	A	69	4.580	11.333	7.569	1.00	249.69
	2056	OE1	GLN	A	69	4.451	10.865	6.436	1.00	249.69
	2057	NE2	GLN	A	69	3.888	10.885	8.615	1.00	249.69
	2058	C	GLN	A	69	7.798	14.111	7.224	1.00	233.18
	2059	O	GLN	A	69	8.485	13.796	6.254	1.00	233.18
35	2060	N	HIS	A	70	8.206	13.942	8.477	1.00	249.54
	2061	CA	HIS	A	70	9.508	13.348	8.757	1.00	249.54
	2062	CB	HIS	A	70	10.202	14.086	9.904	1.00	249.69
	2063	CG	HIS	A	70	10.674	15.458	9.536	1.00	249.69
	2064	CD2	HIS	A	70	10.459	16.662	10.116	1.00	249.69
40	2065	ND1	HIS	A	70	11.475	15.699	8.439	1.00	249.69
	2066	CE1	HIS	A	70	11.731	16.992	8.359	1.00	249.69
	2067	NE2	HIS	A	70	11.126	17.600	9.366	1.00	249.69
	2068	C	HIS	A	70	9.393	11.867	9.084	1.00	249.54
	2069	O	HIS	A	70	8.327	11.270	8.917	1.00	249.54
45	2070	N	GLN	A	71	10.496	11.283	9.549	1.00	249.69
	2071	CA	GLN	A	71	10.546	9.863	9.894	1.00	249.69
	2072	CB	GLN	A	71	11.944	9.520	10.429	1.00	249.69
	2073	CG	GLN	A	71	12.318	8.033	10.415	1.00	249.69
	2074	CD	GLN	A	71	12.356	7.432	9.015	1.00	249.69
50	2075	OE1	GLN	A	71	12.933	8.009	8.090	1.00	249.69
	2076	NE2	GLN	A	71	11.749	6.257	8.859	1.00	249.69
	2077	C	GLN	A	71	9.474	9.485	10.925	1.00	249.69
	2078	O	GLN	A	71	8.737	8.505	10.747	1.00	249.69
	2079	N	GLN	A	72	9.383	10.270	11.995	1.00	249.69
55	2080	CA	GLN	A	72	8.413	10.013	13.056	1.00	249.69
	2081	CB	GLN	A	72	9.148	9.484	14.292	1.00	249.69
	2082	CG	GLN	A	72	8.266	9.132	15.487	1.00	249.69
	2083	CD	GLN	A	72	9.085	8.768	16.717	1.00	249.69
	2084	OE1	GLN	A	72	9.910	7.853	16.679	1.00	249.69
60	2085	NE2	GLN	A	72	8.860	9.486	17.817	1.00	249.69
	2086	C	GLN	A	72	7.634	11.288	13.402	1.00	249.69
	2087	O	GLN	A	72	7.602	11.722	14.558	1.00	249.69
	2088	N	VAL	A	73	7.011	11.891	12.393	1.00	249.69
	2089	CA	VAL	A	73	6.233	13.108	12.595	1.00	249.69
65	2090	CB	VAL	A	73	7.036	14.377	12.200	1.00	239.35
	2091	CG1	VAL	A	73	6.321	15.615	12.720	1.00	239.35
	2092	CG2	VAL	A	73	8.449	14.304	12.750	1.00	239.35
	2093	C	VAL	A	73	4.979	13.047	11.731	1.00	249.69
	2094	O	VAL	A	73	5.014	12.526	10.619	1.00	249.69
70	2095	N	ASN	A	74	3.875	13.578	12.245	1.00	249.69

	2096	CA	ASN	A	74	2.627	13.580	11.494	1.00	249.69
	2097	CB	ASN	A	74	1.448	13.799	12.450	1.00	244.75
	2098	CG	ASN	A	74	1.421	12.775	13.581	1.00	244.75
	2099	OD1	ASN	A	74	1.672	11.588	13.354	1.00	244.75
5	2100	ND2	ASN	A	74	1.112	13.230	14.793	1.00	244.75
	2101	C	ASN	A	74	2.667	14.663	10.404	1.00	249.69
	2102	O	ASN	A	74	2.979	15.828	10.680	1.00	249.69
	2103	N	GLU	A	75	2.362	14.262	9.167	1.00	249.69
	2104	CA	GLU	A	75	2.370	15.160	8.008	1.00	249.69
10	2105	CB	GLU	A	75	1.656	14.485	6.826	1.00	249.69
	2106	CG	GLU	A	75	0.447	13.641	7.216	1.00	249.69
	2107	CD	GLU	A	75	-0.086	12.806	6.064	1.00	249.69
	2108	OE1	GLU	A	75	0.722	12.115	5.408	1.00	249.69
	2109	OE2	GLU	A	75	-1.312	12.831	5.820	1.00	249.69
15	2110	C	GLU	A	75	1.786	16.556	8.262	1.00	249.69
	2111	O	GLU	A	75	0.776	16.714	8.954	1.00	249.69
	2112	N	SER	A	76	2.437	17.562	7.682	1.00	249.69
	2113	CA	SER	A	76	2.037	18.959	7.833	1.00	249.69
	2114	CB	SER	A	76	3.093	19.877	7.212	1.00	185.73
20	2115	OG	SER	A	76	3.026	19.638	5.796	1.00	185.73
	2116	C	SER	A	76	0.691	19.291	7.206	1.00	249.69
	2117	O	SER	A	76	0.212	18.589	6.316	1.00	249.69
	2118	N	GLU	A	77	0.093	20.382	7.677	1.00	249.69
	2119	CA	GLU	A	77	-1.187	20.845	7.153	1.00	249.69
25	2120	CB	GLU	A	77	-1.695	22.053	7.952	1.00	249.63
	2121	CG	GLU	A	77	-2.038	21.734	9.394	1.00	249.63
	2122	CD	GLU	A	77	-3.175	20.742	9.515	1.00	249.63
	2123	OE1	GLU	A	77	-3.606	20.194	8.477	1.00	249.63
	2124	OE2	GLU	A	77	-3.633	20.508	10.653	1.00	249.63
30	2125	C	GLU	A	77	-0.961	21.250	5.701	1.00	249.69
	2126	O	GLU	A	77	-0.262	22.226	5.423	1.00	249.69
	2127	N	PRO	A	78	-1.556	20.502	4.757	1.00	227.00
	2128	CD	PRO	A	78	-2.599	19.491	4.999	1.00	247.88
	2129	CA	PRO	A	78	-1.413	20.781	3.321	1.00	227.00
35	2130	CB	PRO	A	78	-2.583	20.012	2.710	1.00	247.88
	2131	CG	PRO	A	78	-2.752	18.854	3.641	1.00	227.00
	2132	C	PRO	A	78	-1.488	22.271	2.998	1.00	227.00
	2133	O	PRO	A	78	-2.039	23.054	3.771	1.00	169.93
	2134	N	VAL	A	79	-0.910	22.665	1.871	1.00	169.93
40	2135	CA	VAL	A	79	-0.966	24.059	1.435	1.00	154.03
	2136	CB	VAL	A	79	0.390	24.785	1.549	1.00	154.03
	2137	CG1	VAL	A	79	0.329	26.125	0.825	1.00	154.03
	2138	CG2	VAL	A	79	0.721	25.022	3.014	1.00	169.93
	2139	C	VAL	A	79	-1.342	23.987	-0.017	1.00	169.93
45	2140	O	VAL	A	79	-0.883	23.087	-0.710	1.00	161.75
	2141	N	TYR	A	80	-2.175	24.911	-0.487	1.00	161.75
	2142	CA	TYR	A	80	-2.581	24.874	-1.888	1.00	221.72
	2143	CB	TYR	A	80	-4.096	25.028	-2.025	1.00	221.72
	2144	CG	TYR	A	80	-4.606	24.573	-3.372	1.00	221.72
50	2145	CD1	TYR	A	80	-4.874	23.227	-3.618	1.00	221.72
	2146	CE1	TYR	A	80	-5.296	22.792	-4.874	1.00	221.72
	2147	CD2	TYR	A	80	-4.773	25.478	-4.418	1.00	221.72
	2148	CE2	TYR	A	80	-5.193	25.052	-5.679	1.00	221.72
	2149	CZ	TYR	A	80	-5.451	23.708	-5.896	1.00	221.72
55	2150	OH	TYR	A	80	-5.860	23.276	-7.134	1.00	161.75
	2151	C	TYR	A	80	-1.895	25.939	-2.725	1.00	161.75
	2152	O	TYR	A	80	-1.812	27.096	-2.329	1.00	159.92
	2153	N	LEU	A	81	-1.405	25.534	-3.889	1.00	159.92
	2154	CA	LEU	A	81	-0.741	26.451	-4.789	1.00	117.26
60	2155	CB	LEU	A	81	0.652	25.851	-5.138	1.00	117.26
	2156	CG	LEU	A	81	1.353	26.823	-6.188	1.00	117.26
	2157	CD1	LEU	A	81	1.556	28.213	-5.608	1.00	117.26
	2158	CD2	LEU	A	81	2.692	26.221	-6.600	1.00	159.92
	2159	C	LEU	A	81	-1.550	26.562	-6.067	1.00	159.92
65	2160	O	LEU	A	81	-1.879	25.541	-6.678	1.00	176.90
	2161	N	GLU	A	82	-1.879	27.786	-6.476	1.00	176.90
	2162	CA	GLU	A	82	-2.637	27.978	-7.709	1.00	239.33
	2163	CB	GLU	A	82	-3.850	28.697	-7.427	1.00	239.33
	2164	CG	GLU	A	82	-5.021	28.382	-8.454	1.00	239.33
70	2165	CD	GLU	A	82	-6.337	29.072	-8.166	1.00	239.33

	2166	OE1	GLU	A	82	-6.678	29.235	-6.970	1.00	239.33
	2167	OE2	GLU	A	82	-7.038	29.437	-9.139	1.00	239.33
	2168	C	GLU	A	82	-1.815	28.772	-8.720	1.00	176.90
	2169	O	GLU	A	82	-1.176	29.768	-8.369	1.00	176.90
5	2170	N	VAL	A	83	-1.818	28.315	-9.973	1.00	167.08
	2171	CA	VAL	A	83	-1.078	28.988	-11.050	1.00	167.08
	2172	CB	VAL	A	83	-0.163	28.034	-11.817	1.00	127.07
	2173	CG1	VAL	A	83	0.595	28.807	-12.899	1.00	127.07
	2174	CG2	VAL	A	83	0.800	27.368	-10.847	1.00	127.07
10	2175	C	VAL	A	83	-2.036	29.634	-12.043	1.00	167.08
	2176	O	VAL	A	83	-3.077	29.071	-12.390	1.00	136.71
	2177	N	PHE	A	84	-1.653	30.810	-12.524	1.00	136.71
	2178	CA	PHE	A	84	-2.502	31.588	-13.412	1.00	180.02
	2179	CB	PHE	A	84	-3.039	32.805	-12.669	1.00	180.02
15	2180	CG	PHE	A	84	-3.878	32.481	-11.481	1.00	180.02
	2181	CD1	PHE	A	84	-3.296	32.143	-10.263	1.00	180.02
	2182	CD2	PHE	A	84	-5.259	32.534	-11.575	1.00	180.02
	2183	CE1	PHE	A	84	-4.085	31.871	-9.157	1.00	180.02
	2184	CE2	PHE	A	84	-6.055	32.266	-10.484	1.00	180.02
20	2185	CZ	PHE	A	84	-5.471	31.933	-9.274	1.00	180.02
	2186	C	PHE	A	84	-1.917	32.125	-14.692	1.00	136.71
	2187	O	PHE	A	84	-0.710	32.289	-14.838	1.00	136.71
	2188	N	SER	A	85	-2.822	32.440	-15.606	1.00	185.25
	2189	CA	SER	A	85	-2.470	33.050	-16.871	1.00	185.25
25	2190	CB	SER	A	85	-2.639	32.088	-18.036	1.00	191.52
	2191	OG	SER	A	85	-2.269	32.736	-19.246	1.00	191.52
	2192	C	SER	A	85	-3.462	34.193	-17.012	1.00	185.25
	2193	O	SER	A	85	-4.680	33.960	-17.105	1.00	185.25
	2194	N	ASP	A	86	-2.940	35.422	-17.002	1.00	167.09
30	2195	CA	ASP	A	86	-3.769	36.623	-17.117	1.00	167.09
	2196	CB	ASP	A	86	-4.744	36.701	-15.951	1.00	156.75
	2197	CG	ASP	A	86	-6.072	37.252	-16.358	1.00	156.75
	2198	OD1	ASP	A	86	-6.110	38.341	-16.985	1.00	156.75
	2199	OD2	ASP	A	86	-7.083	36.587	-16.045	1.00	156.75
35	2200	C	ASP	A	86	-2.888	37.852	-17.101	1.00	167.09
	2201	O	ASP	A	86	-1.708	37.760	-16.775	1.00	167.09
	2202	N	TRP	A	87	-3.455	39.005	-17.438	1.00	147.13
	2203	CA	TRP	A	87	-2.665	40.233	-17.435	1.00	147.13
	2204	CB	TRP	A	87	-3.446	41.371	-18.079	1.00	200.84
40	2205	CG	TRP	A	87	-3.221	41.441	-19.553	1.00	200.84
	2206	CD2	TRP	A	87	-4.022	40.824	-20.563	1.00	200.84
	2207	CE2	TRP	A	87	-3.413	41.103	-21.798	1.00	200.84
	2208	CE3	TRP	A	87	-5.199	40.061	-20.542	1.00	200.84
	2209	CD1	TRP	A	87	-2.185	42.053	-20.202	1.00	200.84
45	2210	NE1	TRP	A	87	-2.292	41.854	-21.551	1.00	200.84
	2211	CZ2	TRP	A	87	-3.942	40.645	-23.002	1.00	200.84
	2212	CZ3	TRP	A	87	-5.726	39.602	-21.752	1.00	200.84
	2213	CH2	TRP	A	87	-5.095	39.899	-22.861	1.00	200.84
	2214	C	TRP	A	87	-2.233	40.608	-16.017	1.00	147.13
50	2215	O	TRP	A	87	-1.040	40.785	-15.743	1.00	147.13
	2216	N	LEU	A	88	-3.198	40.715	-15.108	1.00	135.82
	2217	CA	LEU	A	88	-2.886	41.049	-13.725	1.00	135.82
	2218	CB	LEU	A	88	-3.469	42.416	-13.366	1.00	139.19
	2219	CG	LEU	A	88	-2.870	43.605	-14.1?1	1.00	139.19
55	2220	CD1	LEU	A	88	-3.435	44.912	-13.593	1.00	139.19
	2221	CD2	LEU	A	88	-1.360	43.608	-14.008	1.00	139.19
	2222	C	LEU	A	88	-3.417	39.996	-12.772	1.00	135.82
	2223	O	LEU	A	88	-4.496	39.439	-12.976	1.00	135.82
	2224	N	LEU	A	89	-2.644	39.710	-11.736	1.00	146.34
60	2225	CA	LEU	A	89	-3.051	38.737	-10.728	1.00	148.34
	2226	CB	LEU	A	89	-2.210	37.466	-10.826	1.00	125.53
	2227	CG	LEU	A	89	-2.519	36.431	-9.741	1.00	125.53
	2228	CD1	LEU	A	89	-4.026	36.143	-9.713	1.00	125.53
	2229	CD2	LEU	A	89	-1.719	35.168	-10.009	1.00	125.53
65	2230	C	LEU	A	89	-2.854	39.355	-9.354	1.00	146.34
	2231	O	LEU	A	89	-1.785	39.903	-9.070	1.00	146.34
	2232	N	LEU	A	90	-3.875	39.282	-8.502	1.00	124.61
	2233	CA	LEU	A	90	-3.762	39.862	-7.173	1.00	124.61
	2234	CB	LEU	A	90	-5.132	40.294	-6.687	1.00	89.03
70	2235	CG	LEU	A	90	-5.136	40.759	-5.234	1.00	89.03

	2236	CD1	LEU	A	90	-4.192	41.932	-5.091	1.00	89.03
	2237	CD2	LEU	A	90	-6.549	41.132	-4.782	1.00	89.03
	2238	C	LEU	A	90	-3.160	38.861	-6.196	1.00	124.61
	2239	O	LEU	A	90	-3.766	37.842	-5.902	1.00	124.61
5	2240	N	GLN	A	91	-1.972	39.147	-5.686	1.00	143.99
	2241	CA	GLN	A	91	-1.335	38.229	-4.757	1.00	143.99
	2242	CB	GLN	A	91	0.139	38.062	-5.110	1.00	163.37
	2243	CG	GLN	A	91	0.382	37.527	-6.497	1.00	163.37
	2244	CD	GLN	A	91	1.861	37.383	-6.798	1.00	163.37
10	2245	OE1	GLN	A	91	2.620	38.356	-6.721	1.00	163.37
	2246	NE2	GLN	A	91	2.283	36.166	-7.143	1.00	163.37
	2247	C	GLN	A	91	-1.463	38.676	-3.304	1.00	143.99
	2248	O	GLN	A	91	-1.322	39.872	-2.991	1.00	143.99
	2249	N	ALA	A	92	-1.725	37.706	-2.421	1.00	122.21
15	2250	CA	ALA	A	92	-1.862	37.978	-0.991	1.00	122.21
	2251	CB	ALA	A	92	-3.283	37.702	-0.548	1.00	218.43
	2252	C	ALA	A	92	-0.892	37.128	-0.190	1.00	122.21
	2253	O	ALA	A	92	-0.653	35.960	-0.527	1.00	122.21
	2254	N	SER	A	93	-0.338	37.733	0.861	1.00	143.19
20	2255	CA	SER	A	93	0.612	37.067	1.742	1.00	143.19
	2256	CB	SER	A	93	0.964	37.975	2.935	1.00	121.60
	2257	OG	SER	A	93	-0.192	38.446	3.608	1.00	121.60
	2258	C	SER	A	93	-0.030	35.790	2.220	1.00	143.19
	2259	O	SER	A	93	0.452	34.690	1.941	1.00	143.19
25	2260	N	ALA	A	94	-1.121	35.958	2.948	1.00	129.43
	2261	CA	ALA	A	94	-1.880	34.831	3.446	1.00	129.43
	2262	CB	ALA	A	94	-1.688	34.686	4.950	1.00	204.58
	2263	C	ALA	A	94	-3.322	35.190	3.108	1.00	129.43
	2264	O	ALA	A	94	-3.620	36.387	2.969	1.00	129.43
30	2265	N	GLU	A	95	-4.208	34.193	2.955	1.00	144.02
	2266	CA	GLU	A	95	-5.601	34.499	2.632	1.00	144.02
	2267	CB	GLU	A	95	-6.144	33.467	1.668	1.00	173.81
	2268	CG	GLU	A	95	-5.434	33.492	0.344	1.00	173.81
	2269	CD	GLU	A	95	-6.123	32.642	-0.695	1.00	173.81
35	2270	OE1	GLU	A	95	-5.590	32.539	-1.831	1.00	173.81
	2271	OE2	GLU	A	95	-7.201	32.078	-0.378	1.00	173.81
	2272	C	GLU	A	95	-6.488	34.587	3.879	1.00	144.02
	2273	O	GLU	A	95	-7.548	35.222	3.857	1.00	144.02
	2274	N	VAL	A	96	-6.044	33.951	4.963	1.00	165.64
40	2275	CA	VAL	A	96	-6.778	33.966	6.222	1.00	165.64
	2276	CB	VAL	A	96	-7.256	32.573	6.592	1.00	130.98
	2277	CG1	VAL	A	96	-8.370	32.683	7.632	1.00	130.98
	2278	CG2	VAL	A	96	-7.722	31.830	5.359	1.00	130.98
	2279	C	VAL	A	96	-5.864	34.458	7.335	1.00	165.64
45	2280	O	VAL	A	96	-4.743	33.962	7.475	1.00	165.64
	2281	N	VAL	A	97	-6.339	35.404	8.147	1.00	117.82
	2282	CA	VAL	A	97	-5.483	35.949	9.204	1.00	117.82
	2283	CB	VAL	A	97	-4.908	37.299	8.784	1.00	171.13
	2284	CG1	VAL	A	97	-3.692	37.597	9.605	1.00	171.13
50	2285	CG2	VAL	A	97	-4.577	37.296	7.307	1.00	171.13
	2286	C	VAL	A	97	-6.078	36.149	10.585	1.00	117.82
	2287	O	VAL	A	97	-7.269	36.404	10.713	1.00	117.82
	2288	N	MET	A	98	-5.221	36.046	11.606	1.00	130.77
	2289	CA	MET	A	98	-5.592	36.228	13.025	1.00	130.77
55	2290	CB	MET	A	98	-4.587	35.504	13.927	1.00	249.69
	2291	CG	MET	A	98	-4.534	33.992	13.785	1.00	249.69
	2292	SD	MET	A	98	-5.915	33.193	14.587	1.00	249.69
	2293	CE	MET	A	98	-5.438	33.351	16.321	1.00	249.69
	2294	C	MET	A	98	-5.545	37.712	13.360	1.00	130.77
60	2295	O	MET	A	98	-4.509	38.332	13.187	1.00	130.77
	2296	N	GLU	A	99	-6.641	38.276	13.852	1.00	130.20
	2297	CA	GLU	A	99	-6.679	39.701	14.167	1.00	130.20
	2298	CB	GLU	A	99	-7.773	39.889	15.194	1.00	216.65
	2299	CG	GLU	A	99	-8.283	41.423	15.162	1.00	216.65
65	2300	CD	GLU	A	99	-9.161	41.757	16.355	1.00	216.65
	2301	OE1	GLU	A	99	-9.931	40.874	16.795	1.00	216.65
	2302	OE2	GLU	A	99	-9.088	42.904	16.844	1.00	216.65
	2303	C	GLU	A	99	-5.341	40.155	14.729	1.00	130.20
	2304	O	GLU	A	99	-4.832	39.538	15.672	1.00	130.20
70	2305	N	GLY	A	100	-4.752	41.206	14.157	1.00	150.30

Line	Serial	Atom	Res	Chain	ResNum	X	Y	Z	Occ	B
	2306	CA	GLY	A	100	-3.476	41.685	14.674	1.00	150.30
	2307	C	GLY	A	100	-2.232	41.342	13.889	1.00	150.30
	2308	O	GLY	A	100	-1.210	42.016	13.999	1.00	150.30
	2309	N	GLN	A	101	-2.305	40.305	13.043	1.00	149.89
5	2310	CA	GLN	A	101	-1.173	39.891	12.209	1.00	149.89
	2311	CB	GLN	A	101	-1.385	38.471	11.699	1.00	220.06
	2312	CG	GLN	A	101	-1.255	37.429	12.777	1.00	220.06
	2313	CD	GLN	A	101	-0.056	37.694	13.650	1.00	220.06
	2314	OE1	GLN	A	101	-0.048	38.646	14.431	1.00	220.06
10	2315	NE2	GLN	A	101	0.974	36.862	13.516	1.00	220.06
	2316	C	GLN	A	101	-0.918	40.831	11.033	1.00	149.89
	2317	O	GLN	A	101	-1.663	41.773	10.795	1.00	149.89
	2318	N	PRO	A	102	0.161	40.572	10.277	1.00	131.84
	2319	CD	PRO	A	102	1.289	39.692	10.571	1.00	202.39
15	2320	CA	PRO	A	102	0.440	41.436	9.131	1.00	131.84
	2321	CB	PRO	A	102	1.966	39.941	9.067	1.00	202.39
	2322	CG	PRO	A	102	2.222	40.960	9.395	1.00	202.39
	2323	C	PRO	A	102	-0.216	39.749	7.837	1.00	131.84
	2324	O	PRO	A	102	-0.418	41.915	7.627	1.00	131.84
20	2325	N	LEU	A	103	-0.531	41.589	6.960	1.00	120.38
	2326	CA	LEU	A	103	-1.150	41.909	5.695	1.00	120.38
	2327	CB	LEU	A	103	-2.620	41.329	5.782	1.00	119.50
	2328	CG	LEU	A	103	-3.321	39.821	4.569	1.00	119.50
	2329	CD1	LEU	A	103	-3.261	41.816	4.686	1.00	119.50
25	2330	CD2	LEU	A	103	-4.753	42.345	4.475	1.00	119.50
	2331	C	LEU	A	103	-0.542	43.582	4.508	1.00	120.38
	2332	O	LEU	A	103	-0.471	41.629	4.537	1.00	120.38
	2333	N	PHE	A	104	-0.116	42.300	3.462	1.00	130.73
	2334	CA	PHE	A	104	0.451	42.002	2.288	1.00	130.73
30	2335	CB	PHE	A	104	1.943	42.332	2.144	1.00	196.69
	2336	CG	PHE	A	104	2.747	41.480	3.353	1.00	196.69
	2337	CD1	PHE	A	104	2.753	43.499	4.446	1.00	196.69
	2338	CD2	PHE	A	104	3.493	41.787	3.410	1.00	196.69
	2339	CE1	PHE	A	104	3.495	43.815	5.589	1.00	196.69
35	2340	CE2	PHE	A	104	4.237	42.960	4.545	1.00	196.69
	2341	CZ	PHE	A	104	4.238	41.868	5.638	1.00	196.69
	2342	C	PHE	A	104	-0.236	40.673	1.004	1.00	130.73
	2343	O	PHE	A	104	-0.279	42.830	0.695	1.00	130.73
	2344	N	LEU	A	105	-0.774	42.514	0.258	1.00	119.49
40	2345	CA	LEU	A	105	-1.421	43.107	-1.015	1.00	119.49
	2346	CB	LEU	A	105	-2.813	42.614	-1.066	1.00	119.62
	2347	CG	LEU	A	105	-3.735	43.152	0.049	1.00	119.62
	2348	CD1	LEU	A	105	-5.138	41.092	-0.172	1.00	119.62
	2349	CD2	LEU	A	105	-3.738	43.084	0.063	1.00	119.62
45	2350	C	LEU	A	105	-0.579	44.104	-2.137	1.00	119.49
	2351	O	LEU	A	105	0.091	42.446	-1.971	1.00	119.49
	2352	N	ARG	A	106	-0.614	42.926	-3.291	1.00	119.67
	2353	CA	ARG	A	106	0.216	42.109	-4.373	1.00	119.67
	2354	CB	ARG	A	106	1.510	42.493	-4.377	1.00	158.51
50	2355	CG	ARG	A	106	2.513	41.503	-5.412	1.00	158.51
	2356	CD	ARG	A	106	3.656	41.787	-5.450	1.00	158.51
	2357	NE	ARG	A	106	4.522	40.876	-6.581	1.00	158.51
	2358	CZ	ARG	A	106	5.231	39.604	-7.233	1.00	158.51
	2359	NH1	ARG	A	106	5.180	41.239	-6.860	1.00	158.51
55	2360	NH2	ARG	A	106	5.973	42.808	-8.280	1.00	158.51
	2361	C	ARG	A	106	-0.505	41.737	-5.717	1.00	119.67
	2362	O	ARG	A	106	-1.026	43.915	-6.069	1.00	119.67
	2363	N	CYS	A	107	-0.564	43.904	-6.455	1.00	120.58
	2364	CA	CYS	A	107	-1.189	43.480	-7.774	1.00	120.58
60	2365	C	CYS	A	107	-0.053	44.299	-8.666	1.00	120.58
	2366	O	CYS	A	107	0.836	45.304	-8.953	1.00	120.58
	2367	CB	CYS	A	107	-1.645	45.384	-8.168	1.00	140.98
	2368	SG	CYS	A	107	-2.754	42.210	-9.622	1.00	140.98
	2369	N	HIS	A	108	-0.069	41.644	-9.083	1.00	148.29
65	2370	CA	HIS	A	108	1.002	40.222	-9.914	1.00	148.29
	2371	CB	HIS	A	108	1.309	39.660	-9.470	1.00	171.13
	2372	CG	HIS	A	108	2.556	38.483	-10.068	1.00	171.13
	2373	CD2	HIS	A	108	2.793	40.308	-10.691	1.00	171.13
	2374	ND1	HIS	A	108	3.773	39.549	-10.001	1.00	171.13
70	2375	CE1	HIS	A	108	4.702		-10.548	1.00	171.13

	Serial	Atom	Res	Chain	#	X	Y	Z	Occ	B
		NE2	HIS	A	108	4.136	38.434	-10.975	1.00	171.13
	2376	C	HIS	A	108	0.759	41.632	-11.411	1.00	148.29
	2377	O	HIS	A	108	-0.248	41.082	-11.896	1.00	148.29
	2378	N	GLY	A	109	1.701	42.229	-12.136	1.00	189.63
5	2379	CA	GLY	A	109	1.593	42.286	-13.579	1.00	189.63
	2380	C	GLY	A	109	2.109	41.002	-14.172	1.00	189.63
	2381	O	GLY	A	109	2.735	40.217	-13.469	1.00	189.63
	2382	N	TRP	A	110	1.836	40.782	-15.454	1.00	151.88
	2383	CA	TRP	A	110	2.302	39.582	-16.136	1.00	151.88
10	2384	CB	TRP	A	110	1.381	39.246	-17.307	1.00	208.61
	2385	CG	TRP	A	110	1.896	38.147	-18.184	1.00	208.61
	2386	CD2	TRP	A	110	1.495	36.764	-18.170	1.00	208.61
	2387	CE2	TRP	A	110	2.277	36.100	-19.135	1.00	208.61
	2388	CE3	TRP	A	110	0.556	36.022	-17.434	1.00	208.61
15	2389	CD1	TRP	A	110	2.863	38.255	-19.134	1.00	208.61
	2390	NE1	TRP	A	110	3.103	37.034	-19.708	1.00	208.61
	2391	CZ2	TRP	A	110	2.147	34.723	-19.387	1.00	208.61
	2392	CZ3	TRP	A	110	0.429	34.653	-17.688	1.00	208.61
	2393	CH2	TRP	A	110	1.218	34.024	-18.658	1.00	208.61
20	2394	C	TRP	A	110	3.747	39.773	-16.615	1.00	151.88
	2395	O	TRP	A	110	4.182	40.909	-16.869	1.00	151.88
	2396	N	ARG	A	111	4.490	38.666	-16.714	1.00	149.24
	2397	CA	ARG	A	111	5.892	38.712	-17.125	1.00	149.24
	2398	CB	ARG	A	111	6.013	39.012	-18.619	1.00	249.69
25	2399	CG	ARG	A	111	6.011	37.777	-19.494	1.00	249.69
	2400	CD	ARG	A	111	6.475	38.106	-20.902	1.00	249.69
	2401	NE	ARG	A	111	7.340	37.059	-21.427	1.00	249.69
	2402	CZ	ARG	A	111	8.490	36.693	-20.868	1.00	249.69
	2403	NH1	ARG	A	111	8.916	37.285	-19.757	1.00	249.69
30	2404	NH2	ARG	A	111	9.215	35.721	-21.411	1.00	249.69
	2405	C	ARG	A	111	6.655	39.777	-16.336	1.00	149.24
	2406	O	ARG	A	111	7.605	40.391	-16.825	1.00	149.24
	2407	N	ASN	A	112	6.219	39.988	-15.107	1.00	174.92
	2408	CA	ASN	A	112	6.837	40.958	-14.231	1.00	174.92
35	2409	CB	ASN	A	112	8.189	40.434	-13.735	1.00	206.21
	2410	CG	ASN	A	112	8.698	41.184	-12.514	1.00	206.21
	2411	OD1	ASN	A	112	8.201	42.256	-12.171	1.00	206.21
	2412	ND2	ASN	A	112	9.703	40.620	-11.858	1.00	206.21
	2413	C	ASN	A	112	7.029	42.293	-14.837	1.00	174.92
40	2414	O	ASN	A	112	7.992	43.001	-14.647	1.00	174.92
	2415	N	TRP	A	113	6.129	42.643	-15.861	1.00	198.50
	2416	CA	TRP	A	113	6.233	43.932	-16.547	1.00	198.50
	2417	CB	TRP	A	113	5.232	44.051	-17.676	1.00	235.99
	2418	CG	TRP	A	113	5.669	43.414	-18.929	1.00	235.99
45	2419	CD2	TRP	A	113	4.825	42.775	-19.896	1.00	235.99
	2420	CE2	TRP	A	113	5.653	42.372	-20.965	1.00	235.99
	2421	CE3	TRP	A	113	3.455	42.498	-19.949	1.00	235.99
	2422	CD1	TRP	A	113	6.927	43.381	-19.440	1.00	235.99
	2423	NE1	TRP	A	113	6.831	42.753	-20.665	1.00	235.99
50	2424	CZ2	TRP	A	113	5.150	41.705	-22.088	1.00	235.99
	2425	CZ3	TRP	A	113	2.952	41.837	-21.067	1.00	235.99
	2426	CH2	TRP	A	113	3.801	41.452	-22.124	1.00	235.99
	2427	C	TRP	A	113	5.948	45.050	-15.563	1.00	198.50
	2428	O	TRP	A	113	5.891	44.821	-14.356	1.00	198.50
55	2429	N	ASP	A	114	5.765	46.262	-16.069	1.00	220.71
	2430	CA	ASP	A	114	5.476	47.388	-15.188	1.00	220.71
	2431	CB	ASP	A	114	6.471	48.542	-15.432	1.00	249.69
	2432	CG	ASP	A	114	7.802	48.353	-14.692	1.00	249.69
	2433	OD1	ASP	A	114	7.791	48.237	-13.446	1.00	249.69
60	2434	OD2	ASP	A	114	8.863	48.329	-15.356	1.00	220.71
	2435	C	ASP	A	114	4.037	47.881	-15.366	1.00	220.71
	2436	O	ASP	A	114	3.569	48.065	-16.501	1.00	122.27
	2437	N	VAL	A	115	3.337	48.072	-14.242	1.00	122.27
	2438	CA	VAL	A	115	1.960	48.556	-14.268	1.00	142.42
65	2439	CB	VAL	A	115	1.032	47.648	-13.440	1.00	142.42
	2440	CG1	VAL	A	115	-0.418	47.957	-13.777	1.00	142.42
	2441	CG2	VAL	A	115	1.328	46.195	-13.716	1.00	122.27
	2442	C	VAL	A	115	1.889	49.978	-13.705	1.00	122.27
	2443	O	VAL	A	115	2.566	50.311	-12.726	1.00	125.74
70	2444	N	TYR	A	116	1.061	50.800	-14.336	1.00	
	2445									

Line	Serial	Atom	Res	Chain	ResNum	X	Y	Z	Occ	B
			TYR	A	116	0.885	52.181	-13.923	1.00	125.74
	2446	CA	TYR	A	116	1.328	53.115	-15.058	1.00	233.81
	2447	CB	TYR	A	116	2.797	53.014	-15.357	1.00	233.81
	2448	CG	TYR	A	116	3.272	52.218	-16.397	1.00	233.81
	2449	CD1	TYR	A	116	4.644	52.092	-16.639	1.00	233.81
5	2450	CE1	TYR	A	116	3.720	52.683	-14.568	1.00	233.81
	2451	CD2	TYR	A	116	5.089	53.566	-14.796	1.00	233.81
	2452	CE2	TYR	A	116	5.551	52.773	-15.832	1.00	233.81
	2453	CZ	TYR	A	116	6.914	52.664	-16.054	1.00	233.81
	2454	OH	TYR	A	116	-0.578	52.470	-13.539	1.00	125.74
10	2455	C	TYR	A	116	-1.451	51.626	-13.747	1.00	125.74
	2456	O	TYR	A	116	-0.833	53.665	-12.992	1.00	145.27
	2457	N	LYS	A	117	-2.176	54.095	-12.586	1.00	145.27
	2458	CA	LYS	A	117	-3.020	54.515	-13.801	1.00	191.01
	2459	CB	LYS	A	117	-2.807	55.955	-14.260	1.00	191.01
15	2460	CG	LYS	A	117	-3.969	56.437	-15.140	1.00	191.01
	2461	CD	LYS	A	117	-5.304	56.363	-15.161	1.00	191.01
	2462	CE	LYS	A	117	-6.504	56.811	-14.377	1.00	191.01
	2463	NZ	LYS	A	117	-2.913	53.014	-11.814	1.00	145.27
	2464	C	LYS	A	117	-4.053	52.653	-12.141	1.00	145.27
20	2465	O	LYS	A	117	-2.269	52.518	-10.767	1.00	149.03
	2466	N	VAL	A	118	-2.858	51.469	-9.959	1.00	149.03
	2467	CA	VAL	A	118	-1.761	50.002	-9.356	1.00	99.24
	2468	CB	VAL	A	118	-2.233	49.921	-8.081	1.00	99.24
	2469	CG1	VAL	A	118	-1.364	49.558	-10.374	1.00	99.24
25	2470	CG2	VAL	A	118	-3.816	51.912	-8.858	1.00	149.03
	2471	C	VAL	A	118	-3.601	52.931	-8.179	1.00	149.03
	2472	O	VAL	A	118	-4.878	51.115	-8.706	1.00	111.26
	2473	N	ILE	A	119	-5.923	51.325	-7.714	1.00	111.26
	2474	CA	ILE	A	119	-7.157	51.950	-8.351	1.00	110.34
30	2475	CB	ILE	A	119	-8.183	52.293	-7.286	1.00	110.34
	2476	CG2	ILE	A	119	-6.752	53.187	-9.108	1.00	110.34
	2477	CG1	ILE	A	119	-7.726	53.537	-10.166	1.00	110.34
	2478	CD1	ILE	A	119	-6.349	49.972	-7.162	1.00	111.26
	2479	C	ILE	A	119	-6.641	49.054	-7.919	1.00	111.26
35	2480	O	ILE	A	119	-6.378	49.843	-5.848	1.00	126.83
	2481	N	TYR	A	120	-6.829	48.603	-5.266	1.00	126.83
	2482	CA	TYR	A	120	-6.039	48.270	-4.015	1.00	126.10
	2483	CB	TYR	A	120	-4.615	47.904	-4.280	1.00	126.10
	2484	CG	TYR	A	120	-3.636	48.884	-4.399	1.00	126.10
40	2485	CD1	TYR	A	120	-2.315	48.542	-4.657	1.00	126.10
	2486	CE1	TYR	A	120	-4.243	46.569	-4.427	1.00	126.10
	2487	CD2	TYR	A	120	-2.930	46.213	-4.687	1.00	126.10
	2488	CE2	TYR	A	120	-1.968	47.197	-4.802	1.00	126.10
	2489	CZ	TYR	A	120	-0.662	46.817	-5.067	1.00	126.83
45	2490	OH	TYR	A	120	-8.280	48.818	-4.889	1.00	126.83
	2491	C	TYR	A	120	-8.672	49.956	-4.606	1.00	106.78
	2492	O	TYR	A	120	-9.084	47.753	-4.890	1.00	106.78
	2493	N	TYR	A	121	-10.496	47.884	-4.516	1.00	155.39
	2494	CA	TYR	A	121	-11.417	47.731	-5.734	1.00	155.39
50	2495	CB	TYR	A	121	-11.362	48.833	-6.777	1.00	155.39
	2496	CG	TYR	A	121	-10.181	49.122	-7.459	1.00	155.39
	2497	CD1	TYR	A	121	-10.149	50.069	-8.499	1.00	155.39
	2498	CE1	TYR	A	121	-12.516	49.522	-7.151	1.00	155.39
	2499	CD2	TYR	A	121	-12.496	50.467	-8.187	1.00	155.39
55	2500	CE2	TYR	A	121	-11.309	50.732	-8.858	1.00	155.39
	2501	CZ	TYR	A	121	-11.272	51.633	-9.903	1.00	106.78
	2502	OH	TYR	A	121	-10.892	46.838	-3.482	1.00	106.78
	2503	C	TYR	A	121	-10.544	45.657	-3.611	1.00	141.82
	2504	O	TYR	A	121	-11.618	47.278	-2.457	1.00	141.82
60	2505	N	LYS	A	122	-12.108	46.362	-1.440	1.00	249.31
	2506	CA	LYS	A	122	-11.511	46.674	-0.080	1.00	249.31
	2507	CB	LYS	A	122	-11.983	45.716	0.997	1.00	249.31
	2508	CG	LYS	A	122	-11.631	46.233	2.367	1.00	249.31
	2509	CD	LYS	A	122	-12.252	45.380	3.451	1.00	249.31
65	2510	CE	LYS	A	122	-12.022	46.005	4.773	1.00	141.82
	2511	NZ	LYS	A	122	-13.631	46.511	-1.375	1.00	141.82
	2512	C	LYS	A	122	-14.136	47.587	-1.042	1.00	127.31
	2513	O	LYS	A	122				1.00	127.31
	2514	N	ASP	A	123	-14.349	45.433	-1.703	1.00	127.31
70	2515	CA	ASP	A	123	-15.801	45.436	-1.701	1.00	127.31

2516	CB	ASP	A	123	-16.344	45.574	-0.276	1.00	199.26
2516	CB	ASP	A	123	-16.186	44.302	0.531	1.00	199.26
2517	CG	ASP	A	123	-16.571	43.223	0.031	1.00	199.26
2518	OD1	ASP	A	123	-15.685	44.378	1.668	1.00	199.26
2519	OD2	ASP	A	123	-16.395	46.531	-2.584	1.00	127.31
2520	C	ASP	A	123	-17.238	47.311	-2.132	1.00	127.31
2521	O	ASP	A	123	-15.955	48.579	-3.842	1.00	152.83
2522	N	GLY	A	124	-16.468	47.561	-4.788	1.00	152.83
2523	CA	GLY	A	124	-16.067	49.007	-4.590	1.00	152.83
2524	C	GLY	A	124	-16.394	49.847	-5.425	1.00	152.83
2525	O	GLY	A	124	-15.355	49.297	-3.502	1.00	121.95
2526	N	GLU	A	125	-14.912	50.668	-3.185	1.00	121.95
2527	CA	GLU	A	125	-15.037	50.926	-1.673	1.00	249.20
2528	CB	GLU	A	125	-16.464	51.006	-1.143	1.00	249.20
2529	CG	GLU	A	125	-17.154	52.304	-1.519	1.00	249.20
2530	CD	GLU	A	125	-16.680	53.373	-1.081	1.00	249.20
2531	OE1	GLU	A	125	-18.168	52.253	-2.250	1.00	249.20
2532	OE2	GLU	A	125	-13.479	50.956	-3.612	1.00	121.95
2533	C	GLU	A	125	-12.616	50.071	-3.548	1.00	121.95
2534	O	GLU	A	125	-13.236	52.185	-4.059	1.00	117.59
2535	N	ALA	A	126	-11.886	52.572	-4.444	1.00	117.59
2536	CA	ALA	A	126	-11.912	53.935	-5.116	1.00	242.07
2537	CB	ALA	A	126	-11.102	52.638	-3.129	1.00	117.59
2538	C	ALA	A	126	-11.619	53.123	-2.132	1.00	117.59
2539	O	ALA	A	126	-9.862	52.176	-3.112	1.00	119.50
2540	N	LEU	A	127	-9.140	52.177	-1.857	1.00	119.50
2541	CA	LEU	A	127	-8.845	50.751	-1.411	1.00	117.16
2542	CB	LEU	A	127	-8.750	50.671	0.099	1.00	117.16
2543	CG	LEU	A	127	-10.045	51.245	0.705	1.00	117.16
2544	CD1	LEU	A	127	-8.534	49.234	0.528	1.00	117.16
2545	CD2	LEU	A	127	-7.859	52.960	-1.813	1.00	119.50
2546	C	LEU	A	127	-7.738	53.890	-1.030	1.00	119.50
2547	O	LEU	A	127	-6.880	52.566	-2.616	1.00	140.05
2548	N	LYS	A	128	-5.603	53.269	-2.661	1.00	140.05
2549	CA	LYS	A	128	-4.503	52.411	-2.036	1.00	182.59
2550	CB	LYS	A	128	-4.725	52.060	-0.576	1.00	182.59
2551	CG	LYS	A	128	-4.526	53.260	0.337	1.00	182.59
2552	CD	LYS	A	128	-4.657	52.855	1.804	1.00	182.59
2553	CE	LYS	A	128	-4.240	53.938	2.743	1.00	182.59
2554	NZ	LYS	A	128	-5.293	53.534	-4.127	1.00	140.05
2555	C	LYS	A	128	-5.875	52.899	-5.010	1.00	140.05
2556	O	LYS	A	128	-4.386	54.467	-4.393	1.00	141.11
2557	N	TYR	A	129	-4.021	54.780	-5.779	1.00	141.11
2558	CA	TYR	A	129	-4.977	55.812	-6.344	1.00	146.88
2559	CB	TYR	A	129	-4.437	56.491	-7.574	1.00	146.88
2560	CG	TYR	A	129	-4.560	55.909	-8.824	1.00	146.88
2561	CD1	TYR	A	129	-4.010	56.518	-9.957	1.00	146.88
2562	CE1	TYR	A	129	-3.749	57.705	-7.474	1.00	146.88
2563	CD2	TYR	A	129	-3.191	58.313	-8.593	1.00	146.88
2564	CE2	TYR	A	129	-3.327	57.717	-9.835	1.00	146.88
2565	CZ	TYR	A	129	-2.781	58.324	-10.846	1.00	146.88
2566	OH	TYR	A	129	-2.588	55.294	-5.941	1.00	141.11
2567	C	TYR	A	129	-2.098	56.070	-5.107	1.00	141.11
2568	O	TYR	A	129	-1.919	54.861	-7.014	1.00	137.60
2569	N	TRP	A	130	-0.545	55.292	-7.282	1.00	137.60
2570	CA	TRP	A	130	0.487	54.377	-6.621	1.00	197.40
2571	CB	TRP	A	130	0.244	54.027	-5.190	1.00	197.40
2572	CG	TRP	A	130	0.940	54.526	-4.060	1.00	197.40
2573	CD2	TRP	A	130	0.426	53.878	-2.911	1.00	197.40
2574	CE2	TRP	A	130	1.974	55.458	-3.892	1.00	197.40
2575	CE3	TRP	A	130	-0.661	53.124	-4.702	1.00	197.40
2576	CD1	TRP	A	130	-0.561	53.018	-3.335	1.00	197.40
2577	NE1	TRP	A	130	0.893	54.128	-1.624	1.00	197.40
2578	CZ2	TRP	A	130	2.452	55.713	-2.598	1.00	197.40
2579	CZ3	TRP	A	130	1.906	55.055	-1.484	1.00	197.40
2580	CH2	TRP	A	130	-0.262	55.287	-8.780	1.00	137.60
2581	C	TRP	A	130	-1.055	54.764	-9.576	1.00	137.60
2582	O	TRP	A	130	0.879	55.868	-9.156	1.00	159.17
2583	N	TYR	A	131	1.313	55.920	-10.554	1.00	159.17
2584	CA	TYR	A	131	2.164	57.155	-10.798	1.00	169.09
2585	CB	TYR	A	131					

No.	Atom	Name	Res	Chain	Seq	X	Y	Z	Occ	B
	2586	CG	TYR	A	131	2.407	57.426	-12.241	1.00	169.09
	2587	CD1	TYR	A	131	1.394	57.927	-13.051	1.00	169.09
	2588	CE1	TYR	A	131	1.603	58.144	-14.415	1.00	169.09
	2589	CD2	TYR	A	131	3.642	57.150	-12.821	1.00	169.09
5	2590	CE2	TYR	A	131	3.863	57.363	-14.183	1.00	169.09
	2591	CZ	TYR	A	131	2.842	57.858	-14.974	1.00	169.09
	2592	OH	TYR	A	131	3.073	58.051	-16.318	1.00	159.17
	2593	C	TYR	A	131	2.152	54.655	-10.756	1.00	159.17
	2594	O	TYR	A	131	1.619	53.613	-11.140	1.00	172.97
10	2595	N	GLU	A	132	3.464	54.754	-10.524	1.00	172.97
	2596	CA	GLU	A	132	4.328	53.577	-10.594	1.00	249.69
	2597	CB	GLU	A	132	5.777	53.933	-10.237	1.00	249.69
	2598	CG	GLU	A	132	6.593	54.598	-11.341	1.00	249.69
	2599	CD	GLU	A	132	7.784	53.750	-11.767	1.00	249.69
15	2600	OE1	GLU	A	132	8.097	52.767	-11.058	1.00	172.97
	2601	OE2	GLU	A	132	8.411	54.063	-12.804	1.00	172.97
	2602	C	GLU	A	132	3.677	52.838	-9.436	1.00	204.08
	2603	O	GLU	A	132	3.531	53.413	-8.343	1.00	204.08
	2604	N	ASN	A	133	3.285	51.580	-9.628	1.00	217.94
20	2605	CA	ASN	A	133	2.559	50.925	-8.545	1.00	217.94
	2606	CB	ASN	A	133	1.839	49.637	-9.065	1.00	217.94
	2607	CG	ASN	A	133	2.705	48.389	-9.085	1.00	217.94
	2608	OD1	ASN	A	133	3.862	48.418	-9.493	1.00	204.08
	2609	ND2	ASN	A	133	2.114	47.262	-8.676	1.00	204.08
25	2610	C	ASN	A	133	3.229	50.722	-7.190	1.00	188.50
	2611	O	ASN	A	133	4.322	51.214	-6.922	1.00	188.50
	2612	N	HIS	A	134	2.512	50.050	-6.314	1.00	249.69
	2613	CA	HIS	A	134	2.986	49.818	-4.979	1.00	249.69
	2614	CB	HIS	A	134	2.434	50.910	-4.067	1.00	249.69
30	2615	CG	HIS	A	134	3.005	50.881	-2.679	1.00	249.69
	2616	CD2	HIS	A	134	2.405	50.671	-1.481	1.00	249.69
	2617	ND1	HIS	A	134	4.338	51.055	-2.429	1.00	249.69
	2618	CE1	HIS	A	134	4.557	50.953	-1.120	1.00	249.69
	2619	NE2	HIS	A	134	3.399	50.720	-0.530	1.00	249.69
35	2620	C	HIS	A	134	2.485	48.456	-4.542	1.00	188.50
	2621	O	HIS	A	134	2.068	47.636	-5.374	1.00	188.50
	2622	N	ASN	A	135	2.518	48.217	-3.234	1.00	122.11
	2623	CA	ASN	A	135	2.076	46.946	-2.670	1.00	122.11
	2624	CB	ASN	A	135	3.274	45.986	-2.547	1.00	249.69
40	2625	CG	ASN	A	135	3.803	45.530	-3.906	1.00	249.69
	2626	OD1	ASN	A	135	3.010	45.158	-4.776	1.00	249.69
	2627	ND2	ASN	A	135	5.128	45.534	-4.086	1.00	249.69
	2628	C	ASN	A	135	1.431	47.190	-1.301	1.00	122.11
	2629	O	ASN	A	135	2.081	47.042	-0.271	1.00	122.11
45	2630	N	ILE	A	136	0.151	47.572	-1.313	1.00	110.87
	2631	CA	ILE	A	136	-0.653	47.846	-0.115	1.00	110.87
	2632	CB	ILE	A	136	-2.147	47.756	-0.452	1.00	153.19
	2633	CG2	ILE	A	136	-2.474	46.406	-1.055	1.00	153.19
	2634	CG1	ILE	A	136	-2.873	47.869	0.801	1.00	153.19
50	2635	CD1	ILE	A	136	-4.463	47.811	0.553	1.00	153.19
	2636	C	ILE	A	136	-0.350	46.912	1.075	1.00	110.87
	2637	O	ILE	A	136	-0.773	45.732	1.121	1.00	110.87
	2638	N	SER	A	137	0.351	47.475	2.061	1.00	139.22
	2639	CA	SER	A	137	0.763	46.734	3.254	1.00	139.22
55	2640	CB	SER	A	137	2.242	46.951	3.488	1.00	151.42
	2641	OG	SER	A	137	2.597	46.432	4.746	1.00	151.42
	2642	C	SER	A	137	0.032	47.027	4.554	1.00	139.22
	2643	O	SER	A	137	-0.378	48.149	4.823	1.00	139.22
	2644	N	ILE	A	138	-0.080	45.991	5.374	1.00	158.60
60	2645	CA	ILE	A	138	-0.760	46.072	6.659	1.00	158.60
	2646	CB	ILE	A	138	-2.136	45.423	6.577	1.00	139.81
	2647	CG2	ILE	A	138	-2.695	45.183	7.958	1.00	139.81
	2648	CG1	ILE	A	138	-3.058	46.314	5.766	1.00	139.81
	2649	CD1	ILE	A	138	-4.349	45.652	5.392	1.00	139.81
65	2650	C	ILE	A	138	0.014	45.396	7.780	1.00	158.60
	2651	O	ILE	A	138	0.321	44.203	7.716	1.00	158.60
	2652	N	THR	A	139	0.309	46.174	8.816	1.00	172.47
	2653	CA	THR	A	139	0.300	45.695	9.975	1.00	172.47
	2654	CB	THR	A	139	1.053	46.877	10.697	1.00	249.69
70	2655	OG1	THR	A	139	1.698	47.853	10.990	1.00	249.69

	2656	CG2	THR	A	139	2.763	47.522	9.811	1.00	249.69
	2657	C	THR	A	139	0.107	44.974	10.920	1.00	172.47
	2658	O	THR	A	139	0.027	43.744	10.930	1.00	172.47
	2659	N	ASN	A	140	-0.601	45.760	11.719	1.00	189.96
5	2660	CA	ASN	A	140	-1.573	45.233	12.662	1.00	189.96
	2661	CB	ASN	A	140	-1.738	46.209	13.830	1.00	189.00
	2662	CG	ASN	A	140	-2.767	45.750	14.835	1.00	189.00
	2663	OD1	ASN	A	140	-3.887	45.403	14.466	1.00	189.00
	2664	ND2	ASN	A	140	-2.398	45.764	16.111	1.00	189.00
10	2665	C	ASN	A	140	-2.877	45.113	11.879	1.00	189.96
	2666	O	ASN	A	140	-3.367	46.110	11.335	1.00	189.96
	2667	N	ALA	A	141	-3.437	43.904	11.818	1.00	161.77
	2668	CA	ALA	A	141	-4.669	43.674	11.062	1.00	161.77
	2669	CB	ALA	A	141	-4.569	42.364	10.287	1.00	147.99
15	2670	C	ALA	A	141	-5.962	43.694	11.874	1.00	161.77
	2671	O	ALA	A	141	-6.105	42.992	12.888	1.00	161.77
	2672	N	THR	A	142	-6.902	44.510	11.402	1.00	148.72
	2673	CA	THR	A	142	-8.208	44.652	12.032	1.00	148.72
	2674	CB	THR	A	142	-8.792	46.049	11.793	1.00	197.74
20	2675	OG1	THR	A	142	-7.820	47.046	12.140	1.00	197.74
	2676	CG2	THR	A	142	-10.036	46.245	12.636	1.00	197.74
	2677	C	THR	A	142	-9.126	43.636	11.376	1.00	148.72
	2678	O	THR	A	142	-8.849	43.153	10.277	1.00	148.72
	2679	N	VAL	A	143	-10.224	43.310	12.037	1.00	167.20
25	2680	CA	VAL	A	143	-11.143	42.347	11.456	1.00	167.20
	2681	CB	VAL	A	143	-12.142	41.824	12.479	1.00	139.08
	2682	CG1	VAL	A	143	-13.146	42.910	12.826	1.00	139.08
	2683	CG2	VAL	A	143	-12.838	40.590	11.934	1.00	139.08
	2684	C	VAL	A	143	-11.830	43.001	10.334	1.00	167.20
30	2685	O	VAL	A	143	-12.432	42.315	9.446	1.00	167.20
	2686	N	GLU	A	144	-12.047	44.327	10.372	1.00	193.27
	2687	CA	GLU	A	144	-12.785	45.043	9.333	1.00	193.27
	2688	CB	GLU	A	144	-13.048	46.488	9.742	1.00	249.50
	2689	CG	GLU	A	144	-13.868	46.624	11.002	1.00	249.50
35	2690	CD	GLU	A	144	-13.060	47.202	12.141	1.00	249.50
	2691	OE1	GLU	A	144	-12.590	48.352	12.003	1.00	249.50
	2692	OE2	GLU	A	144	-12.888	46.511	13.170	1.00	249.50
	2693	C	GLU	A	144	-12.022	45.019	8.019	1.00	193.27
	2694	O	GLU	A	144	-12.572	45.370	6.981	1.00	193.27
40	2695	N	ASP	A	145	-10.755	44.606	8.069	1.00	179.52
	2696	CA	ASP	A	145	-9.931	44.524	6.866	1.00	179.52
	2697	CB	ASP	A	145	-8.449	44.383	7.228	1.00	162.18
	2698	CG	ASP	A	145	-7.836	45.691	7.667	1.00	162.18
	2699	OD1	ASP	A	145	-7.903	46.662	6.883	1.00	162.18
45	2700	OD2	ASP	A	145	-7.286	45.750	8.786	1.00	162.18
	2701	C	ASP	A	145	-10.357	43.348	6.000	1.00	179.52
	2702	O	ASP	A	145	-10.003	43.286	4.819	1.00	179.52
	2703	N	SER	A	146	-11.117	42.421	6.592	1.00	145.41
	2704	CA	SER	A	146	-11.600	41.223	5.886	1.00	145.41
50	2705	CB	SER	A	146	-12.318	40.267	6.856	1.00	152.87
	2706	OG	SER	A	146	-11.477	39.816	7.907	1.00	152.87
	2707	C	SER	A	146	-12.565	41.619	4.782	1.00	145.41
	2708	O	SER	A	146	-13.518	42.349	5.037	1.00	145.41
	2709	N	GLY	A	147	-12.323	41.140	3.563	1.00	168.10
55	2710	CA	GLY	A	147	-13.215	41.477	2.467	1.00	168.10
	2711	C	GLY	A	147	-12.794	40.871	1.149	1.00	168.10
	2712	O	GLY	A	147	-12.011	39.907	1.129	1.00	168.10
	2713	N	THR	A	148	-13.306	41.428	0.048	1.00	117.05
	2714	CA	THR	A	148	-12.961	40.922	-1.283	1.00	117.05
60	2715	CB	THR	A	148	-14.234	40.419	-2.014	1.00	146.29
	2716	OG1	THR	A	148	-14.738	41.446	-2.867	1.00	146.29
	2717	CG2	THR	A	148	-15.327	40.059	-1.012	1.00	146.29
	2718	C	THR	A	148	-12.235	42.004	-2.116	1.00	117.05
	2719	O	THR	A	148	-12.833	43.019	-2.502	1.00	117.05
65	2720	N	TYR	A	149	-10.948	41.776	-2.386	1.00	131.53
	2721	CA	TYR	A	149	-10.136	42.735	-3.128	1.00	131.53
	2722	CB	TYR	A	149	-8.772	42.906	-2.453	1.00	104.84
	2723	CG	TYR	A	149	-8.803	43.338	-1.003	1.00	104.84
	2724	CD1	TYR	A	149	-9.126	42.435	0.010	1.00	104.84
70	2725	CE1	TYR	A	149	-9.127	42.823	1.361	1.00	104.84

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	2726	CD2	TYR A	149	-8.477	44.643	-0.639	1.00	104.84
	2727	CE2	TYR A	149	-8.467	45.042	0.700	1.00	104.84
	2728	CZ	TYR A	149	-8.792	44.133	1.696	1.00	104.84
	2729	OH	TYR A	149	-8.778	44.535	3.019	1.00	104.84
5	2730	C	TYR A	149	-9.881	42.371	-4.589	1.00	131.53
	2731	O	TYR A	149	-10.064	41.216	-4.989	1.00	131.53
	2732	N	TYR A	150	-9.454	43.380	-5.362	1.00	105.68
	2733	CA	TYR A	150	-9.090	43.272	-6.784	1.00	105.68
	2734	CB	TYR A	150	-10.319	43.023	-7.660	1.00	139.51
10	2735	CG	TYR A	150	-11.173	44.231	-7.964	1.00	139.51
	2736	CD1	TYR A	150	-10.738	45.210	-8.856	1.00	139.51
	2737	CE1	TYR A	150	-11.568	46.306	-9.205	1.00	139.51
	2738	CD2	TYR A	150	-12.456	44.369	-7.413	1.00	139.51
	2739	CE2	TYR A	150	-13.294	45.456	-7.759	1.00	139.51
15	2740	CZ	TYR A	150	-12.839	46.418	-8.660	1.00	139.51
	2741	OH	TYR A	150	-13.648	47.469	-9.041	1.00	105.68
	2742	C	TYR A	150	-8.429	44.587	-7.146	1.00	105.68
	2743	O	TYR A	150	-8.720	45.604	-6.525	1.00	99.57
	2744	N	CYS A	151	-7.536	44.585	-8.128	1.00	99.57
20	2745	CA	CYS A	151	-6.868	45.830	-8.510	1.00	99.57
	2746	C	CYS A	151	-6.994	46.133	-9.992	1.00	99.57
	2747	O	CYS A	151	-7.274	45.244	-10.786	1.00	148.54
	2748	CB	CYS A	151	-5.393	45.773	-8.136	1.00	148.54
	2749	SG	CYS A	151	-4.448	44.452	-8.958	1.00	107.45
25	2750	N	THR A	152	-6.782	47.396	-10.359	1.00	107.45
	2751	CA	THR A	152	-6.857	47.838	-11.756	1.00	135.55
	2752	CB	THR A	152	-8.058	48.753	-11.986	1.00	135.55
	2753	OG1	THR A	152	-7.802	50.045	-11.407	1.00	135.55
	2754	CG2	THR A	152	-9.295	48.160	-11.345	1.00	107.45
30	2755	C	THR A	152	-5.600	48.637	-12.118	1.00	107.45
	2756	O	THR A	152	-5.043	49.358	-11.285	1.00	123.72
	2757	N	GLY A	153	-5.159	48.518	-13.359	1.00	123.72
	2758	CA	GLY A	153	-3.971	49.241	-13.744	1.00	123.72
	2759	C	GLY A	153	-3.749	49.248	-15.239	1.00	123.72
35	2760	O	GLY A	153	-4.388	48.477	-15.965	1.00	129.98
	2761	N	LYS A	154	-2.834	50.113	-15.691	1.00	129.98
	2762	CA	LYS A	154	-2.515	50.256	-17.107	1.00	212.29
	2763	CB	LYS A	154	-2.490	51.740	-17.481	1.00	212.29
	2764	CG	LYS A	154	-2.291	52.012	-18.945	1.00	212.29
40	2765	CD	LYS A	154	-2.351	53.502	-19.225	1.00	212.29
	2766	CE	LYS A	154	-2.074	53.803	-20.693	1.00	212.29
	2767	NZ	LYS A	154	-2.101	55.266	-20.986	1.00	129.98
	2768	C	LYS A	154	-1.179	49.591	-17.445	1.00	129.98
	2769	O	LYS A	154	-0.130	49.969	-16.923	1.00	168.08
45	2770	N	VAL A	155	-1.242	48.579	-18.311	1.00	168.08
	2771	CA	VAL A	155	-0.071	47.827	-18.769	1.00	187.90
	2772	CB	VAL A	155	-0.355	46.305	-18.759	1.00	187.90
	2773	CG1	VAL A	155	0.825	45.540	-19.304	1.00	187.90
	2774	CG2	VAL A	155	-0.658	45.849	-17.343	1.00	168.08
50	2775	C	VAL A	155	0.193	48.277	-20.196	1.00	168.08
	2776	O	VAL A	155	-0.717	48.244	-21.025	1.00	179.87
	2777	N	TRP A	156	1.429	48.672	-20.493	1.00	179.87
	2778	CA	TRP A	156	1.765	49.167	-21.834	1.00	249.69
	2779	CB	TRP A	156	1.399	48.169	-22.954	1.00	249.69
55	2780	CG	TRP A	156	2.200	46.890	-23.019	1.00	249.69
	2781	CD2	TRP A	156	3.591	46.752	-23.359	1.00	249.69
	2782	CE2	TRP A	156	3.900	45.367	-23.302	1.00	249.69
	2783	CE3	TRP A	156	4.606	47.657	-23.714	1.00	249.69
	2784	CD1	TRP A	156	1.740	45.625	-22.774	1.00	249.69
60	2785	NE1	TRP A	156	2.754	44.707	-22.945	1.00	249.69
	2786	CZ2	TRP A	156	5.175	44.871	-23.993	1.00	249.69
	2787	CZ3	TRP A	156	5.876	47.161	-23.921	1.00	179.87
	2788	CH2	TRP A	156	6.148	45.779	-22.020	1.00	179.87
	2789	C	TRP A	156	0.905	50.400	-21.535	1.00	176.07
65	2790	O	TRP A	156	1.242	51.485	-22.712	1.00	176.07
	2791	N	GLN A	157	-0.221	50.212	-22.959	1.00	249.69
	2792	CA	GLN A	157	-1.161	51.301	-24.313	1.00	249.69
	2793	CB	GLN A	157	-0.864	51.955	-24.311	1.00	249.69
	2794	CG	GLN A	157	0.381	52.851	-23.412	1.00	249.69
70	2795	CD	GLN A	157	0.232	54.078			

Line	Atom #	Atom	Res	Chain	ResNum	X	Y	Z	Occ	B
		OE1	GLN	A	157	-0.638	54.922	-23.635	1.00	249.69
	2796	NE2	GLN	A	157	1.086	54.180	-22.391	1.00	249.69
	2797	C	GLN	A	157	-2.843	50.904	-22.872	1.00	176.07
	2798	O	GLN	A	157	-3.504	51.584	-23.430	1.00	176.07
	2799	N	LEU	A	158	-2.937	49.811	-22.171	1.00	165.71
5	2800	CA	LEU	A	158	-4.320	49.375	-21.989	1.00	165.71
	2801	CB	LEU	A	158	-4.9??	48.122	-22.809	1.00	232.32
	2802	CG	LEU	A	158	-4.809	48.278	-24.317	1.00	232.32
	2803	CD1	LEU	A	158	-5.868	47.274	-24.764	1.00	232.32
	2804	CD2	LEU	A	158	-5.267	49.687	-24.663	1.00	232.32
10	2805	C	LEU	A	158	-4.642	49.105	-20.520	1.00	165.71
	2806	O	LEU	A	158	-3.764	48.726	-19.741	1.00	165.71
	2807	N	ASP	A	159	-5.903	49.301	-20.148	1.00	172.26
	2808	CA	ASP	A	159	-6.321	49.080	-18.772	1.00	172.26
	2809	CB	ASP	A	159	-7.518	49.974	-18.431	1.00	159.32
15	2810	CG	ASP	A	159	-7.259	51.435	-18.725	1.00	159.32
	2811	OD1	ASP	A	159	-6.345	52.022	-18.103	1.00	159.32
	2812	OD2	ASP	A	159	-7.974	51.995	-19.586	1.00	159.32
	2813	C	ASP	A	159	-6.7??	47.618	-18.556	1.00	172.26
	2814	O	ASP	A	159	-7.192	46.960	-19.479	1.00	172.26
20	2815	N	TYR	A	160	-6.468	47.113	-17.343	1.00	165.86
	2816	CA	TYR	A	160	-6.826	45.741	-17.016	1.00	165.86
	2817	CB	TYR	A	160	-5.667	44.810	-17.253	1.00	170.32
	2818	CG	TYR	A	160	-5.121	44.887	-18.643	1.00	170.32
	2819	CD1	TYR	A	160	-4.101	45.789	-18.959	1.00	170.32
25	2820	CE1	TYR	A	160	-3.558	45.844	-20.241	1.00	170.32
	2821	CD2	TYR	A	160	-5.600	44.042	-19.645	1.00	170.32
	2822	CE2	TYR	A	160	-5.072	44.088	-20.937	1.00	170.32
	2823	CZ	TYR	A	160	-4.046	44.988	-21.228	1.00	170.32
	2824	OH	TYR	A	160	-3.493	45.018	-22.495	1.00	170.32
30	2825	C	TYR	A	160	-7.301	45.590	-15.586	1.00	165.86
	2826	O	TYR	A	160	-6.845	46.289	-14.675	1.00	165.86
	2827	N	GLU	A	161	-8.228	44.660	-15.410	1.00	140.66
	2828	CA	GLU	A	161	-8.828	44.380	-14.119	1.00	140.66
	2829	CB	GLU	A	161	-10.356	44.448	-14.272	1.00	201.20
35	2830	CG	GLU	A	161	-11.197	44.125	-13.044	1.00	201.20
	2831	CD	GLU	A	161	-12.653	44.551	-13.222	1.00	201.20
	2832	OE1	GLU	A	161	-13.525	44.011	-12.499	1.00	201.20
	2833	OE2	GLU	A	161	-12.920	45.434	-14.076	1.00	201.20
	2834	C	GLU	A	161	-8.339	42.987	-13.688	1.00	140.66
40	2835	O	GLU	A	161	-8.148	42.095	-14.523	1.00	140.66
	2836	N	SER	A	162	-8.109	42.815	-12.389	1.00	133.72
	2837	CA	SER	A	162	-7.628	41.552	-11.841	1.00	133.72
	2838	CB	SER	A	162	-6.687	41.835	-10.672	1.00	153.53
	2839	OG	SER	A	162	-7.366	42.515	-9.616	1.00	153.53
45	2840	C	SER	A	162	-8.766	40.686	-11.341	1.00	133.72
	2841	O	SER	A	162	-9.852	41.187	-11.066	1.00	133.72
	2842	N	GLU	A	163	-8.517	39.386	-11.222	1.00	190.14
	2843	CA	GLU	A	163	-9.539	38.488	-10.699	1.00	190.14
	2844	CB	GLU	A	163	-9.037	37.041	-10.704	1.00	249.69
50	2845	CG	GLU	A	163	-8.981	36.372	-12.079	1.00	249.69
	2846	CD	GLU	A	163	-10.356	36.015	-12.616	1.00	249.69
	2847	OE1	GLU	A	163	-11.096	35.284	-11.928	1.00	249.69
	2848	OE2	GLU	A	163	-10.694	36.462	-13.730	1.00	249.69
	2849	C	GLU	A	163	-9.764	38.962	-9.264	1.00	190.14
55	2850	O	GLU	A	163	-8.835	39.462	-8.631	1.00	190.14
	2851	N	PRO	A	164	-10.991	38.833	-8.736	1.00	116.57
	2852	CD	PRO	A	164	-12.208	38.343	-9.412	1.00	155.66
	2853	CA	PRO	A	164	-11.302	39.267	-7.368	1.00	116.57
	2854	CB	PRO	A	164	-12.814	39.411	-7.394	1.00	155.66
60	2855	CG	PRO	A	164	-13.205	38.276	-8.263	1.00	155.66
	2856	C	PRO	A	164	-10.827	38.258	-6.325	1.00	116.57
	2857	O	PRO	A	164	-10.826	37.056	-6.578	1.00	116.57
	2858	N	LEU	A	165	-10.441	38.735	-5.150	1.00	151.49
	2859	CA	LEU	A	165	-9.849	37.832	-4.122	1.00	151.49
65	2860	CB	LEU	A	165	-8.413	37.855	-4.030	1.00	116.01
	2861	CG	LEU	A	165	-7.716	37.061	-2.995	1.00	116.01
	2862	CD1	LEU	A	165	-8.414	35.693	-2.953	1.00	116.01
	2863	CD2	LEU	A	165	-6.244	36.924	-3.335	1.00	116.01
	2864	C	LEU	A	165	-10.570	38.031	-2.739	1.00	151.49
70	2865	C								

	Serial	Atom	Res	Chain	ResNo	X	Y	Z	Occ	B
	2866	O	LEU	A	165	-10.651	39.156	-2.252	1.00	151.49
	2867	N	ASN	A	166	-10.996	36.932	-2.113	1.00	136.62
	2868	CA	ASN	A	166	-11.583	36.988	-0.779	1.00	136.62
	2869	CB	ASN	A	166	-12.582	35.861	-0.576	1.00	179.00
5	2870	CG	ASN	A	166	-13.998	36.278	-0.898	1.00	179.00
	2871	OD1	ASN	A	166	-14.338	37.458	-0.835	1.00	179.00
	2872	ND2	ASN	A	166	-14.839	35.305	-1.223	1.00	179.00
	2873	C	ASN	A	166	-10.535	36.890	0.307	1.00	136.62
	2874	O	ASN	A	166	-9.561	36.155	0.165	1.00	136.62
10	2875	N	ILE	A	167	-10.741	37.619	1.401	1.00	136.70
	2876	CA	ILE	A	167	-9.795	37.605	2.521	1.00	136.70
	2877	CB	ILE	A	167	-8.857	38.814	2.472	1.00	129.99
	2878	CG2	ILE	A	167	-7.953	38.809	3.694	1.00	129.99
	2879	CG1	ILE	A	167	-8.012	38.756	1.209	1.00	129.99
15	2880	CD1	ILE	A	167	-7.114	39.934	1.059	1.00	129.99
	2881	C	ILE	A	167	-10.496	37.621	3.867	1.00	136.70
	2882	O	ILE	A	167	-11.317	38.494	4.126	1.00	136.70
	2883	N	THR	A	168	-10.148	36.685	4.738	1.00	125.45
	2884	CA	THR	A	168	-10.808	36.66	6.016	1.00	125.45
20	2885	CB	THR	A	168	-11.677	35.424	6.131	1.00	120.45
	2886	OG1	THR	A	168	-12.602	35.394	5.041	1.00	120.45
	2887	CG2	THR	A	168	-12.451	35.445	7.433	1.00	120.45
	2888	C	THR	A	168	-9.910	36.749	7.232	1.00	125.45
	2889	O	THR	A	168	-8.989	35.928	7.431	1.00	125.45
25	2890	N	VAL	A	169	-10.194	37.757	8.050	1.00	104.30
	2891	CA	VAL	A	169	-9.444	37.979	9.276	1.00	104.30
	2892	CB	VAL	A	169	-9.061	39.471	9.422	1.00	108.18
	2893	CG1	VAL	A	169	-8.798	39.826	10.864	1.00	108.18
	2894	CG2	VAL	A	169	-7.798	39.750	8.602	1.00	108.18
30	2895	C	VAL	A	169	-10.333	37.534	10.433	1.00	104.30
	2896	O	VAL	A	169	-11.331	38.182	10.729	1.00	104.30
	2897	N	ILE	A	170	-9.972	36.416	11.069	1.00	193.03
	2898	CA	ILE	A	170	-10.727	35.860	12.191	1.00	193.03
	2899	CB	ILE	A	170	-10.701	34.321	12.132	1.00	177.52
35	2900	CG2	ILE	A	170	-11.108	33.853	10.743	1.00	177.52
	2901	CG1	ILE	A	170	-9.291	33.800	12.404	1.00	177.52
	2902	CD1	ILE	A	170	-9.174	32.283	12.422	1.00	177.52
	2903	C	ILE	A	170	-10.133	36.337	13.513	1.00	193.03
	2904	O	ILE	A	170	-9.014	36.850	13.542	1.00	193.03
40	2905	N	LYS	A	171	-10.858	36.172	14.614	1.00	156.56
	2906	CA	LYS	A	171	-10.335	36.621	15.921	1.00	156.56
	2907	CB	LYS	A	171	-11.244	37.705	16.466	1.00	223.67
	2908	CG	LYS	A	171	-12.675	37.247	16.553	1.00	223.67
	2909	CD	LYS	A	171	-13.639	38.405	16.449	1.00	223.67
45	2910	CE	LYS	A	171	-13.412	39.423	17.548	1.00	223.67
	2911	NZ	LYS	A	171	-14.415	40.529	17.484	1.00	223.67
	2912	C	LYS	A	171	-10.169	35.507	16.984	1.00	156.56
	2913	O	LYS	A	171	-9.911	35.776	18.164	1.00	156.56
	2914	C1	NAG	A	221	13.115	30.531	-12.704	1.00	229.93
50	2915	C2	NAG	A	221	13.292	32.012	-13.027	1.00	229.93
	2916	N2	NAG	A	221	11.991	32.635	-13.150	1.00	229.93
	2917	C7	NAG	A	221	11.855	33.943	-12.957	1.00	229.93
	2918	O7	NAG	A	221	12.801	34.685	-12.679	1.00	229.93
	2919	C8	NAG	A	221	10.451	34.518	-13.100	1.00	229.93
55	2920	C3	NAG	A	221	14.066	32.185	-14.322	1.00	229.93
	2921	O3	NAG	A	221	14.354	33.560	-14.516	1.00	229.93
	2922	C4	NAG	A	221	15.380	31.386	-14.319	1.00	229.93
	2923	O4	NAG	A	221	15.903	31.411	-15.666	1.00	229.93
	2924	C5	NAG	A	221	15.121	29.925	-13.874	1.00	229.93
60	2925	O5	NAG	A	221	14.399	29.895	-12.623	1.00	229.93
	2926	C6	NAG	A	221	16.390	29.114	-13.656	1.00	229.93
	2927	O6	NAG	A	221	17.244	29.725	-12.701	1.00	229.93
	2928	C1	NAG	A	222	17.240	31.098	-15.903	1.00	249.69
	2929	C2	NAG	A	222	17.830	32.101	-16.914	1.00	249.69
65	2930	N2	NAG	A	222	17.769	33.452	-16.374	1.00	249.69
	2931	C7	NAG	A	222	18.879	34.168	-16.205	1.00	249.69
	2932	O7	NAG	A	222	20.003	33.746	-16.487	1.00	249.69
	2933	C8	NAG	A	222	18.718	35.569	-15.634	1.00	249.69
	2934	C3	NAG	A	222	17.038	32.023	-18.236	1.00	249.69
70	2935	O3	NAG	A	222	17.639	32.861	-19.217	1.00	249.69

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	2936	C4	NAG	A	222	16.979	30.571	-18.752	1.00	249.69
	2937	O4	NAG	A	222	16.114	30.501	-19.878	1.00	249.69
	2938	C5	NAG	A	222	16.463	29.634	-17.646	1.00	249.69
	2939	O5	NAG	A	222	17.286	29.769	-16.459	1.00	249.69
5	2940	C6	NAG	A	222	16.462	28.165	-18.038	1.00	249.69
	2941	O6	NAG	A	222	15.210	27.555	-17.749	1.00	249.69
	2942	C1	NAG	A	242	-3.871	18.493	-8.371	1.00	249.50
	2943	C2	NAG	A	242	-3.270	18.370	-9.775	1.00	249.50
	2944	N2	NAG	A	242	-1.860	18.040	-9.718	1.00	249.50
10	2945	C7	NAG	A	242	-1.426	16.919	-10.287	1.00	249.50
	2946	O7	NAG	A	242	-2.178	16.128	-10.862	1.00	249.50
	2947	C8	NAG	A	242	0.063	16.621	-10.205	1.00	249.50
	2948	C3	NAG	A	242	-3.480	19.691	-10.511	1.00	249.50
	2949	O3	NAG	A	242	-2.951	19.600	-11.829	1.00	249.50
15	2950	C4	NAG	A	242	-4.979	20.019	-10.567	1.00	249.50
	2951	O4	NAG	A	242	-5.159	21.345	-11.115	1.00	249.50
	2952	C5	NAG	A	242	-5.622	19.952	-9.158	1.00	249.50
	2953	O5	NAG	A	242	-5.285	18.711	-8.481	1.00	249.50
	2954	C6	NAG	A	242	-7.140	20.004	-9.235	1.00	249.50
20	2955	O6	NAG	A	242	-7.650	21.225	-8.725	1.00	249.50
	2956	C1	NAG	A	243	-5.905	21.444	-12.280	1.00	249.69
	2957	C2	NAG	A	243	-6.423	22.875	-12.441	1.00	249.69
	2958	N2	NAG	A	243	-7.258	23.262	-11.323	1.00	249.69
	2959	C7	NAG	A	243	-7.047	24.432	-10.724	1.00	249.69
25	2960	O7	NAG	A	243	-6.150	25.215	-11.062	1.00	249.69
	2961	C8	NAG	A	243	-7.964	24.787	-9.565	1.00	249.69
	2962	C3	NAG	A	243	-7.210	22.971	-13.739	1.00	249.69
	2963	O3	NAG	A	243	-7.711	24.291	-13.913	1.00	249.69
	2964	C4	NAG	A	243	-6.286	22.613	-14.888	1.00	249.69
30	2965	O4	NAG	A	243	-7.053	22.760	-16.068	1.00	249.69
	2966	C5	NAG	A	243	-5.731	21.178	-14.681	1.00	249.69
	2967	O5	NAG	A	243	-5.049	21.113	-13.392	1.00	249.69
	2968	C6	NAG	A	243	-4.717	20.769	-15.727	1.00	249.69
	2969	O6	NAG	A	243	-3.570	21.598	-15.679	1.00	249.69
35	2970	C1	MAN	A	244	-6.484	23.132	-17.256	1.00	249.69
	2971	C2	MAN	A	244	-7.225	22.291	-18.199	1.00	249.69
	2972	O2	MAN	A	244	-8.623	22.309	-17.842	1.00	249.69
	2973	C3	MAN	A	244	-6.903	22.695	-19.610	1.00	249.69
	2974	O3	MAN	A	244	-7.502	21.811	-20.538	1.00	249.69
40	2975	C4	MAN	A	244	-7.252	24.155	-19.854	1.00	249.69
	2976	O4	MAN	A	244	-6.977	24.497	-21.200	1.00	249.69
	2977	C5	MAN	A	244	-6.404	24.996	-18.895	1.00	249.69
	2978	O5	MAN	A	244	-6.748	24.610	-17.507	1.00	249.69
	2979	C6	MAN	A	244	-6.499	26.518	-19.137	1.00	249.69
45	2980	O6	MAN	A	244	-7.631	27.105	-18.519	1.00	249.69
	2981	C1	NAG	A	250	17.983	21.117	-1.207	1.00	249.69
	2982	C2	NAG	A	250	19.036	22.142	-0.738	1.00	249.69
	2983	N2	NAG	A	250	19.037	22.235	0.709	1.00	249.69
	2984	C7	NAG	A	250	20.062	21.752	1.406	1.00	249.69
50	2985	O7	NAG	A	250	21.042	21.214	0.876	1.00	249.69
	2986	C8	NAG	A	250	19.990	21.883	2.924	1.00	249.69
	2987	C3	NAG	A	250	18.721	23.516	-1.350	1.00	249.69
	2988	O3	NAG	A	250	19.736	24.449	-1.001	1.00	249.69
	2989	C4	NAG	A	250	18.617	23.400	-2.878	1.00	249.69
55	2990	O4	NAG	A	250	18.193	24.648	-3.416	1.00	249.69
	2991	C5	NAG	A	250	17.612	22.286	-3.261	1.00	249.69
	2992	O5	NAG	A	250	17.986	21.032	-2.636	1.00	249.69
	2993	C6	NAG	A	250	17.526	22.023	-4.759	1.00	249.69
	2994	O6	NAG	A	250	16.887	20.775	-5.028	1.00	249.69
60	2995	C1	NAG	A	274	0.355	12.405	15.723	1.00	249.69
	2996	C2	NAG	A	274	-0.462	13.289	16.690	1.00	249.69
	2997	N2	NAG	A	274	0.423	14.159	17.448	1.00	249.69
	2998	C7	NAG	A	274	-0.025	15.313	17.944	1.00	249.69
	2999	O7	NAG	A	274	-1.188	15.702	17.799	1.00	249.69
65	3000	C8	NAG	A	274	0.966	16.171	18.721	1.00	249.69
	3001	C3	NAG	A	274	-1.276	12.407	17.651	1.00	249.69
	3002	O3	NAG	A	274	-2.130	13.222	18.443	1.00	249.69
	3003	C4	NAG	A	274	-2.117	11.387	16.868	1.00	249.69
	3004	O4	NAG	A	274	-2.765	10.493	17.768	1.00	249.69
70	3005	C5	NAG	A	274	-1.221	10.596	15.901	1.00	249.69

3006	O5	NAG	A	274	-0.517	11.505	15.017	1.00	249.69
3007	C6	NAG	A	274	-2.018	9.637	15.026	1.00	249.69
3008	O6	NAG	A	274	-1.206	9.058	14.010	1.00	249.69
3009	C1	NAG	A	335	5.793	44.302	-4.488	1.00	249.69
3010	C2	NAG	A	335	6.924	43.869	-3.512	1.00	249.69
3011	N2	NAG	A	335	6.696	44.490	-2.220	1.00	249.69
3012	C7	NAG	A	335	6.442	43.744	-1.148	1.00	249.69
3013	O7	NAG	A	335	6.394	42.513	-1.175	1.00	249.69
3014	C8	NAG	A	335	6.211	44.481	0.156	1.00	249.69
3015	C3	NAG	A	335	8.352	44.222	-3.983	1.00	249.69
3016	O3	NAG	A	335	9.296	43.421	-3.281	1.00	249.69
3017	C4	NAG	A	335	8.520	43.993	-5.483	1.00	249.69
3018	O4	NAG	A	335	9.821	44.401	-5.897	1.00	249.69
3019	C5	NAG	A	335	7.450	44.802	-6.205	1.00	249.69
3020	O5	NAG	A	335	6.149	44.255	-5.895	1.00	249.69
3021	C6	NAG	A	335	7.609	44.762	-7.718	1.00	249.69
3022	O6	NAG	A	335	7.688	46.071	-8.267	1.00	249.69
3023	C1	NAG	A	340	-3.087	46.639	17.035	1.00	249.69
3024	C2	NAG	A	340	-3.935	45.839	18.030	1.00	249.69
3025	N2	NAG	A	340	-4.856	44.975	17.311	1.00	249.69
3026	C7	NAG	A	340	-4.995	43.695	17.659	1.00	249.69
3027	O7	NAG	A	340	-4.379	43.170	18.595	1.00	249.69
3028	C8	NAG	A	340	-5.979	42.868	16.843	1.00	249.69
3029	C3	NAG	A	340	-4.707	46.820	18.927	1.00	249.69
3030	O3	NAG	A	340	-5.434	46.110	19.924	1.00	249.69
3031	C4	NAG	A	340	-3.738	47.802	19.596	1.00	249.69
3032	O4	NAG	A	340	-4.485	48.790	20.299	1.00	249.69
3033	C5	NAG	A	340	-2.841	48.473	18.533	1.00	249.69
3034	O5	NAG	A	340	-2.166	47.471	17.739	1.00	249.69
3035	C6	NAG	A	340	-1.781	49.371	19.114	1.00	249.69
3036	O6	NAG	A	340	-0.846	49.785	18.103	1.00	221.62
3037	C1	NAG	A	366	-16.179	35.618	-1.670	1.00	221.62
3038	C2	NAG	A	366	-16.600	34.642	-2.761	1.00	221.62
3039	N2	NAG	A	366	-15.672	34.736	-3.871	1.00	221.62
3040	C7	NAG	A	366	-14.602	33.944	-3.922	1.00	221.62
3041	O7	NAG	A	366	-14.351	33.096	-3.062	1.00	221.62
3042	C8	NAG	A	366	-13.672	34.112	-5.114	1.00	221.62
3043	C3	NAG	A	366	-18.011	34.981	-3.236	1.00	221.62
3044	O3	NAG	A	366	-18.470	33.973	-4.125	1.00	221.62
3045	C4	NAG	A	366	-18.991	35.113	-2.065	1.00	221.62
3046	O4	NAG	A	366	-20.223	35.683	-2.557	1.00	221.62
3047	C5	NAG	A	366	-18.409	36.017	-0.964	1.00	221.62
3048	O5	NAG	A	366	-17.100	35.560	-0.585	1.00	221.62
3049	C6	NAG	A	366	-19.246	36.056	0.304	1.00	221.62
3050	O6	NAG	A	366	-18.758	37.042	1.205	1.00	221.62
3051	C1	NAG	A	367	-21.391	34.987	-2.286	1.00	249.69
3052	C2	NAG	A	367	-22.592	35.932	-2.385	1.00	249.69
3053	N2	NAG	A	367	-22.437	37.053	-1.478	1.00	249.69
3054	C7	NAG	A	367	-22.260	38.275	-1.969	1.00	249.69
3055	O7	NAG	A	367	-22.222	38.512	-3.181	1.00	249.69
3056	C8	NAG	A	367	-22.101	39.407	-0.966	1.00	249.69
3057	C3	NAG	A	367	-23.858	35.142	-2.058	1.00	249.69
3058	O3	NAG	A	367	-24.998	35.986	-2.163	1.00	249.69
3059	C4	NAG	A	367	-23.984	33.958	-3.031	1.00	249.69
3060	O4	NAG	A	367	-25.101	33.153	-2.664	1.00	249.69
3061	C5	NAG	A	367	-22.694	33.108	-3.015	1.00	249.69
3062	O5	NAG	A	367	-21.528	33.838	-3.257	1.00	249.69
3063	C6	NAG	A	367	-22.696	32.031	-4.083	1.00	249.69
3064	O6	NAG	A	367	-21.707	32.291	-5.071	1.00	249.69
3065	CB	LYS	B	4	31.112	63.164	23.840	1.00	249.69
3066	CG	LYS	B	4	31.172	64.583	23.260	1.00	249.69
3067	CD	LYS	B	4	31.232	65.658	24.353	1.00	249.69
3068	CE	LYS	B	4	31.339	67.065	23.748	1.00	249.69
3069	NZ	LYS	B	4	31.384	68.141	24.779	1.00	249.69
3070	C	LYS	B	4	32.410	62.191	21.928	1.00	249.69
3071	O	LYS	B	4	33.409	62.759	22.371	1.00	249.69
3072	N	LYS	B	4	31.072	60.721	23.434	1.00	249.69
3073	CA	LYS	B	4	31.141	62.056	22.777	1.00	223.70
3074	N	PRO	B	5	32.389	61.656	20.698	1.00	195.56
3075	CD	PRO	B	5	31.376	60.752	20.128	1.00	

	3076	CA	PRO	B	5	33.562	61.750	19.825	1.00	223.70
	3077	CB	PRO	B	5	33.387	60.550	18.906	1.00	195.56
	3078	CG	PRO	B	5	31.904	60.498	18.724	1.00	195.56
	3079	C	PRO	B	5	33.598	63.077	19.060	1.00	223.70
5	3080	O	PRO	B	5	32.576	63.741	18.895	1.00	223.70
	3081	N	LYS	B	6	34.780	63.472	18.605	1.00	208.07
	3082	CA	LYS	B	6	34.916	64.713	17.858	1.00	208.07
	3083	CB	LYS	B	6	35.357	65.849	18.783	1.00	245.96
	3084	CG	LYS	B	6	35.467	67.195	18.074	1.00	245.96
10	3085	CD	LYS	B	6	35.756	68.337	19.039	1.00	245.96
	3086	CE	LYS	B	6	35.816	69.677	18.304	1.00	245.96
	3087	NZ	LYS	B	6	35.973	70.834	19.231	1.00	245.96
	3088	C	LYS	B	6	35.920	64.543	16.721	1.00	208.07
	3089	O	LYS	B	6	37.122	64.371	16.946	1.00	208.07
15	3090	N	VAL	B	7	35.414	64.603	15.497	1.00	211.91
	3091	CA	VAL	B	7	36.245	64.443	14.312	1.00	211.91
	3092	CB	VAL	B	7	35.379	64.356	13.053	1.00	105.28
	3093	CG1	VAL	B	7	36.218	63.818	11.881	1.00	105.28
	3094	CG2	VAL	B	7	34.151	63.495	13.325	1.00	105.28
20	3095	C	VAL	B	7	37.258	65.565	14.107	1.00	211.91
	3096	O	VAL	B	7	36.903	66.741	14.033	1.00	211.91
	3097	N	SER	B	8	38.524	65.185	14.009	1.00	208.76
	3098	CA	SER	B	8	39.599	66.141	13.797	1.00	208.76
	3099	CB	SER	B	8	40.749	65.846	14.770	1.00	216.01
25	3100	OG	SER	B	8	41.085	64.465	14.777	1.00	216.01
	3101	C	SER	B	8	40.084	66.033	12.348	1.00	208.76
	3102	O	SER	B	8	39.830	65.031	11.685	1.00	208.76
	3103	N	LEU	B	9	40.767	67.061	11.853	1.00	194.89
	3104	CA	LEU	B	9	41.278	67.030	10.487	1.00	194.89
30	3105	CB	LEU	B	9	40.528	68.017	9.599	1.00	159.88
	3106	CG	LEU	B	9	39.017	67.914	9.401	1.00	159.88
	3107	CD1	LEU	B	9	38.658	68.762	8.190	1.00	159.88
	3108	CD2	LEU	B	9	38.575	66.489	9.175	1.00	159.88
	3109	C	LEU	B	9	42.760	67.363	10.413	1.00	194.89
35	3110	O	LEU	B	9	43.318	67.981	11.315	1.00	194.89
	3111	N	ASN	B	10	43.390	66.956	9.319	1.00	186.22
	3112	CA	ASN	B	10	44.801	67.229	9.113	1.00	186.22
	3113	CB	ASN	B	10	45.653	66.253	9.914	1.00	231.85
	3114	CG	ASN	B	10	47.090	66.704	10.015	1.00	231.85
40	3115	OD1	ASN	B	10	47.381	67.753	10.592	1.00	231.85
	3116	ND2	ASN	B	10	47.999	65.921	9.445	1.00	231.85
	3117	C	ASN	B	10	45.157	67.123	7.638	1.00	186.22
	3118	O	ASN	B	10	45.137	66.030	7.059	1.00	186.22
	3119	N	PRO	B	11	45.503	68.262	6.991	1.00	188.99
45	3120	CD	PRO	B	11	45.868	68.247	5.571	1.00	219.87
	3121	CA	PRO	B	11	45.592	69.622	7.539	1.00	188.99
	3122	CB	PRO	B	11	45.872	70.458	6.284	1.00	219.87
	3123	CG	PRO	B	11	46.650	69.526	5.431	1.00	219.87
	3124	C	PRO	B	11	44.336	70.101	8.267	1.00	188.99
50	3125	O	PRO	B	11	43.282	69.480	8.188	1.00	188.99
	3126	N	PRO	B	12	44.443	71.222	9.003	1.00	172.73
	3127	CD	PRO	B	12	45.661	71.989	9.311	1.00	135.97
	3128	CA	PRO	B	12	43.290	71.755	9.739	1.00	172.73
	3129	CB	PRO	B	12	43.920	72.837	10.623	1.00	135.97
55	3130	CG	PRO	B	12	45.375	72.451	10.702	1.00	135.97
	3131	C	PRO	B	12	42.274	72.344	8.744	1.00	172.73
	3132	O	PRO	B	12	41.079	72.406	9.017	1.00	172.73
	3133	N	TRP	B	13	42.788	72.770	7.593	1.00	154.67
	3134	CA	TRP	B	13	42.024	73.371	6.503	1.00	154.67
60	3135	CB	TRP	B	13	42.952	73.560	5.300	1.00	165.26
	3136	CG	TRP	B	13	44.249	74.215	5.658	1.00	165.26
	3137	CD2	TRP	B	13	44.455	75.194	6.673	1.00	165.26
	3138	CE2	TRP	B	13	45.818	75.545	6.650	1.00	165.26
	3139	CE3	TRP	B	13	43.612	75.818	7.601	1.00	165.26
65	3140	CD1	TRP	B	13	45.469	74.009	5.073	1.00	165.26
	3141	NE1	TRP	B	13	46.419	74.806	5.668	1.00	165.26
	3142	CZ2	TRP	B	13	46.356	76.486	7.521	1.00	165.26
	3143	CZ3	TRP	B	13	44.146	76.753	8.464	1.00	165.26
	3144	CH2	TRP	B	13	45.506	77.080	8.420	1.00	165.26
70	3145	C	TRP	B	13	40.840	72.520	6.088	1.00	154.67

	Atom	Name	Res	Chain	Seq	X	Y	Z	Occ	B
	3146	O	TRP	B	13	41.023	71.414	5.593	1.00	154.67
	3147	N	ASN	B	14	39.827	73.038	6.265	1.00	126.91
	3148	CA	ASN	B	14	38.416	72.290	5.885	1.00	126.91
	3149	CB	ASN	B	14	37.397	72.308	7.035	1.00	191.01
5	3150	CG	ASN	B	14	36.877	73.687	7.331	1.00	191.01
	3151	OD1	ASN	B	14	37.643	74.604	7.635	1.00	191.01
	3152	ND2	ASN	B	14	35.564	73.848	7.246	1.00	191.01
	3153	C	ASN	B	14	37.778	72.796	4.590	1.00	126.91
	3154	O	ASN	B	14	36.595	72.577	4.336	1.00	126.91
10	3155	N	ARG	B	15	38.606	73.477	3.799	1.00	109.47
	3156	CA	ARG	B	15	38.240	74.033	2.509	1.00	109.47
	3157	CB	ARG	B	15	38.096	75.576	2.571	1.00	119.97
	3158	CG	ARG	B	15	37.202	76.153	3.671	1.00	119.97
	3159	CD	ARG	B	15	37.010	77.677	3.482	1.00	119.97
15	3160	NE	ARG	B	15	36.034	78.008	2.444	1.00	119.97
	3161	CZ	ARG	B	15	36.135	79.040	1.615	1.00	119.97
	3162	NH1	ARG	B	15	37.176	79.846	1.693	1.00	119.97
	3163	NH2	ARG	B	15	35.187	79.273	0.715	1.00	119.97
	3164	C	ARG	B	15	39.432	73.688	1.616	1.00	109.47
20	3165	O	ARG	B	15	40.462	74.353	1.689	1.00	109.47
	3166	N	ILE	B	16	39.307	72.675	0.769	1.00	122.07
	3167	CA	ILE	B	16	40.431	72.294	-0.072	1.00	122.07
	3168	CB	ILE	B	16	40.914	70.905	0.303	1.00	121.17
	3169	CG2	ILE	B	16	41.691	70.954	1.608	1.00	121.17
25	3170	CG1	ILE	B	16	39.708	69.975	0.377	1.00	121.17
	3171	CD1	ILE	B	16	40.058	68.526	0.495	1.00	121.17
	3172	C	ILE	B	16	40.206	72.279	-1.571	1.00	122.07
	3173	O	ILE	B	16	39.087	72.146	-2.041	1.00	122.07
	3174	N	PHE	B	17	41.299	72.390	-2.314	1.00	169.19
30	3175	CA	PHE	B	17	41.255	72.361	-3.770	1.00	169.19
	3176	CB	PHE	B	17	42.595	72.815	-4.351	1.00	156.59
	3177	CG	PHE	B	17	42.685	74.285	-4.609	1.00	156.59
	3178	CD1	PHE	B	17	43.888	74.960	-4.420	1.00	156.59
	3179	CD2	PHE	B	17	41.586	74.990	-5.076	1.00	156.59
35	3180	CE1	PHE	B	17	43.987	76.315	-4.690	1.00	156.59
	3181	CE2	PHE	B	17	41.684	76.350	-5.349	1.00	156.59
	3182	CZ	PHE	B	17	42.886	77.013	-5.156	1.00	169.19
	3183	C	PHE	B	17	40.970	70.947	-4.258	1.00	169.19
	3184	O	PHE	B	17	40.883	70.006	-3.460	1.00	133.30
40	3185	N	LYS	B	18	40.853	70.811	-5.575	1.00	133.30
	3186	CA	LYS	B	18	40.573	69.531	-6.208	1.00	237.07
	3187	CB	LYS	B	18	39.922	69.777	-7.575	1.00	237.07
	3188	CG	LYS	B	18	39.500	68.537	-8.339	1.00	237.07
	3189	CD	LYS	B	18	38.720	68.925	-9.585	1.00	237.07
45	3190	CE	LYS	B	18	38.347	67.714	-10.424	1.00	237.07
	3191	NZ	LYS	B	18	39.539	67.079	-11.054	1.00	133.30
	3192	C	LYS	B	18	41.851	68.693	-6.363	1.00	133.30
	3193	O	LYS	B	18	42.864	69.166	-6.884	1.00	182.54
	3194	N	GLY	B	19	41.799	67.448	-5.899	1.00	182.54
50	3195	CA	GLY	B	19	42.942	66.562	-6.017	1.00	182.54
	3196	C	GLY	B	19	43.823	66.498	-4.794	1.00	182.54
	3197	O	GLY	B	19	44.703	65.642	-4.724	1.00	116.49
	3198	N	GLU	B	20	43.591	67.391	-3.835	1.00	116.49
	3199	CA	GLU	B	20	44.396	67.424	-2.606	1.00	185.38
55	3200	CB	GLU	B	20	44.276	68.800	-1.920	1.00	185.38
	3201	CG	GLU	B	20	44.484	70.019	-2.822	1.00	185.38
	3202	CD	GLU	B	20	44.476	71.336	-2.047	1.00	185.38
	3203	OE1	GLU	B	20	43.513	71.585	-1.288	1.00	185.38
	3204	OE2	GLU	B	20	45.433	72.125	-2.205	1.00	116.49
60	3205	C	GLU	B	20	43.948	66.330	-1.622	1.00	116.49
	3206	O	GLU	B	20	42.816	65.854	-1.729	1.00	130.57
	3207	N	ASN	B	21	44.810	65.944	-0.669	1.00	130.57
	3208	CA	ASN	B	21	44.430	64.911	0.300	1.00	248.12
	3209	CB	ASN	B	21	45.473	63.791	0.353	1.00	248.12
65	3210	CG	ASN	B	21	46.097	63.492	-0.992	1.00	248.12
	3211	OD1	ASN	B	21	45.414	63.347	-2.004	1.00	248.12
	3212	ND2	ASN	B	21	47.420	63.384	-0.980	1.00	130.57
	3213	C	ASN	B	21	44.229	65.432	1.730	1.00	130.57
	3214	O	ASN	B	21	44.972	66.308	2.194	1.00	161.15
70	3215	N	VAL	B	22	43.243	64.865	2.428	1.00	

3216	CA	VAL	B	22	42.933	65.242	3.810	1.00	161.15
3217	CB	VAL	B	22	41.702	66.157	3.876	1.00	160.53
3218	CG1	VAL	B	22	40.447	65.365	3.549	1.00	160.53
3219	CG2	VAL	B	22	41.584	66.778	5.249	1.00	160.53
3220	C	VAL	B	22	42.633	64.002	4.652	1.00	161.15
3221	O	VAL	B	22	42.062	63.035	4.141	1.00	161.15
3222	N	THR	B	23	42.985	64.041	5.940	1.00	186.22
3223	CA	THR	B	23	42.771	62.898	6.849	1.00	186.22
3224	CB	THR	B	23	44.108	62.440	7.478	1.00	249.25
3225	OG1	THR	B	23	45.086	62.250	6.448	1.00	249.25
3226	CG2	THR	B	23	43.919	61.136	8.238	1.00	249.25
3227	C	THR	B	23	41.804	63.173	8.004	1.00	186.22
3228	O	THR	B	23	42.015	64.109	8.783	1.00	186.22
3229	N	LEU	B	24	40.764	62.345	8.132	1.00	183.26
3230	CA	LEU	B	24	39.782	62.522	9.208	1.00	183.26
3231	CB	LEU	B	24	38.339	62.398	8.677	1.00	177.01
3232	CG	LEU	B	24	37.949	62.842	7.258	1.00	177.01
3233	CD1	LEU	B	24	36.435	62.918	7.183	1.00	177.01
3234	CD2	LEU	B	24	38.553	!90	6.910	1.00	177.01
3235	C	LEU	B	24	39.974	61.501	10.329	1.00	183.26
3236	O	LEU	B	24	39.661	60.321	10.162	1.00	183.26
3237	N	THR	B	25	40.476	61.965	11.472	1.00	238.46
3238	CA	THR	B	25	40.717	61.111	12.636	1.00	238.46
3239	CB	THR	B	25	42.027	61.517	13.351	1.00	207.80
3240	OG1	THR	B	25	43.116	61.448	12.424	1.00	207.80
3241	CG2	THR	B	25	42.312	60.594	14.527	1.00	207.80
3242	C	THR	B	25	39.562	61.234	13.632	1.00	238.46
3243	O	THR	B	25	39.133	62.342	13.949	1.00	238.46
3244	N	CYS	B	26	39.069	60.099	14.126	1.00	203.48
3245	CA	CYS	B	26	37.965	60.098	15.088	1.00	203.48
3246	C	CYS	B	26	38.484	60.356	16.500	1.00	203.48
3247	O	CYS	B	26	39.563	59.880	16.861	1.00	203.48
3248	CB	CYS	B	26	37.227	58.767	15.036	1.00	181.40
3249	SG	CYS	B	26	35.662	58.718	15.964	1.00	181.40
3250	N	ASN	B	27	37.708	61.100	17.294	1.00	249.69
3251	CA	ASN	B	27	38.087	61.472	18.666	1.00	249.69
3252	CB	ASN	B	27	36.876	61.388	19.608	1.00	249.69
3253	CG	ASN	B	27	37.148	62.023	20.969	1.00	249.69
3254	OD1	ASN	B	27	37.644	63.155	21.060	1.00	249.69
3255	ND2	ASN	B	27	36.820	61.299	22.033	1.00	249.69
3256	C	ASN	B	27	39.259	60.677	19.254	1.00	249.69
3257	O	ASN	B	27	39.081	59.605	19.837	1.00	249.69
3258	N	GLY	B	28	40.455	61.234	19.090	1.00	244.48
3259	CA	GLY	B	28	41.676	60.619	19.577	1.00	244.48
3260	C	GLY	B	28	42.824	61.439	19.026	1.00	244.48
3261	O	GLY	B	28	42.970	61.561	17.809	1.00	244.48
3262	N	ASN	B	29	43.638	62.008	19.912	1.00	249.69
3263	CA	ASN	B	29	44.763	62.853	19.497	1.00	249.69
3264	CB	ASN	B	29	45.261	63.688	20.698	1.00	249.69
3265	CG	ASN	B	29	46.236	64.797	20.295	1.00	249.69
3266	OD1	ASN	B	29	48.441	65.073	19.106	1.00	249.69
3267	ND2	ASN	B	29	46.830	65.444	21.293	1.00	249.69
3268	C	ASN	B	29	45.830	62.076	18.865	1.00	249.69
3269	O	ASN	B	29	46.375	62.412	17.757	1.00	249.69
3270	N	ASN	B	30	46.412	61.034	19.543	1.00	249.69
3271	CA	ASN	B	30	47.543	60.279	19.017	1.00	249.69
3272	CB	ASN	B	30	48.783	60.555	19.881	1.00	249.69
3273	CG	ASN	B	30	49.224	62.017	19.831	1.00	249.69
3274	OD1	ASN	B	30	49.500	62.634	20.869	1.00	249.69
3275	ND2	ASN	B	30	49.301	62.574	18.622	1.00	249.69
3276	C	ASN	B	30	47.341	58.772	18.864	1.00	249.69
3277	O	ASN	B	30	47.289	58.267	17.736	1.00	249.69
3278	N	PHE	B	31	47.227	58.056	19.985	1.00	249.69
3279	CA	PHE	B	31	47.068	56.598	19.833	1.00	249.69
3280	CB	PHE	B	31	48.220	55.917	20.703	1.00	249.69
3281	CG	PHE	B	31	49.601	56.344	20.239	1.00	249.69
3282	CD1	PHE	B	31	50.151	57.556	20.662	1.00	249.69
3283	CD2	PHE	B	31	50.335	55.552	19.345	1.00	249.69
3284	CE1	PHE	B	31	51.403	57.976	20.203	1.00	249.69
3285	CE2	PHE	B	31	51.589	55.967	18.881	1.00	249.69

	3286	CZ	PHE	B	31	52.121	57.182	19.313	1.00	249.69
	3287	C	PHE	B	31	45.718	56.071	20.433	1.00	249.69
	3288	O	PHE	B	31	45.325	56.313	21.577	1.00	249.69
	3289	N	PHE	B	32	45.027	55.341	19.556	1.00	249.69
5	3290	CA	PHE	B	32	43.717	54.761	19.859	1.00	249.69
	3291	CB	PHE	B	32	42.670	55.314	18.875	1.00	249.69
	3292	CG	PHE	B	32	41.238	55.081	19.304	1.00	249.69
	3293	CD1	PHE	B	32	40.722	55.709	20.443	1.00	249.69
	3294	CD2	PHE	B	32	40.404	54.237	18.565	1.00	249.69
10	3295	CE1	PHE	B	32	39.398	55.499	20.835	1.00	249.69
	3296	CE2	PHE	B	32	39.081	54.022	18.950	1.00	249.69
	3297	CZ	PHE	B	32	38.578	54.655	20.087	1.00	249.69
	3298	C	PHE	B	32	43.771	53.220	19.785	1.00	249.69
	3299	O	PHE	B	32	44.746	52.646	19.285	1.00	249.69
15	3300	N	GLU	B	33	42.714	52.559	20.259	1.00	249.69
	3301	CA	GLU	B	33	42.688	51.104	20.273	1.00	249.69
	3302	CB	GLU	B	33	42.563	50.633	21.724	1.00	249.69
	3303	CG	GLU	B	33	42.965	49.185	21.932	1.00	249.69
	3304	CD	GLU	B	33	44.299	48.858	21.285	1.00	249.69
20	3305	OE1	GLU	B	33	45.257	49.641	21.471	1.00	249.69
	3306	OE2	GLU	B	33	44.389	47.819	20.593	1.00	249.69
	3307	C	GLU	B	33	41.644	50.384	19.409	1.00	249.69
	3308	O	GLU	B	33	41.991	49.478	18.645	1.00	249.69
	3309	N	VAL	B	34	40.375	50.773	19.532	1.00	249.69
25	3310	CA	VAL	B	34	39.290	50.129	18.784	1.00	247.84
	3311	CB	VAL	B	34	37.920	50.767	19.158	1.00	247.84
	3312	CG1	VAL	B	34	36.794	50.060	18.427	1.00	247.84
	3313	CG2	VAL	B	34	37.698	50.681	20.661	1.00	249.69
	3314	C	VAL	B	34	39.448	50.119	17.252	1.00	249.69
30	3315	O	VAL	B	34	40.059	51.023	16.663	1.00	249.69
	3316	N	SER	B	35	38.895	49.077	16.627	1.00	249.69
	3317	CA	SER	B	35	38.934	48.909	15.175	1.00	249.69
	3318	CB	SER	B	35	39.389	47.500	14.806	1.00	240.73
	3319	OG	SER	B	35	38.373	46.555	15.104	1.00	240.73
35	3320	C	SER	B	35	37.529	49.126	14.625	1.00	249.69
	3321	O	SER	B	35	37.305	49.055	13.412	1.00	249.69
	3322	N	SER	B	36	36.583	49.371	15.533	1.00	249.69
	3323	CA	SER	B	36	35.186	49.611	15.162	1.00	249.69
	3324	CB	SER	B	36	34.233	48.825	16.081	1.00	249.69
40	3325	OG	SER	B	36	34.184	49.372	17.391	1.00	249.69
	3326	C	SER	B	36	34.857	51.108	15.231	1.00	249.69
	3327	O	SER	B	36	34.462	51.639	16.278	1.00	249.69
	3328	N	THR	B	37	35.037	51.780	14.102	1.00	249.69
	3329	CA	THR	B	37	34.765	53.198	14.004	1.00	249.69
45	3330	CB	THR	B	37	36.076	53.989	13.773	1.00	184.28
	3331	OG1	THR	B	37	36.977	53.759	14.866	1.00	184.28
	3332	CG2	THR	B	37	35.787	55.477	13.679	1.00	184.28
	3333	C	THR	B	37	33.808	53.375	12.823	1.00	249.69
	3334	O	THR	B	37	33.964	52.726	11.782	1.00	249.69
50	3335	N	LYS	B	38	32.809	54.236	12.988	1.00	236.74
	3336	CA	LYS	B	38	31.831	54.464	11.930	1.00	236.74
	3337	CB	LYS	B	38	30.421	54.378	12.519	1.00	245.72
	3338	CG	LYS	B	38	30.118	53.037	13.196	1.00	245.72
	3339	CD	LYS	B	38	28.713	52.984	13.820	1.00	245.72
55	3340	CE	LYS	B	38	28.418	51.615	14.417	1.00	245.72
	3341	NZ	LYS	B	38	27.042	51.521	14.992	1.00	245.72
	3342	C	LYS	B	38	32.035	55.806	11.227	1.00	236.74
	3343	O	LYS	B	38	32.415	56.797	11.847	1.00	236.74
	3344	N	TRP	B	39	31.805	55.821	9.920	1.00	197.18
60	3345	CA	TRP	B	39	31.948	57.042	9.141	1.00	197.18
	3346	CB	TRP	B	39	33.131	56.937	8.184	1.00	174.88
	3347	CG	TRP	B	39	34.474	56.888	8.840	1.00	174.88
	3348	CD2	TRP	B	39	35.068	57.877	9.709	1.00	174.88
	3349	CE2	TRP	B	39	36.391	57.457	9.977	1.00	174.88
65	3350	CE3	TRP	B	39	34.614	59.069	10.278	1.00	174.88
	3351	CD1	TRP	B	39	35.433	55.942	8.634	1.00	174.88
	3352	NE1	TRP	B	39	36.589	56.276	9.311	1.00	174.88
	3353	CZ2	TRP	B	39	37.265	58.190	10.788	1.00	174.88
	3354	CZ3	TRP	B	39	35.488	59.797	11.082	1.00	174.88
70	3355	CH2	TRP	B	39	36.798	59.357	11.324	1.00	174.88

						x	y	z	occ	B
	3356	C	TRP	B	39	30.667	57.211	8.335	1.00	197.18
	3357	O	TRP	B	39	30.215	56.251	7.708	1.00	197.18
	3358	N	PHE	B	40	30.086	58.413	8.348	1.00	186.05
	3359	CA	PHE	B	40	28.848	58.653	7.609	1.00	186.05
5	3360	CB	PHE	B	40	27.674	58.878	8.572	1.00	216.66
	3361	CG	PHE	B	40	27.425	57.738	9.528	1.00	216.66
	3362	CD1	PHE	B	40	28.199	57.602	10.679	1.00	216.66
	3363	CD2	PHE	B	40	26.396	56.824	9.297	1.00	216.66
	3364	CE1	PHE	B	40	27.951	56.578	11.590	1.00	216.66
10	3365	CE2	PHE	B	40	26.139	55.800	10.194	1.00	216.66
	3366	CZ	PHE	B	40	26.917	55.674	11.345	1.00	216.66
	3367	C	PHE	B	40	28.896	59.825	6.616	1.00	196.05
	3368	O	PHE	B	40	28.336	60.888	6.877	1.00	196.05
	3369	N	HIS	B	41	29.552	59.613	5.476	1.00	132.87
15	3370	CA	HIS	B	41	29.665	60.618	4.418	1.00	132.87
	3371	CB	HIS	B	41	30.576	60.097	3.315	1.00	148.70
	3372	CG	HIS	B	41	30.772	61.067	2.198	1.00	148.70
	3373	CD2	HIS	B	41	30.886	60.877	0.864	1.00	148.70
	3374	ND1	HIS	B	41	30.949	62.416	2.414	1.00	148.70
20	3375	CE1	HIS	B	41	31.166	63.019	1.259	1.00	148.70
	3376	NE2	HIS	B	41	31.135	62.108	0.304	1.00	148.70
	3377	C	HIS	B	41	28.311	60.975	3.804	1.00	132.87
	3378	O	HIS	B	41	27.783	60.210	2.996	1.00	132.87
	3379	N	ASN	B	42	27.777	62.147	4.163	1.00	209.30
25	3380	CA	ASN	B	42	26.467	62.614	3.684	1.00	209.30
	3381	CB	ASN	B	42	26.371	62.546	2.148	1.00	240.31
	3382	CG	ASN	B	42	27.092	63.700	1.461	1.00	240.31
	3383	OD1	ASN	B	42	28.241	63.989	1.789	1.00	240.31
	3384	ND2	ASN	B	42	26.427	64.350	0.505	1.00	240.31
30	3385	C	ASN	B	42	25.375	61.745	4.316	1.00	209.30
	3386	O	ASN	B	42	24.271	61.613	3.774	1.00	209.30
	3387	N	GLY	B	43	25.695	61.168	5.475	1.00	171.14
	3388	CA	GLY	B	43	24.758	60.306	6.176	1.00	171.14
	3389	C	GLY	B	43	24.985	58.836	5.841	1.00	171.14
35	3390	O	GLY	B	43	24.963	57.969	6.717	1.00	171.14
	3391	N	SER	B	44	25.211	58.563	4.560	1.00	214.62
	3392	CA	SER	B	44	25.444	57.207	4.071	1.00	214.62
	3393	CB	SER	B	44	25.676	57.228	2.555	1.00	249.69
	3394	OG	SER	B	44	24.567	57.774	1.864	1.00	249.69
40	3395	C	SER	B	44	26.651	56.559	4.733	1.00	214.62
	3396	O	SER	B	44	27.757	57.088	4.657	1.00	214.62
	3397	N	LEU	B	45	26.448	55.404	5.359	1.00	180.32
	3398	CA	LEU	B	45	27.555	54.713	6.008	1.00	180.32
	3399	CB	LEU	B	45	27.095	53.361	6.558	1.00	218.81
45	3400	CG	LEU	B	45	28.170	52.573	7.318	1.00	218.81
	3401	CD1	LEU	B	45	28.753	53.429	8.432	1.00	218.81
	3402	CD2	LEU	B	45	27.568	51.300	7.883	1.00	218.81
	3403	C	LEU	B	45	28.722	54.516	5.030	1.00	180.32
	3404	O	LEU	B	45	28.517	54.379	3.819	1.00	180.32
50	3405	N	SER	B	46	29.942	54.517	5.565	1.00	248.98
	3406	CA	SER	B	46	31.145	54.357	4.757	1.00	248.98
	3407	CB	SER	B	46	32.188	55.405	5.149	1.00	249.38
	3408	OG	SER	B	46	33.322	55.338	4.301	1.00	249.38
	3409	C	SER	B	46	31.747	52.957	4.898	1.00	248.98
55	3410	O	SER	B	46	31.351	52.195	5.773	1.00	248.98
	3411	N	GLU	B	47	32.72/	52.670	4.045	1.00	249.69
	3412	CA	GLU	B	47	33.387	51.365	4.032	1.00	249.69
	3413	CB	GLU	B	47	33.757	50.996	2.593	1.00	249.69
	3414	CG	GLU	B	47	32.553	50.869	1.674	1.00	249.69
60	3415	CD	GLU	B	47	32.945	50.524	0.256	1.00	249.69
	3416	OE1	GLU	B	47	33.631	51.350	-0.388	1.00	249.69
	3417	OE2	GLU	B	47	32.572	49.426	-0.214	1.00	249.69
	3418	C	GLU	B	47	34.618	51.211	4.926	1.00	249.69
	3419	O	GLU	B	47	35.099	50.096	5.132	1.00	249.69
65	3420	N	GLU	B	48	35.139	52.316	5.446	1.00	184.88
	3421	CA	GLU	B	48	36.297	52.225	6.316	1.00	184.88
	3422	CB	GLU	B	48	37.110	53.523	6.288	1.00	208.21
	3423	CG	GLU	B	48	38.293	53.542	7.265	1.00	208.21
	3424	CD	GLU	B	48	39.366	52.513	6.941	1.00	208.21
70	3425	OE1	GLU	B	48	40.084	52.698	5.937	1.00	208.21

	3426	OE2	GLU	B	48	39.493	51.517	7.685	1.00	208.21
	3427	C	GLU	B	48	35.834	51.929	7.738	1.00	184.88
	3428	O	GLU	B	48	34.687	52.213	8.104	1.00	184.88
	3429	N	THR	B	49	36.731	51.348	8.530	1.00	237.20
5	3430	CA	THR	B	49	36.443	51.003	9.917	1.00	237.20
	3431	CB	THR	B	49	36.348	49.477	10.090	1.00	231.33
	3432	OG1	THR	B	49	37.542	48.864	9.586	1.00	231.33
	3433	CG2	THR	B	49	35.144	48.933	9.336	1.00	231.33
	3434	C	THR	B	49	37.540	51.551	10.829	1.00	237.20
10	3435	O	THR	B	49	37.303	51.819	12.006	1.00	237.20
	3436	N	ASN	B	50	38.739	51.713	10.278	1.00	222.02
	3437	CA	ASN	B	50	39.863	52.246	11.036	1.00	222.02
	3438	CB	ASN	B	50	41.101	52.350	10.132	1.00	245.81
	3439	CG	ASN	B	50	42.369	52.650	10.910	1.00	245.81
15	3440	OD1	ASN	B	50	42.309	53.119	12.045	1.00	245.81
	3441	ND2	ASN	B	50	43.520	52.400	10.299	1.00	245.81
	3442	C	ASN	B	50	39.447	53.636	11.531	1.00	222.02
	3443	O	ASN	B	50	38.625	54.290	10.901	1.00	222.02
	3444	N	SER	B	51	40.004	54.089	12.651	1.00	208.27
20	3445	CA	SER	B	51	39.652	55.405	13.176	1.00	208.27
	3446	CB	SER	B	51	40.219	55.590	14.590	1.00	249.69
	3447	OG	SER	B	51	41.624	55.785	14.565	1.00	249.69
	3448	C	SER	B	51	40.135	56.555	12.276	1.00	208.27
	3449	O	SER	B	51	39.672	57.690	12.416	1.00	208.27
25	3450	N	SER	B	52	41.059	56.265	11.360	1.00	249.32
	3451	CA	SER	B	52	41.588	57.283	10.446	1.00	249.32
	3452	CB	SER	B	52	43.125	57.283	10.456	1.00	193.43
	3453	OG	SER	B	52	43.642	57.584	11.741	1.00	193.43
	3454	C	SER	B	52	41.106	57.076	9.014	1.00	249.32
30	3455	O	SER	B	52	41.596	56.199	8.299	1.00	249.32
	3456	N	LEU	B	53	40.147	57.895	8.601	1.00	187.33
	3457	CA	LEU	B	53	39.601	57.820	7.255	1.00	187.33
	3458	CB	LEU	B	53	38.107	58.131	7.283	1.00	113.92
	3459	CG	LEU	B	53	37.410	58.539	5.975	1.00	113.92
35	3460	CD1	LEU	B	53	37.839	57.637	4.810	1.00	113.92
	3461	CD2	LEU	B	53	35.889	58.503	6.185	1.00	113.92
	3462	C	LEU	B	53	40.310	58.794	6.331	1.00	187.33
	3463	O	LEU	B	53	40.085	60.010	6.397	1.00	187.33
	3464	N	ASN	B	54	41.169	58.261	5.467	1.00	190.27
40	3465	CA	ASN	B	54	41.899	59.112	4.547	1.00	190.27
	3466	CB	ASN	B	54	43.209	58.458	4.126	1.00	248.26
	3467	CG	ASN	B	54	44.214	58.414	5.254	1.00	248.26
	3468	OD1	ASN	B	54	44.519	59.432	5.876	1.00	248.26
	3469	ND2	ASN	B	54	44.737	57.232	5.525	1.00	248.26
45	3470	C	ASN	B	54	41.096	59.481	3.320	1.00	190.27
	3471	O	ASN	B	54	40.134	58.800	2.957	1.00	190.27
	3472	N	ILE	B	55	41.515	60.580	2.700	1.00	195.13
	3473	CA	ILE	B	55	40.900	61.127	1.503	1.00	195.13
	3474	CB	ILE	B	55	40.101	62.413	1.829	1.00	126.27
50	3475	CG2	ILE	B	55	39.946	63.268	0.581	1.00	126.27
	3476	CG1	ILE	B	55	38.743	62.032	2.431	1.00	126.27
	3477	CD1	ILE	B	55	37.857	63.206	2.786	1.00	126.27
	3478	C	ILE	B	55	42.017	61.473	0.540	1.00	195.13
	3479	O	ILE	B	55	42.836	62.346	0.825	1.00	195.13
55	3480	N	VAL	B	56	42.057	60.789	-0.594	1.00	178.85
	3481	CA	VAL	B	56	43.099	61.058	-1.569	1.00	178.85
	3482	CB	VAL	B	56	43.587	59.773	-2.227	1.00	249.69
	3483	CG1	VAL	B	56	44.960	60.002	-2.841	1.00	249.69
	3484	CG2	VAL	B	56	43.642	58.662	-1.189	1.00	249.69
60	3485	C	VAL	B	56	42.580	62.012	-2.630	1.00	178.85
	3486	O	VAL	B	56	41.612	62.729	-2.376	1.00	178.85
	3487	N	ASN	B	57	43.217	62.025	-3.804	1.00	192.84
	3488	CA	ASN	B	57	42.832	62.923	-4.895	1.00	192.84
	3489	CB	ASN	B	57	43.085	62.261	-6.239	1.00	201.25
65	3490	CG	ASN	B	57	44.560	62.119	-6.530	1.00	201.25
	3491	OD1	ASN	B	57	45.309	63.090	-6.446	1.00	201.25
	3492	ND2	ASN	B	57	44.988	60.908	-6.875	1.00	201.25
	3493	C	ASN	B	57	41.397	63.405	-4.791	1.00	192.84
	3494	O	ASN	B	57	40.470	62.757	-5.267	1.00	192.84
70	3495	N	ALA	B	58	41.253	64.565	-4.151	1.00	127.65

	3496	CA	ALA	B	58	39.980	65.227	-3.870	1.00	127.65
	3497	CB	ALA	B	58	40.256	66.555	-3.201	1.00	133.74
	3498	C	ALA	B	58	39.029	65.436	-5.041	1.00	127.65
	3499	O	ALA	B	58	39.244	66.294	-5.891	1.00	127.65
5	3500	N	LYS	B	59	37.956	64.658	-5.060	1.00	124.63
	3501	CA	LYS	B	59	36.946	64.744	-6.109	1.00	124.63
	3502	CB	LYS	B	59	36.504	63.344	-6.550	1.00	240.20
	3503	CG	LYS	B	59	37.632	62.491	-7.108	1.00	240.20
	3504	CD	LYS	B	59	37.182	61.069	-7.421	1.00	240.20
10	3505	CE	LYS	B	59	38.354	60.214	-7.901	1.00	240.20
	3506	NZ	LYS	B	59	37.959	58.816	-8.237	1.00	240.20
	3507	C	LYS	B	59	35.778	65.493	-5.511	1.00	124.63
	3508	O	LYS	B	59	35.423	65.278	-4.355	1.00	124.63
	3509	N	PHE	B	60	35.188	66.378	-6.301	1.00	146.51
15	3510	CA	PHE	B	60	34.064	67.179	-5.839	1.00	146.51
	3511	CB	PHE	B	60	33.350	67.788	-7.049	1.00	206.05
	3512	CG	PHE	B	60	34.189	68.770	-7.815	1.00	206.05
	3513	CD1	PHE	B	60	33.968	68.976	-9.169	1.00	206.05
	3514	CD2	PHE	B	60	35.193	69.499	-7.177	1.00	206.05
20	3515	CE1	PHE	B	60	34.732	69.890	-9.882	1.00	206.05
	3516	CE2	PHE	B	60	35.963	70.417	-7.877	1.00	206.05
	3517	CZ	PHE	B	60	35.732	70.612	-9.234	1.00	206.05
	3518	C	PHE	B	60	33.073	66.407	-4.968	1.00	146.51
	3519	O	PHE	B	60	32.479	66.957	-4.044	1.00	146.51
25	3520	N	GLU	B	61	32.911	65.125	-5.257	1.00	158.05
	3521	CA	GLU	B	61	31.977	64.284	-4.520	1.00	158.05
	3522	CB	GLU	B	61	31.872	62.911	-5.197	1.00	249.69
	3523	CG	GLU	B	61	31.394	62.950	-6.651	1.00	249.69
	3524	CD	GLU	B	61	32.288	63.798	-7.556	1.00	249.69
30	3525	OE1	GLU	B	61	33.522	63.580	-7.574	1.00	249.69
	3526	OE2	GLU	B	61	31.753	64.685	-8.256	1.00	249.69
	3527	C	GLU	B	61	32.391	64.113	-3.067	1.00	158.05
	3528	O	GLU	B	61	31.555	63.831	-2.213	1.00	158.05
	3529	N	ASP	B	62	33.682	64.285	-2.789	1.00	134.92
35	3530	CA	ASP	B	62	34.200	64.139	-1.426	1.00	134.92
	3531	CB	ASP	B	62	35.729	64.128	-1.432	1.00	133.92
	3532	CG	ASP	B	62	36.294	63.118	-2.393	1.00	133.92
	3533	OD1	ASP	B	62	35.669	62.048	-2.551	1.00	133.92
	3534	OD2	ASP	B	62	37.364	63.397	-2.972	1.00	134.92
40	3535	C	ASP	B	62	33.709	65.279	-0.543	1.00	134.92
	3536	O	ASP	B	62	33.663	65.143	0.685	1.00	128.21
	3537	N	SER	B	63	33.358	66.400	-1.177	1.00	128.21
	3538	CA	SER	B	63	32.857	67.553	-0.449	1.00	212.43
	3539	CB	SER	B	63	32.552	68.710	-1.407	1.00	212.43
45	3540	OG	SER	B	63	33.696	69.095	-2.153	1.00	128.21
	3541	C	SER	B	63	31.574	67.137	0.261	1.00	128.21
	3542	O	SER	B	63	30.660	66.629	-0.377	1.00	137.99
	3543	N	GLY	B	64	31.500	67.347	1.571	1.00	137.99
	3544	CA	GLY	B	64	30.298	66.963	2.274	1.00	137.99
50	3545	C	GLY	B	64	30.367	66.973	3.784	1.00	137.99
	3546	O	GLY	B	64	31.282	67.545	4.385	1.00	125.38
	3547	N	GLU	B	65	29.378	66.312	4.383	1.00	125.38
	3548	CA	GLU	B	65	29.219	66.217	5.830	1.00	249.57
	3549	CB	GLU	B	65	27.747	66.504	6.159	1.00	249.57
55	3550	CG	GLU	B	65	27.329	66.290	7.594	1.00	249.57
	3551	CD	GLU	B	65	25.818	66.198	7.731	1.00	249.57
	3552	OE1	GLU	B	65	25.227	65.270	7.143	1.00	249.57
	3553	OE2	GLU	B	65	25.217	67.046	8.416	1.00	125.38
	3554	C	GLU	B	65	29.617	64.843	6.339	1.00	125.38
60	3555	O	GLU	B	65	29.050	63.844	5.900	1.00	138.71
	3556	N	TYR	B	66	30.575	64.790	7.265	1.00	138.71
	3557	CA	TYR	B	66	31.029	63.510	7.826	1.00	186.43
	3558	CB	TYR	B	66	32.512	63.294	7.560	1.00	186.43
	3559	CG	TYR	B	66	32.917	63.170	6.122	1.00	186.43
65	3560	CD1	TYR	B	66	32.997	64.287	5.302	1.00	186.43
	3561	CE1	TYR	B	66	33.473	64.189	3.998	1.00	186.43
	3562	CD2	TYR	B	66	33.309	61.943	5.607	1.00	186.43
	3563	CE2	TYR	B	66	33.785	61.827	4.314	1.00	186.43
	3564	CZ	TYR	B	66	33.871	62.957	3.508	1.00	186.43
70	3565	OH	TYR	B	66	34.375	62.850	2.220	1.00	186.43

	Atom #	Atom	Res	Chain	Res #	X	Y	Z	Occ	B
	3566	C	TYR	B	66	30.823	63.378	9.345	1.00	138.71
	3567	O	TYR	B	66	30.510	64.370	10.022	1.00	138.71
	3568	N	LYS	B	67	31.029	62.155	9.862	1.00	179.70
	3569	CA	LYS	B	67	30.895	61.847	11.295	1.00	179.70
5	3570	CB	LYS	B	67	29.456	62.047	11.754	1.00	159.69
	3571	CG	LYS	B	67	28.447	61.317	10.919	1.00	159.69
	3572	CD	LYS	B	67	27.057	61.654	11.392	1.00	159.69
	3573	CE	LYS	B	67	26.005	61.334	10.324	1.00	159.69
	3574	NZ	LYS	B	67	24.591	61.613	10.773	1.00	159.69
10	3575	C	LYS	B	67	31.323	60.434	11.691	1.00	179.70
	3576	O	LYS	B	67	31.284	59.505	10.885	1.00	179.70
	3577	N	CYS	B	68	31.723	60.285	12.953	1.00	162.03
	3578	CA	CYS	B	68	32.142	58.993	13.489	1.00	162.03
	3579	C	CYS	B	68	31.445	58.691	14.810	1.00	162.03
15	3580	O	CYS	B	68	31.102	59.589	15.578	1.00	162.03
	3581	CB	CYS	B	68	33.670	58.915	13.665	1.00	220.63
	3582	SG	CYS	B	68	34.426	59.969	14.951	1.00	220.63
	3583	N	GLN	B	69	31.239	57.402	15.049	1.00	249.69
	3584	CA	GLN	B	69	30.573	56.906	16.245	1.00	249.69
20	3585	CB	GLN	B	69	29.078	56.763	15.965	1.00	222.67
	3586	CG	GLN	B	69	28.343	55.832	16.904	1.00	222.67
	3587	CD	GLN	B	69	26.898	55.619	16.496	1.00	222.67
	3588	OE1	GLN	B	69	26.612	55.268	15.351	1.00	222.67
	3589	NE2	GLN	B	69	25.977	55.823	17.435	1.00	222.67
25	3590	C	GLN	B	69	31.168	55.546	16.606	1.00	249.69
	3591	O	GLN	B	69	31.580	54.788	15.727	1.00	249.69
	3592	N	HIS	B	70	31.219	55.235	17.897	1.00	249.63
	3593	CA	HIS	B	70	31.762	53.956	18.331	1.00	249.63
	3594	CB	HIS	B	70	32.637	54.139	19.570	1.00	248.69
30	3595	CG	HIS	B	70	33.932	54.841	19.289	1.00	248.69
	3596	CD2	HIS	B	70	34.500	55.925	19.864	1.00	248.69
	3597	ND1	HIS	B	70	34.798	54.422	18.304	1.00	248.69
	3598	CE1	HIS	B	70	35.852	55.223	18.283	1.00	248.69
	3599	NE2	HIS	B	70	35.696	56.141	19.217	1.00	249.63
35	3600	C	HIS	B	70	30.656	52.952	18.618	1.00	249.63
	3601	O	HIS	B	70	29.488	53.196	18.308	1.00	249.69
	3602	N	GLN	B	71	31.032	51.824	19.211	1.00	249.69
	3603	CA	GLN	B	71	30.087	50.755	19.541	1.00	249.69
	3604	CB	GLN	B	71	30.836	49.613	20.251	1.00	249.69
40	3605	CG	GLN	B	71	30.136	48.247	20.254	1.00	249.69
	3606	CD	GLN	B	71	29.921	47.672	18.850	1.00	249.69
	3607	OE1	GLN	B	71	30.834	47.657	18.016	1.00	249.69
	3608	NE2	GLN	B	71	28.710	47.183	18.594	1.00	249.69
	3609	C	GLN	B	71	28.923	51.253	20.410	1.00	249.69
45	3610	O	GLN	B	71	27.756	50.990	20.118	1.00	249.69
	3611	N	GLN	B	72	29.243	51.983	21.471	1.00	249.69
	3612	CA	GLN	B	72	28.217	52.506	22.371	1.00	249.69
	3613	CB	GLN	B	72	28.211	51.678	23.671	1.00	249.69
	3614	CG	GLN	B	72	27.259	52.118	24.772	1.00	249.69
50	3615	CD	GLN	B	72	27.523	51.390	26.084	1.00	249.69
	3616	OE1	GLN	B	72	27.540	50.159	26.130	1.00	249.69
	3617	NE2	GLN	B	72	27.729	52.151	27.156	1.00	249.69
	3618	C	GLN	B	72	28.463	53.997	22.656	1.00	249.69
	3619	O	GLN	B	72	28.598	54.423	23.809	1.00	249.69
55	3620	N	VAL	B	73	28.533	54.787	21.588	1.00	249.69
	3621	CA	VAL	B	73	28.747	56.226	21.718	1.00	227.88
	3622	CB	VAL	B	73	30.224	56.626	21.458	1.00	227.88
	3623	CG1	VAL	B	73	30.454	58.055	21.917	1.00	227.88
	3624	CG2	VAL	B	73	31.167	55.684	22.175	1.00	249.69
60	3625	C	VAL	B	73	27.875	56.941	20.690	1.00	249.69
	3626	O	VAL	B	73	27.681	56.449	19.579	1.00	249.69
	3627	N	ASN	B	74	27.348	58.101	21.062	1.00	249.69
	3628	CA	ASN	B	74	26.504	58.866	20.156	1.00	218.87
	3629	CB	ASN	B	74	25.675	59.883	20.956	1.00	218.87
65	3630	CG	ASN	B	74	24.852	59.227	22.059	1.00	218.87
	3631	OD1	ASN	B	74	24.270	58.159	21.845	1.00	218.87
	3632	ND2	ASN	B	74	24.793	59.865	23.226	1.00	249.69
	3633	C	ASN	B	74	27.368	59.564	19.100	1.00	249.69
	3634	O	ASN	B	74	28.342	60.240	19.428	1.00	242.43
70	3635	N	GLU	B	75	27.005	59.383	17.833	1.00	242.43

	3636	CA	GLU	B	75	27.735	59.968	16.704	1.00	242.43
	3637	CB	GLU	B	75	26.889	59.853	15.429	1.00	240.14
	3638	CG	GLU	B	75	25.394	60.044	15.649	1.00	240.14
	3639	CD	GLU	B	75	24.571	59.681	14.423	1.00	240.14
5	3640	OE1	GLU	B	75	24.782	58.580	13.867	1.00	240.14
	3641	OE2	GLU	B	75	23.709	60.493	14.021	1.00	240.14
	3642	C	GLU	B	75	28.199	61.410	16.900	1.00	242.43
	3643	O	GLU	B	75	27.478	62.241	17.453	1.00	242.43
	3644	N	SER	B	76	29.413	61.690	16.427	1.00	249.69
10	3645	CA	SER	B	76	30.030	63.012	16.552	1.00	249.69
	3646	CB	SER	B	76	31.491	62.960	16.091	1.00	193.15
	3647	OG	SER	B	76	31.574	62.865	14.681	1.00	193.15
	3648	C	SER	B	76	29.323	64.104	15.766	1.00	249.69
	3649	O	SER	B	76	28.595	63.825	14.813	1.00	249.69
15	3650	N	GLU	B	77	29.555	65.351	16.175	1.00	227.37
	3651	CA	GLU	B	77	28.969	66.496	15.500	1.00	227.37
	3652	CB	GLU	B	77	29.300	67.790	16.252	1.00	249.69
	3653	CG	GLU	B	77	28.667	67.874	17.635	1.00	249.69
	3654	CD	GLU	B	77	27.144	67.885	17.588	1.00	249.69
20	3655	OE1	GLU	B	77	26.566	67.679	16.493	1.00	249.69
	3656	OE2	GLU	B	77	26.521	68.094	18.654	1.00	249.69
	3657	C	GLU	B	77	29.556	66.554	14.099	1.00	227.37
	3658	O	GLU	B	77	30.747	66.802	13.926	1.00	227.37
	3659	N	PRO	B	78	28.708	66.324	13.072	1.00	151.66
25	3660	CD	PRO	B	78	27.233	66.271	13.163	1.00	139.99
	3661	CA	PRO	B	78	29.168	66.339	11.671	1.00	151.66
	3662	CB	PRO	B	78	27.852	66.486	10.892	1.00	139.99
	3663	CG	PRO	B	78	26.833	65.808	11.784	1.00	139.99
	3664	C	PRO	B	78	30.136	67.473	11.369	1.00	151.66
30	3665	O	PRO	B	78	30.182	68.466	12.086	1.00	151.66
	3666	N	VAL	B	79	30.929	67.306	10.321	1.00	174.84
	3667	CA	VAL	B	79	31.855	68.352	9.905	1.00	174.84
	3668	CB	VAL	B	79	33.336	68.021	10.222	1.00	152.46
	3669	CG1	VAL	B	79	34.256	69.029	9.536	1.00	152.46
35	3670	CG2	VAL	B	79	33.566	68.076	11.714	1.00	152.46
	3671	C	VAL	B	79	31.682	68.435	8.405	1.00	174.84
	3672	O	VAL	B	79	31.482	67.408	7.752	1.00	174.84
	3673	N	TYR	B	80	31.738	69.642	7.850	1.00	124.58
	3674	CA	TYR	B	80	31.564	69.771	6.414	1.00	124.58
40	3675	CB	TYR	B	80	30.573	70.877	6.084	1.00	201.47
	3676	CG	TYR	B	80	30.044	70.777	4.675	1.00	201.47
	3677	CD1	TYR	B	80	28.979	69.936	4.370	1.00	201.47
	3678	CE1	TYR	B	80	28.515	69.801	3.072	1.00	201.47
	3679	CD2	TYR	B	80	30.636	71.484	3.641	1.00	201.47
45	3680	CE2	TYR	B	80	30.180	71.356	2.334	1.00	201.47
	3681	CZ	TYR	B	80	29.122	70.514	2.057	1.00	201.47
	3682	OH	TYR	B	80	28.676	70.383	0.762	1.00	201.47
	3683	C	TYR	B	80	32.861	70.049	5.704	1.00	124.58
	3684	O	TYR	B	80	33.655	70.887	6.140	1.00	124.58
50	3685	N	LEU	B	81	33.082	69.344	4.606	1.00	114.91
	3686	CA	LEU	B	81	34.296	69.544	3.839	1.00	114.91
	3687	CB	LEU	B	81	35.033	68.223	3.661	1.00	104.59
	3688	CG	LEU	B	81	36.234	68.327	2.720	1.00	104.59
	3689	CD1	LEU	B	81	37.234	69.306	3.327	1.00	104.59
55	3690	CD2	LEU	B	81	36.881	66.972	2.487	1.00	104.59
	3691	C	LEU	B	81	33.917	70.087	2.482	1.00	114.91
	3692	O	LEU	B	81	33.039	69.517	1.836	1.00	114.91
	3693	N	GLU	B	82	34.545	71.184	2.049	1.00	120.70
	3694	CA	GLU	B	82	34.244	71.734	0.725	1.00	120.70
60	3695	CB	GLU	B	82	33.716	73.163	0.833	1.00	201.66
	3696	CG	GLU	B	82	32.820	73.551	-0.332	1.00	201.66
	3697	CD	GLU	B	82	32.280	74.954	-0.214	1.00	201.66
	3698	OE1	GLU	B	82	32.022	75.401	0.925	1.00	201.66
	3699	OE2	GLU	B	82	32.100	75.610	-1.264	1.00	201.66
65	3700	C	GLU	B	82	35.482	71.691	-0.174	1.00	120.70
	3701	O	GLU	B	82	36.583	72.004	0.276	1.00	120.70
	3702	N	VAL	B	83	35.299	71.276	-1.430	1.00	157.10
	3703	CA	VAL	B	83	36.398	71.204	-2.390	1.00	157.10
	3704	CB	VAL	B	83	36.519	69.829	-3.035	1.00	142.28
70	3705	CG1	VAL	B	83	37.699	69.820	-4.005	1.00	142.28

						x	y	z	occ	B
	3706	CG2	VAL	B	83	36.708	68.770	-1.955	1.00	142.28
	3707	C	VAL	B	83	36.227	72.239	-3.494	1.00	157.10
	3708	O	VAL	B	83	35.120	72.455	-3.992	1.00	157.10
	3709	N	PHE	B	84	37.344	72.845	-3.895	1.00	122.91
5	3710	CA	PHE	B	84	37.331	73.921	-4.875	1.00	122.91
	3711	CB	PHE	B	84	37.654	75.240	-4.180	1.00	156.44
	3712	CG	PHE	B	84	36.687	75.629	-3.106	1.00	156.44
	3713	CD1	PHE	B	84	36.773	75.093	-1.821	1.00	156.44
	3714	CD2	PHE	B	84	35.696	76.562	-3.382	1.00	156.44
10	3715	CE1	PHE	B	84	35.885	75.485	-0.833	1.00	156.44
	3716	CE2	PHE	B	84	34.805	76.958	-2.401	1.00	156.44
	3717	CZ	PHE	B	84	34.903	76.419	-1.121	1.00	156.44
	3718	C	PHE	B	84	38.259	73.854	-6.045	1.00	122.91
	3719	O	PHE	B	84	39.300	73.198	-6.007	1.00	122.91
15	3720	N	SER	B	85	37.884	74.614	-7.064	1.00	152.63
	3721	CA	SER	B	85	38.690	74.765	-8.267	1.00	152.63
	3722	CB	SER	B	85	38.054	74.080	-9.467	1.00	143.15
	3723	OG	SER	B	85	38.872	74.255	-10.617	1.00	143.15
	3724	C	SER	B	85	38.741	76.262	-8.523	1.00	152.63
20	3725	O	SER	B	85	37.715	76.882	-8.796	1.00	152.63
	3726	N	ASP	B	86	39.933	76.836	-8.412	1.00	139.36
	3727	CA	ASP	B	86	40.120	78.263	-8.613	1.00	139.36
	3728	CB	ASP	B	86	39.314	79.047	-7.577	1.00	172.94
	3729	CG	ASP	B	86	38.724	80.313	-8.143	1.00	172.94
25	3730	OD1	ASP	B	86	39.476	81.114	-8.744	1.00	172.94
	3731	OD2	ASP	B	86	37.505	80.511	-7.977	1.00	172.94
	3732	C	ASP	B	86	41.606	78.609	-8.458	1.00	139.36
	3733	O	ASP	B	86	42.379	77.794	-7.963	1.00	139.36
	3734	N	TRP	B	87	42.003	79.814	-8.863	1.00	121.62
30	3735	CA	TRP	B	87	43.393	80.224	-8.745	1.00	121.62
	3736	CB	TRP	B	87	43.617	81.544	-9.459	1.00	247.13
	3737	CG	TRP	B	87	43.989	81.344	-10.891	1.00	247.13
	3738	CD2	TRP	B	87	43.103	81.328	-12.013	1.00	247.13
	3739	CE2	TRP	B	87	43.881	81.063	-13.164	1.00	247.13
35	3740	CE3	TRP	B	87	41.722	81.521	-12.166	1.00	247.13
	3741	CD1	TRP	B	87	45.237	81.085	-11.386	1.00	247.13
	3742	NE1	TRP	B	87	45.183	80.918	-12.752	1.00	247.13
	3743	CZ2	TRP	B	87	43.328	80.982	-14.445	1.00	247.13
	3744	CZ3	TRP	B	87	41.170	81.442	-13.443	1.00	247.13
40	3745	CH2	TRP	B	87	41.973	81.171	-14.563	1.00	247.13
	3746	C	TRP	B	87	43.788	80.336	-7.288	1.00	121.62
	3747	O	TRP	B	87	44.771	79.726	-6.870	1.00	121.62
	3748	N	LEU	B	88	43.030	81.106	-6.510	1.00	133.11
	3749	CA	LEU	B	88	43.333	81.246	-5.092	1.00	133.11
45	3750	CB	LEU	B	88	43.787	82.678	-4.789	1.00	136.45
	3751	CG	LEU	B	88	45.105	83.123	-5.444	1.00	136.45
	3752	CD1	LEU	B	88	45.489	84.525	-4.973	1.00	136.45
	3753	CD2	LEU	B	88	46.196	82.131	-5.093	1.00	136.45
	3754	C	LEU	B	88	42.137	80.876	-4.219	1.00	133.11
50	3755	O	LEU	B	88	40.985	81.159	-4.577	1.00	133.11
	3756	N	LEU	B	89	42.413	80.222	-3.086	1.00	126.96
	3757	CA	LEU	B	89	41.363	79.834	-2.143	1.00	126.96
	3758	CB	LEU	B	89	41.152	78.335	-2.153	1.00	166.49
	3759	CG	LEU	B	89	40.113	77.865	-1.131	1.00	166.49
55	3760	CD1	LEU	B	89	38.812	78.646	-1.306	1.00	166.49
	3761	CD2	LEU	B	89	39.881	76.365	-1.300	1.00	126.96
	3762	C	LEU	B	89	41.777	80.255	-0.749	1.00	126.96
	3763	O	LEU	B	89	42.900	79.978	-0.336	1.00	113.68
	3764	N	LEU	B	90	40.883	80.929	-0.029	1.00	113.68
60	3765	CA	LEU	B	90	41.196	81.391	1.326	1.00	125.93
	3766	CB	LEU	B	90	40.422	82.674	1.646	1.00	125.93
	3767	CG	LEU	B	90	40.536	83.133	3.101	1.00	125.93
	3768	CD1	LEU	B	90	41.984	83.406	3.418	1.00	125.93
	3769	CD2	LEU	B	90	39.691	84.379	3.334	1.00	113.68
65	3770	C	LEU	B	90	40.856	80.326	2.356	1.00	113.68
	3771	O	LEU	B	90	39.693	80.010	2.566	1.00	98.97
	3772	N	GLN	B	91	41.870	79.780	3.010	1.00	98.97
	3773	CA	GLN	B	91	41.644	78.731	4.000	1.00	171.07
	3774	CB	GLN	B	91	42.662	77.614	3.842	1.00	171.07
70	3775	CG	GLN	B	91	42.650	76.964	2.481	1.00	

Line	Serial	Atom	Res	Chain	Res#	X	Y	Z	Occ	B
	3776	CD	GLN	B	91	43.685	75.865	2.363	1.00	171.07
	3777	OE1	GLN	B	91	44.878	76.095	2.555	1.00	171.07
	3778	NE2	GLN	B	91	43.232	74.660	2.046	1.00	171.07
	3779	C	GLN	B	91	41.707	79.237	5.422	1.00	98.97
5	3780	O	GLN	B	91	42.592	80.023	5.780	1.00	98.97
	3781	N	ALA	B	92	40.769	78.773	6.244	1.00	123.57
	3782	CA	ALA	B	92	40.707	79.189	7.645	1.00	123.57
	3783	CB	ALA	B	92	39.422	79.967	7.914	1.00	155.46
	3784	C	ALA	B	92	40.774	77.974	8.537	1.00	123.57
10	3785	O	ALA	B	92	40.215	76.918	8.208	1.00	123.57
	3786	N	SER	B	93	41.473	78.126	9.662	1.00	119.49
	3787	CA	SER	B	93	41.631	77.046	10.652	1.00	119.49
	3788	CB	SER	B	93	42.377	77.561	11.897	1.00	144.43
	3789	OG	SER	B	93	41.794	78.730	12.443	1.00	144.43
15	3790	C	SER	B	93	40.238	76.547	11.026	1.00	119.49
	3791	O	SER	B	93	39.891	75.389	10.783	1.00	119.49
	3792	N	ALA	B	94	39.447	77.448	11.605	1.00	139.25
	3793	CA	ALA	B	94	38.072	77.173	11.989	1.00	139.25
	3794	CB	ALA	B	94	37.961	77.053	13.497	1.00	173.88
20	3795	C	ALA	B	94	37.289	78.378	11.484	1.00	139.25
	3796	O	ALA	B	94	37.843	79.465	11.346	1.00	139.25
	3797	N	GLU	B	95	36.010	78.197	11.188	1.00	153.31
	3798	CA	GLU	B	95	35.217	79.312	10.694	1.00	153.31
	3799	CB	GLU	B	95	34.219	78.813	9.648	1.00	193.17
25	3800	CG	GLU	B	95	34.894	78.235	8.419	1.00	193.17
	3801	CD	GLU	B	95	33.929	77.974	7.284	1.00	193.17
	3802	OE1	GLU	B	95	34.372	77.478	6.230	1.00	193.17
	3803	OE2	GLU	B	95	32.727	78.269	7.442	1.00	193.17
	3804	C	GLU	B	95	34.493	80.058	11.817	1.00	153.31
30	3805	O	GLU	B	95	34.153	81.241	11.678	1.00	153.31
	3806	N	VAL	B	96	34.272	79.364	12.930	1.00	119.30
	3807	CA	VAL	B	96	33.599	79.942	14.087	1.00	119.30
	3808	CB	VAL	B	96	32.262	79.239	14.355	1.00	135.82
	3809	CG1	VAL	B	96	31.387	80.129	15.250	1.00	135.82
35	3810	CG2	VAL	B	96	31.566	78.905	13.045	1.00	135.82
	3811	C	VAL	B	96	34.482	79.788	15.330	1.00	119.30
	3812	O	VAL	B	96	34.967	78.690	15.622	1.00	119.30
	3813	N	VAL	B	97	34.664	80.871	16.082	1.00	139.44
	3814	CA	VAL	B	97	35.530	80.799	17.247	1.00	139.44
40	3815	CB	VAL	B	97	36.882	81.401	16.927	1.00	116.73
	3816	CG1	VAL	B	97	37.890	80.880	17.910	1.00	116.73
	3817	CG2	VAL	B	97	37.283	81.074	15.506	1.00	116.73
	3818	C	VAL	B	97	35.070	81.451	18.543	1.00	139.44
	3819	O	VAL	B	97	34.355	82.445	18.528	1.00	139.44
45	3820	N	MET	B	98	35.528	80.882	19.659	1.00	148.58
	3821	CA	MET	B	98	35.228	81.363	21.015	1.00	148.58
	3822	CB	MET	B	98	35.399	80.224	22.034	1.00	249.69
	3823	CG	MET	B	98	34.439	79.059	21.898	1.00	249.69
	3824	SD	MET	B	98	32.799	79.444	22.531	1.00	249.69
50	3825	CE	MET	B	98	33.078	79.331	24.290	1.00	249.69
	3826	C	MET	B	98	36.217	82.467	21.365	1.00	148.58
	3827	O	MET	B	98	37.425	82.250	21.304	1.00	148.58
	3828	N	GLU	B	99	35.721	83.636	21.756	1.00	152.43
	3829	CA	GLU	B	99	36.604	84.754	22.102	1.00	152.43
55	3830	CB	GLU	B	99	35.865	85.773	22.970	1.00	244.45
	3831	CG	GLU	B	99	36.447	87.177	22.890	1.00	244.45
	3832	CD	GLU	B	99	35.891	88.095	23.954	1.00	244.45
	3833	OE1	GLU	B	99	34.681	87.989	24.264	1.00	244.45
	3834	OE2	GLU	B	99	36.663	88.930	24.468	1.00	244.45
60	3835	C	GLU	B	99	37.831	84.264	22.859	1.00	152.43
	3836	O	GLU	B	99	37.708	83.591	23.877	1.00	152.43
	3837	N	GLY	B	100	39.015	84.586	22.363	1.00	146.37
	3838	CA	GLY	B	100	40.216	84.144	23.053	1.00	146.37
	3839	C	GLY	B	100	41.006	83.025	22.397	1.00	146.37
65	3840	O	GLY	B	100	42.205	82.880	22.659	1.00	146.37
	3841	N	GLN	B	101	40.353	82.237	21.552	1.00	128.49
	3842	CA	GLN	B	101	41.009	81.129	20.851	1.00	128.49
	3843	CB	GLN	B	101	39.964	80.177	20.290	1.00	190.16
	3844	CG	GLN	B	101	39.253	79.391	21.346	1.00	190.16
70	3845	CD	GLN	B	101	40.226	78.874	22.370	1.00	190.16

3846	OE1	GLN	B	101	40.792	79.645	23.140	1.00	190.16
3847	NE2	GLN	B	101	40.441	77.565	22.378	1.00	190.16
3848	C	GLN	B	101	41.952	81.596	19.731	1.00	128.49
3849	O	GLN	B	101	42.038	82.780	19.407	1.00	128.49
3850	N	PRO	B	102	42.675	80.637	19.115	1.00	164.10
3851	CD	PRO	B	102	42.886	79.258	19.540	1.00	192.64
3852	CA	PRO	B	102	43.581	81.010	18.018	1.00	164.10
3853	CB	PRO	B	102	44.669	79.950	18.152	1.00	192.64
3854	CG	PRO	B	102	43.863	78.733	18.490	1.00	192.64
3855	C	PRO	B	102	42.928	80.983	16.652	1.00	164.10
3856	O	PRO	B	102	42.017	80.208	16.389	1.00	164.10
3857	N	LEU	B	103	43.418	81.831	15.761	1.00	147.70
3858	CA	LEU	B	103	42.870	81.913	14.425	1.00	147.70
3859	CB	LEU	B	103	41.981	83.136	14.328	1.00	111.28
3860	CG	LEU	B	103	41.244	83.102	13.004	1.00	111.28
3861	CD1	LEU	B	103	40.261	81.951	13.100	1.00	111.28
3862	CD2	LEU	B	103	40.546	84.415	12.716	1.00	111.28
3863	C	LEU	B	103	43.939	81.997	13.331	1.00	147.70
3864	O	LEU	B	103	44.797	82.868	13.379	1.00	147.70
3865	N	PHE	B	104	43.890	81.112	12.339	1.00	122.26
3866	CA	PHE	B	104	44.880	81.157	11.261	1.00	122.26
3867	CB	PHE	B	104	45.820	79.951	11.311	1.00	249.69
3868	CG	PHE	B	104	46.501	79.766	12.627	1.00	249.69
3869	CD1	PHE	B	104	45.816	79.216	13.707	1.00	249.69
3870	CD2	PHE	B	104	47.831	80.137	12.793	1.00	249.69
3871	CE1	PHE	B	104	46.444	79.041	14.939	1.00	249.69
3872	CE2	PHE	B	104	48.467	79.967	14.020	1.00	249.69
3873	CZ	PHE	B	104	47.773	79.416	15.096	1.00	249.69
3874	C	PHE	B	104	44.227	81.185	9.885	1.00	122.26
3875	O	PHE	B	104	43.451	80.290	9.546	1.00	122.26
3876	N	LEU	B	105	44.541	82.207	9.093	1.00	122.11
3877	CA	LEU	B	105	44.001	82.309	7.743	1.00	122.11
3878	CB	LEU	B	105	43.390	83.676	7.495	1.00	103.82
3879	CG	LEU	B	105	42.270	84.000	8.466	1.00	103.82
3880	CD1	LEU	B	105	41.606	85.309	8.040	1.00	103.82
3881	CD2	LEU	B	105	41.254	82.847	8.512	1.00	103.82
3882	C	LEU	B	105	45.130	82.083	6.776	1.00	122.11
3883	O	LEU	B	105	46.272	82.387	7.065	1.00	122.11
3884	N	ARG	B	106	44.820	81.560	5.608	1.00	131.12
3885	CA	ARG	B	106	45.870	81.289	4.645	1.00	131.12
3886	CB	ARG	B	106	46.287	79.828	4.792	1.00	175.38
3887	CG	ARG	B	106	47.384	79.387	3.874	1.00	175.38
3888	CD	ARG	B	106	47.593	77.897	3.980	1.00	175.38
3889	NE	ARG	B	106	48.544	77.460	2.972	1.00	175.38
3890	CZ	ARG	B	106	48.536	76.259	2.404	1.00	175.38
3891	NH1	ARG	B	106	47.618	75.361	2.743	1.00	175.38
3892	NH2	ARG	B	106	49.438	75.963	1.477	1.00	175.38
3893	C	ARG	B	106	45.418	81.578	3.220	1.00	131.12
3894	O	ARG	B	106	44.374	81.096	2.784	1.00	131.12
3895	N	CYS	B	107	46.184	82.394	2.507	1.00	139.30
3896	CA	CYS	B	107	45.852	82.704	1.124	1.00	139.30
3897	C	CYS	B	107	46.515	81.564	0.378	1.00	139.30
3898	O	CYS	B	107	47.747	81.560	0.228	1.00	139.30
3899	CB	CYS	B	107	46.472	84.034	0.698	1.00	152.04
3900	SG	CYS	B	107	45.853	84.704	-0.878	1.00	152.04
3901	N	HIS	B	108	45.703	80.604	-0.073	1.00	155.54
3902	CA	HIS	B	108	46.205	79.419	-0.771	1.00	155.54
3903	CB	HIS	B	108	45.429	78.180	-0.319	1.00	137.70
3904	CG	HIS	B	108	46.047	76.880	-0.745	1.00	137.70
3905	CD2	HIS	B	108	45.514	75.802	-1.357	1.00	137.70
3906	ND1	HIS	B	108	47.366	76.564	-0.486	1.00	137.70
3907	CE1	HIS	B	108	47.609	75.341	-0.919	1.00	137.70
3908	NE2	HIS	B	108	46.506	74.854	-1.453	1.00	137.70
3909	C	HIS	B	108	46.182	79.487	-2.289	1.00	155.54
3910	O	HIS	B	108	45.137	79.731	-2.900	1.00	155.54
3911	N	GLY	B	109	47.351	79.253	-2.881	1.00	164.07
3912	CA	GLY	B	109	47.480	79.271	-4.321	1.00	164.07
3913	C	GLY	B	109	47.090	77.915	-4.866	1.00	164.07
3914	O	GLY	B	109	46.967	76.949	-4.098	1.00	164.07
3915	N	TRP	B	110	46.886	77.833	-6.180	1.00	153.07

	Atom	Name	Res	Chain	#	X	Y	Z	Occ	B
	3916	CA	TRP	B	110	46.506	76.568	-6.812	1.00	153.07
	3917	CB	TRP	B	110	45.719	76.839	-8.097	1.00	171.40
	3918	CG	TRP	B	110	45.467	75.611	-8.920	1.00	171.40
	3919	CD2	TRP	B	110	44.256	74.833	-8.973	1.00	171.40
5	3920	CE2	TRP	B	110	44.496	73.764	-9.855	1.00	171.40
	3921	CE3	TRP	B	110	42.998	74.937	-8.353	1.00	171.40
	3922	CD1	TRP	B	110	46.3??	75.000	-9.745	1.00	171.40
	3923	NE1	TRP	B	110	45.778	73.889	-10.311	1.00	171.40
	3924	CZ2	TRP	B	110	43.521	72.799	-10.140	1.00	171.40
10	3925	CZ3	TRP	B	110	42.026	73.974	-8.639	1.00	171.40
	3926	CH2	TRP	B	110	42.297	72.921	-9.526	1.00	171.40
	3927	C	TRP	B	110	47.743	75.723	-7.098	1.00	153.07
	3928	O	TRP	B	110	48.833	76.257	-7.296	1.00	153.07
	3929	N	ARG	B	111	47.567	74.404	-7.104	1.00	188.19
15	3930	CA	ARG	B	111	48.671	73.481	-7.333	1.00	188.19
	3931	CB	ARG	B	111	49.124	73.522	-8.790	1.00	249.69
	3932	CG	ARG	B	111	48.394	72.532	-9.682	1.00	249.69
	3933	CD	ARG	B	111	49.101	72.359	-11.018	1.00	249.69
	3934	NE	ARG	B	111	49.00?	70.961	-11.448	1.00	249.69
20	3935	CZ	ARG	B	111	49.641	69.965	-10.751	1.00	249.69
	3936	NH1	ARG	B	111	50.241	70.210	-9.587	1.00	249.69
	3937	NH2	ARG	B	111	49.594	68.722	-11.216	1.00	249.69
	3938	C	ARG	B	111	49.845	73.814	-6.431	1.00	188.19
	3939	O	ARG	B	111	50.999	73.588	-6.787	1.00	188.19
25	3940	N	ASN	B	112	49.534	74.350	-5.260	1.00	160.66
	3941	CA	ASN	B	112	50.542	74.729	-4.291	1.00	160.66
	3942	CB	ASN	B	112	51.146	73.478	-3.648	1.00	209.47
	3943	CG	ASN	B	112	51.910	73.791	-2.372	1.00	209.47
	3944	OD1	ASN	B	112	52.226	74.947	-2.083	1.00	209.47
30	3945	ND2	ASN	B	112	52.221	72.757	-1.607	1.00	209.47
	3946	C	ASN	B	112	51.652	75.583	-4.931	1.00	160.66
	3947	O	ASN	B	112	52.808	75.522	-4.489	1.00	160.66
	3948	N	TRP	B	113	51.319	76.368	-5.966	1.00	180.98
	3949	CA	TRP	B	113	52.321	77.223	-6.608	1.00	180.98
35	3950	CB	TRP	B	113	51.781	77.888	-7.863	1.00	248.40
	3951	CG	TRP	B	113	51.824	77.037	-9.064	1.00	248.40
	3952	CD2	TRP	B	113	50.876	77.029	-10.131	1.00	248.40
	3953	CE2	TRP	B	113	51.344	76.102	-11.092	1.00	248.40
	3954	CE3	TRP	B	113	49.678	77.717	-10.370	1.00	248.40
40	3955	CD1	TRP	B	113	52.799	76.145	-9.405	1.00	248.40
	3956	NE1	TRP	B	113	52.513	75.582	-10.623	1.00	248.40
	3957	CZ2	TRP	B	113	50.639	75.845	-12.289	1.00	248.40
	3958	CZ3	TRP	B	113	48.984	77.461	-11.557	1.00	248.40
	3959	CH2	TRP	B	113	49.472	76.530	-12.504	1.00	180.98
45	3960	C	TRP	B	113	52.741	78.311	-5.641	1.00	180.98
	3961	O	TRP	B	113	52.414	78.261	-4.452	1.00	240.61
	3962	N	ASP	B	114	53.465	79.305	-6.144	1.00	240.61
	3963	CA	ASP	B	114	53.905	80.407	-5.292	1.00	249.69
	3964	CB	ASP	B	114	55.427	80.596	-5.390	1.00	249.69
50	3965	CG	ASP	B	114	56.207	79.633	-4.489	1.00	249.69
	3966	OD1	ASP	B	114	55.981	79.644	-3.260	1.00	249.69
	3967	OD2	ASP	B	114	57.054	78.868	-5.007	1.00	240.61
	3968	C	ASP	B	114	53.185	81.707	-5.655	1.00	240.61
	3969	O	ASP	B	114	53.064	82.062	-6.841	1.00	153.55
55	3970	N	VAL	B	115	52.691	82.403	-4.627	1.00	153.55
	3971	CA	VAL	B	115	51.976	83.665	-4.828	1.00	153.55
	3972	CB	VAL	B	115	50.603	83.666	-4.135	1.00	146.14
	3973	CG1	VAL	B	115	49.770	84.824	-4.640	1.00	146.14
	3974	CG2	VAL	B	115	49.887	82.359	-4.385	1.00	146.14
60	3975	C	VAL	B	115	52.790	84.823	-4.256	1.00	153.55
	3976	O	VAL	B	115	53.410	84.708	-3.194	1.00	153.55
	3977	N	TYR	B	116	52.781	85.939	-4.975	1.00	165.97
	3978	CA	TYR	B	116	53.518	87.128	-4.575	1.00	165.97
	3979	CB	TYR	B	116	54.595	87.441	-5.619	1.00	249.69
65	3980	CG	TYR	B	116	55.660	86.371	-5.722	1.00	249.69
	3981	CD1	TYR	B	116	55.612	85.393	-6.716	1.00	249.69
	3982	CE1	TYR	B	116	56.582	84.386	-6.784	1.00	249.69
	3983	CD2	TYR	B	116	56.700	86.319	-4.802	1.00	249.69
	3984	CE2	TYR	B	116	57.671	85.322	-4.857	1.00	249.69
70	3985	CZ	TYR	B	116	57.611	84.360	-5.847	1.00	249.69

	Atom #	Name	Res	Chain	Res #	X	Y	Z	Occ	B
	3986	OH	TYR	B	116	58.575	83.375	-5.898	1.00	249.69
	3987	C	TYR	B	116	52.593	88.332	-4.405	1.00	165.97
	3988	O	TYR	B	116	51.423	88.278	-4.782	1.00	165.97
	3989	N	LYS	B	117	53.129	89.413	-3.840	1.00	123.89
5	3990	CA	LYS	B	117	52.369	90.641	-3.609	1.00	123.89
	3991	CB	LYS	B	117	52.154	91.413	-4.924	1.00	248.40
	3992	CG	LYS	B	117	53.310	92.323	-5.333	1.00	248.40
	3993	CD	LYS	B	117	52.850	93.384	-6.340	1.00	248.40
	3994	CE	LYS	B	117	51.729	94.253	-5.761	1.00	248.40
10	3995	NZ	LYS	B	117	51.232	95.311	-6.687	1.00	248.40
	3996	C	LYS	B	117	51.019	90.378	-2.948	1.00	123.89
	3997	O	LYS	B	117	49.972	90.844	-3.409	1.00	123.89
	3998	N	VAL	B	118	51.055	89.650	-1.846	1.00	126.95
	3999	CA	VAL	B	118	49.843	89.314	-1.142	1.00	126.95
15	4000	CB	VAL	B	118	50.033	87.999	-0.408	1.00	114.58
	4001	CG1	VAL	B	118	49.078	87.892	0.760	1.00	114.58
	4002	CG2	VAL	B	118	49.789	86.867	-1.372	1.00	114.58
	4003	C	VAL	B	118	49.299	90.352	-0.177	1.00	126.95
	4004	O	VAL	B	118	50.051	91.007	0.547	1.00	126.95
20	4005	N	ILE	B	119	47.972	90.477	-0.179	1.00	120.13
	4006	CA	ILE	B	119	47.244	91.402	0.686	1.00	120.13
	4007	CB	ILE	B	119	46.813	92.633	-0.073	1.00	113.05
	4008	CG2	ILE	B	119	46.149	93.628	0.860	1.00	113.05
	4009	CG1	ILE	B	119	48.021	93.233	-0.750	1.00	113.05
25	4010	CD1	ILE	B	119	47.645	94.049	-1.930	1.00	113.05
	4011	C	ILE	B	119	45.971	90.716	1.152	1.00	120.13
	4012	O	ILE	B	119	45.244	90.135	0.347	1.00	120.13
	4013	N	TYR	B	120	45.700	90.761	2.448	1.00	131.55
	4014	CA	TYR	B	120	44.475	90.162	2.952	1.00	131.55
30	4015	CB	TYR	B	120	44.704	89.457	4.286	1.00	143.62
	4016	CG	TYR	B	120	45.550	88.215	4.186	1.00	143.62
	4017	CD1	TYR	B	120	46.935	88.292	4.258	1.00	143.62
	4018	CE1	TYR	B	120	47.725	87.153	4.175	1.00	143.62
	4019	CD2	TYR	B	120	44.966	86.963	4.019	1.00	143.62
35	4020	CE2	TYR	B	120	45.733	85.821	3.830	1.00	143.62
	4021	CZ	TYR	B	120	47.117	85.918	4.010	1.00	143.62
	4022	OH	TYR	B	120	47.898	84.776	3.937	1.00	143.62
	4023	C	TYR	B	120	43.506	91.304	3.146	1.00	131.55
	4024	O	TYR	B	120	43.919	92.426	3.396	1.00	131.55
40	4025	N	TYR	B	121	42.221	91.024	3.013	1.00	134.10
	4026	CA	TYR	B	121	41.210	92.047	3.197	1.00	134.10
	4027	CB	TYR	B	121	40.572	92.433	1.867	1.00	128.02
	4028	CG	TYR	B	121	41.444	93.147	0.886	1.00	128.02
	4029	CD1	TYR	B	121	42.598	92.562	0.407	1.00	128.02
45	4030	CE1	TYR	B	121	43.370	93.184	-0.612	1.00	128.02
	4031	CD2	TYR	B	121	41.060	94.376	0.350	1.00	128.02
	4032	CE2	TYR	B	121	41.810	95.003	-0.661	1.00	128.02
	4033	CZ	TYR	B	121	42.970	94.395	-1.142	1.00	128.02
	4034	OH	TYR	B	121	43.710	94.979	-2.155	1.00	128.02
50	4035	C	TYR	B	121	40.085	91.591	4.149	1.00	134.10
	4036	O	TYR	B	121	39.556	90.483	4.039	1.00	134.10
	4037	N	LYS	B	122	39.716	92.457	5.086	1.00	124.90
	4038	CA	LYS	B	122	38.635	92.165	6.013	1.00	124.90
	4039	CB	LYS	B	122	39.152	92.121	7.442	1.00	161.09
55	4040	CG	LYS	B	122	38.059	91.814	8.433	1.00	161.09
	4041	CD	LYS	B	122	38.511	92.092	9.842	1.00	161.09
	4042	CE	LYS	B	122	37.370	91.925	10.817	1.00	161.09
	4043	NZ	LYS	B	122	37.815	92.313	12.166	1.00	161.09
	4044	C	LYS	B	122	37.606	93.289	5.874	1.00	124.90
60	4045	O	LYS	B	122	37.892	94.448	6.146	1.00	124.90
	4046	N	ASP	B	123	36.409	92.939	5.437	1.00	160.91
	4047	CA	ASP	B	123	35.338	93.908	5.250	1.00	160.91
	4048	CB	ASP	B	123	34.877	94.474	6.591	1.00	179.88
	4049	CG	ASP	B	123	34.061	93.486	7.385	1.00	179.88
65	4050	OD1	ASP	B	123	33.105	92.913	6.817	1.00	179.88
	4051	OD2	ASP	B	123	34.365	93.289	8.583	1.00	179.88
	4052	C	ASP	B	123	35.719	95.056	4.324	1.00	160.91
	4053	O	ASP	B	123	35.556	96.222	4.671	1.00	160.91
	4054	N	GLY	B	124	36.231	94.718	3.144	1.00	138.47
70	4055	CA	GLY	B	124	36.604	95.728	2.160	1.00	138.47

	4056	C	GLY	B	124	37.853	96.561	2.426	1.00	138.47
	4057	O	GLY	B	124	38.295	97.314	1.543	1.00	138.47
	4058	N	GLU	B	125	38.430	96.420	3.621	1.00	138.22
	4059	CA	GLU	B	125	39.627	97.166	4.009	1.00	138.22
5	4060	CB	GLU	B	125	39.534	97.532	5.496	1.00	228.57
	4061	CG	GLU	B	125	38.461	98.543	5.849	1.00	228.57
	4062	CD	GLU	B	125	38.835	99.938	5.425	1.00	228.57
	4063	OE1	GLU	B	125	39.838	100.460	5.952	1.00	228.57
	4064	OE2	GLU	B	125	38.132	100.515	4.567	1.00	228.57
10	4065	C	GLU	B	125	40.934	96.411	3.763	1.00	138.22
	4066	O	GLU	B	125	41.001	95.195	3.933	1.00	138.22
	4067	N	ALA	B	126	41.974	97.132	3.360	1.00	132.93
	4068	CA	ALA	B	126	43.266	96.495	3.155	1.00	132.93
	4069	CB	ALA	B	126	44.225	97.478	2.531	1.00	135.56
15	4070	C	ALA	B	126	43.730	96.115	4.563	1.00	132.93
	4071	O	ALA	B	126	43.549	96.898	5.489	1.00	132.93
	4072	N	LEU	B	127	44.325	94.941	4.751	1.00	121.91
	4073	CA	LEU	B	127	44.734	94.563	6.102	1.00	121.91
	4074	CB	LEU	B	127	43.939	93.352	6.540	1.00	110.11
20	4075	CG	LEU	B	127	43.777	93.371	8.046	1.00	110.11
	4076	CD1	LEU	B	127	43.167	94.684	8.464	1.00	110.11
	4077	CD2	LEU	B	127	42.902	92.200	8.476	1.00	110.11
	4078	C	LEU	B	127	46.214	94.312	6.354	1.00	121.91
	4079	O	LEU	B	127	46.818	94.960	7.211	1.00	121.91
25	4080	N	LYS	B	128	46.781	93.344	5.643	1.00	133.29
	4081	CA	LYS	B	128	48.199	93.025	5.779	1.00	133.29
	4082	CB	LYS	B	128	48.384	91.693	6.524	1.00	231.48
	4083	CG	LYS	B	128	47.832	91.675	7.942	1.00	231.48
	4084	CD	LYS	B	128	48.657	92.524	8.899	1.00	231.48
30	4085	CE	LYS	B	128	48.119	92.423	10.322	1.00	231.48
	4086	NZ	LYS	B	128	49.040	93.021	11.325	1.00	231.48
	4087	C	LYS	B	128	48.770	92.918	4.365	1.00	133.29
	4088	O	LYS	B	128	48.009	92.760	3.392	1.00	133.29
	4089	N	TYR	B	129	50.095	92.999	4.243	1.00	155.64
35	4090	CA	TYR	B	129	50.722	92.894	2.930	1.00	155.64
	4091	CB	TYR	B	129	50.745	94.261	2.262	1.00	155.17
	4092	CG	TYR	B	129	51.721	94.324	1.124	1.00	155.17
	4093	CD1	TYR	B	129	51.372	93.892	-0.149	1.00	155.17
	4094	CE1	TYR	B	129	52.298	93.900	-1.184	1.00	155.17
40	4095	CD2	TYR	B	129	53.026	94.765	1.340	1.00	155.17
	4096	CE2	TYR	B	129	53.965	94.775	0.315	1.00	155.17
	4097	CZ	TYR	B	129	53.593	94.340	-0.950	1.00	155.17
	4098	OH	TYR	B	129	54.521	94.360	-1.976	1.00	155.17
	4099	C	TYR	B	129	52.144	92.321	2.965	1.00	155.64
45	4100	O	TYR	B	129	52.930	92.644	3.857	1.00	155.64
	4101	N	TRP	B	130	52.466	91.477	1.982	1.00	'37.92
	4102	CA	TRP	B	130	53.792	90.873	1.883	1.00	137.92
	4103	CB	TRP	B	130	53.871	89.553	2.659	1.00	181.18
	4104	CG	TRP	B	130	53.301	89.553	4.048	1.00	181.18
50	4105	CD2	TRP	B	130	54.032	89.540	5.275	1.00	181.18
	4106	CE2	TRP	B	130	53.094	89.489	6.329	1.00	181.18
	4107	CE3	TRP	B	130	55.398	89.564	5.588	1.00	181.18
	4108	CD1	TRP	B	130	51.980	89.516	4.397	1.00	181.18
	4109	NE1	TRP	B	130	51.843	89.470	5.767	1.00	181.18
55	4110	CZ2	TRP	B	130	53.470	89.458	7.667	1.00	101.18
	4111	CZ3	TRP	B	130	55.778	89.532	6.928	1.00	181.18
	4112	CH2	TRP	B	130	54.816	89.490	7.949	1.00	137.92
	4113	C	TRP	B	130	54.173	90.577	0.427	1.00	137.92
	4114	O	TRP	B	130	53.340	90.655	-0.480	1.00	207.31
60	4115	N	TYR	B	131	55.439	90.218	0.220	1.00	207.31
	4116	CA	TYR	B	131	55.946	89.871	-1.103	1.00	239.97
	4117	CB	TYR	B	131	57.427	90.207	-1.198	1.00	239.97
	4118	CG	TYR	B	131	57.952	90.151	-2.603	1.00	239.97
	4119	CD1	TYR	B	131	57.608	91.130	-3.530	1.00	239.97
65	4120	CE1	TYR	B	131	58.061	91.065	-4.843	1.00	239.97
	4121	CD2	TYR	B	131	58.768	89.101	-3.020	1.00	239.97
	4122	CE2	TYR	B	131	59.226	89.023	-4.327	1.00	239.97
	4123	CZ	TYR	B	131	58.871	90.007	-5.235	1.00	239.97
	4124	OH	TYR	B	131	59.314	89.922	-6.534	1.00	207.31
70	4125	C	TYR	B	131	55.745	88.361	-1.207	1.00	207.31

	4126	O	TYR	B	131	54.695	87.903	-1.669	1.00	207.31
	4127	N	GLU	B	132	56.760	87.590	-0.805	1.00	245.95
	4128	CA	GLU	B	132	56.632	86.133	-0.780	1.00	245.95
	4129	CB	GLU	B	132	57.906	85.470	-0.236	1.00	249.39
5	4130	CG	GLU	B	132	59.071	85.349	-1.220	1.00	249.39
	4131	CD	GLU	B	132	59.448	83.901	-1.491	1.00	249.39
	4132	OE1	GLU	B	132	58.976	83.011	-0.751	1.00	249.39
	4133	OE2	GLU	B	132	60.223	83.649	-2.438	1.00	249.39
	4134	C	GLU	B	132	55.535	86.097	0.271	1.00	245.95
10	4135	O	GLU	B	132	55.697	86.700	1.341	1.00	245.95
	4136	N	ASN	B	133	54.430	85.403	0.003	1.00	176.11
	4137	CA	ASN	B	133	53.339	85.462	0.965	1.00	176.11
	4138	CB	ASN	B	133	52.010	84.935	0.335	1.00	160.36
	4139	CG	ASN	B	133	51.822	83.434	0.412	1.00	160.36
15	4140	OD1	ASN	B	133	52.741	82.660	0.161	1.00	160.36
	4141	ND2	ASN	B	133	50.589	83.015	0.716	1.00	160.36
	4142	C	ASN	B	133	53.555	84.965	2.388	1.00	176.11
	4143	O	ASN	B	133	54.665	84.633	2.802	1.00	176.11
	4144	N	HIS	B	134	52.479	84.997	3.151	1.00	182.29
20	4145	CA	HIS	B	134	52.525	84.611	4.534	1.00	182.29
	4146	CB	HIS	B	134	52.743	85.860	5.391	1.00	249.69
	4147	CG	HIS	B	134	53.003	85.559	6.845	1.00	249.69
	4148	CD2	HIS	B	134	52.286	85.883	7.951	1.00	249.69
	4149	ND1	HIS	B	134	54.081	84.836	7.264	1.00	249.69
25	4150	CE1	HIS	B	134	54.036	84.709	8.595	1.00	249.69
	4151	NE2	HIS	B	134	52.961	85.335	9.023	1.00	249.69
	4152	C	HIS	B	134	51.200	83.948	4.873	1.00	182.29
	4153	O	HIS	B	134	50.446	83.556	3.984	1.00	182.29
	4154	N	ASN	B	135	50.922	83.832	6.163	1.00	162.56
30	4155	CA	ASN	B	135	49.712	83.206	6.644	1.00	162.56
	4156	CB	ASN	B	135	49.964	81.712	6.908	1.00	240.35
	4157	CG	ASN	B	135	50.213	80.928	5.625	1.00	240.35
	4158	OD1	ASN	B	135	49.484	81.111	4.647	1.00	240.35
	4159	ND2	ASN	B	135	51.216	80.048	5.620	1.00	162.56
35	4160	C	ASN	B	135	49.252	83.905	7.919	1.00	162.56
	4161	O	ASN	B	135	49.536	83.439	9.028	1.00	151.20
	4162	N	ILE	B	136	48.544	85.024	7.745	1.00	151.20
	4163	CA	ILE	B	136	47.996	85.840	8.846	1.00	153.45
	4164	CB	ILE	B	136	46.845	86.737	8.329	1.00	153.45
40	4165	CG2	ILE	B	136	45.775	85.891	7.675	1.00	153.45
	4166	CG1	ILE	B	136	46.230	87.526	9.477	1.00	153.45
	4167	CD1	ILE	B	136	45.072	88.386	9.042	1.00	151.20
	4168	C	ILE	B	136	47.495	85.052	10.063	1.00	151.20
	4169	O	ILE	B	136	46.403	84.466	10.041	1.00	137.33
45	4170	N	SER	B	137	48.291	85.084	11.133	1.00	137.33
	4171	CA	SER	B	137	47.981	84.351	12.353	1.00	185.84
	4172	CB	SER	B	137	49.199	83.553	12.782	1.00	185.84
	4173	OG	SER	B	137	48.986	82.999	14.062	1.00	137.33
	4174	C	SER	B	137	47.481	85.154	13.549	1.00	137.33
50	4175	O	SER	B	137	47.862	86.294	13.764	1.00	147.08
	4176	N	ILE	B	138	46.641	84.509	14.348	1.00	147.08
	4177	CA	ILE	B	138	46.043	85.114	15.529	1.00	140.24
	4178	CB	ILE	B	138	44.592	85.533	15.243	1.00	140.24
	4179	CG2	ILE	B	138	43.867	85.830	16.544	1.00	140.24
55	4180	CG1	ILE	B	138	44.581	86.736	14.307	1.00	140.24
	4181	CD1	ILE	B	138	43.214	87.030	13.737	1.00	147.08
	4182	C	ILE	B	138	46.047	84.165	16.723	1.00	147.08
	4183	O	ILE	B	138	45.494	83.059	16.678	1.00	249.69
	4184	N	THR	B	139	46.666	84.623	17.800	1.00	249.69
60	4185	CA	THR	B	139	46.764	83.857	19.032	1.00	249.31
	4186	CB	THR	B	139	47.944	84.369	19.853	1.00	249.31
	4187	OG1	THR	B	139	47.808	85.783	20.034	1.00	249.31
	4188	CG2	THR	B	139	49.251	84.099	19.122	1.00	249.69
	4189	C	THR	B	139	45.473	84.015	19.832	1.00	249.69
65	4190	O	THR	B	139	44.591	83.158	19.795	1.00	177.26
	4191	N	ASN	B	140	45.382	85.121	20.559	1.00	177.26
	4192	CA	ASN	B	140	44.211	85.439	21.351	1.00	249.69
	4193	CB	ASN	B	140	44.612	86.358	22.504	1.00	249.69
	4194	CG	ASN	B	140	43.435	86.774	23.349	1.00	249.69
70	4195	OD1	ASN	B	140	42.422	87.240	22.822	1.00	249.69

Line	Serial	Atom	Res	Chain	Seq	X	Y	Z	Occ	B
	4196	ND2	ASN	B	140	43.566	86.631	24.665	1.00	249.69
	4197	C	ASN	B	140	43.247	86.161	20.396	1.00	177.26
	4198	O	ASN	B	140	43.596	87.200	19.812	1.00	177.26
	4199	N	ALA	B	141	42.040	85.615	20.236	1.00	147.92
5	4200	CA	ALA	B	141	41.050	86.199	19.327	1.00	147.92
	4201	CB	ALA	B	141	40.337	85.085	18.551	1.00	170.82
	4202	C	ALA	B	141	40.015	87.128	19.867	1.00	147.92
	4203	O	ALA	B	141	39.333	86.783	20.942	1.00	147.92
	4204	N	THR	B	142	39.910	88.316	19.389	1.00	150.18
10	4205	CA	THR	B	142	38.966	89.325	19.840	1.00	150.18
	4206	CB	THR	B	142	39.487	90.741	19.549	1.00	194.09
	4207	OG1	THR	B	142	40.823	90.870	20.055	1.00	194.09
	4208	CG2	THR	B	142	38.595	91.777	20.202	1.00	194.09
	4209	C	THR	B	142	37.681	89.119	19.053	1.00	150.18
15	4210	O	THR	B	142	37.682	88.485	17.996	1.00	150.18
	4211	N	VAL	B	143	36.580	89.650	19.560	1.00	151.70
	4212	CA	VAL	B	143	35.325	89.489	18.859	1.00	151.70
	4213	CB	VAL	B	143	34.128	89.829	19.752	1.00	138.48
	4214	CG1	VAL	B	143	34.053	91.341	19.973	1.00	138.48
20	4215	CG2	VAL	B	143	32.853	89.308	19.122	1.00	138.48
	4216	C	VAL	B	143	35.313	90.418	17.658	1.00	151.70
	4217	O	VAL	B	143	34.595	90.168	16.688	1.00	151.70
	4218	N	GLU	B	144	36.106	91.488	17.716	1.00	158.91
	4219	CA	GLU	B	144	36.149	92.427	16.609	1.00	158.91
25	4220	CB	GLU	B	144	36.870	93.708	16.996	1.00	246.81
	4221	CG	GLU	B	144	36.208	94.445	18.127	1.00	246.81
	4222	CD	GLU	B	144	37.054	94.424	19.371	1.00	246.81
	4223	OE1	GLU	B	144	38.183	94.958	19.317	1.00	246.81
	4224	OE2	GLU	B	144	36.599	93.872	20.396	1.00	246.81
30	4225	C	GLU	B	144	36.827	91.811	15.407	1.00	158.91
	4226	O	GLU	B	144	36.756	92.346	14.312	1.00	158.91
	4227	N	ASP	B	145	37.485	90.676	15.606	1.00	116.08
	4228	CA	ASP	B	145	38.161	89.992	14.501	1.00	116.08
	4229	CB	ASP	B	145	39.135	88.943	15.039	1.00	169.83
35	4230	CG	ASP	B	145	40.399	89.560	15.570	1.00	169.83
	4231	OD1	ASP	B	145	41.061	90.286	14.797	1.00	169.83
	4232	OD2	ASP	B	145	40.728	89.327	16.756	1.00	169.83
	4233	C	ASP	B	145	37.149	89.332	13.575	1.00	116.08
	4234	O	ASP	B	145	37.481	88.992	12.450	1.00	116.08
40	4235	N	SER	B	146	35.918	89.161	14.054	1.00	118.95
	4236	CA	SER	B	146	34.858	88.538	13.267	1.00	118.95
	4237	CB	SER	B	146	33.592	88.361	14.116	1.00	193.19
	4238	OG	SER	B	146	33.830	87.569	15.261	1.00	193.19
	4239	C	SER	B	146	34.511	89.394	12.048	1.00	118.95
45	4240	O	SER	B	146	34.247	90.591	12.186	1.00	118.95
	4241	N	GLY	B	147	34.487	88.787	10.863	1.00	175.20
	4242	CA	GLY	B	147	34.150	89.543	9.668	1.00	175.20
	4243	C	GLY	B	147	34.222	88.715	8.406	1.00	175.20
	4244	O	GLY	B	147	34.162	87.487	8.467	1.00	175.20
50	4245	N	THR	B	148	34.350	89.383	7.260	1.00	119.45
	4246	CA	THR	B	148	34.445	88.689	5.967	1.00	119.45
	4247	CB	THR	B	148	33.224	89.059	5.057	1.00	97.36
	4248	OG1	THR	B	148	33.606	90.066	4.118	1.00	97.36
	4249	CG2	THR	B	148	32.069	89.581	5.907	1.00	97.36
55	4250	C	THR	B	148	35.802	88.969	5.256	1.00	119.45
	4251	O	THR	B	148	36.102	90.077	4.838	1.00	119.45
	4252	N	TYR	B	149	36.618	87.934	5.139	1.00	115.49
	4253	CA	TYR	B	149	37.918	88.061	4.528	1.00	115.49
	4254	CB	TYR	B	149	38.966	87.350	5.381	1.00	121.92
60	4255	CG	TYR	B	149	39.073	87.793	6.830	1.00	121.92
	4256	CD1	TYR	B	149	38.125	87.403	7.771	1.00	121.92
	4257	CE1	TYR	B	149	38.255	87.752	9.102	1.00	121.92
	4258	CD2	TYR	B	149	40.153	88.557	7.264	1.00	121.92
	4259	CE2	TYR	B	149	40.293	88.910	8.578	1.00	121.92
65	4260	CZ	TYR	B	149	39.346	88.509	9.496	1.00	121.92
	4261	OH	TYR	B	149	39.501	88.875	10.821	1.00	121.92
	4262	C	TYR	B	149	38.027	87.492	3.104	1.00	115.49
	4263	O	TYR	B	149	37.182	86.708	2.670	1.00	115.49
	4264	N	TYR	B	150	39.095	87.895	2.402	1.00	105.13
70	4265	CA	TYR	B	150	39.437	87.467	1.042	1.00	105.13

	4266	CB	TYR	B	150	38.454	88.037	0.005	1.00	148.24
	4267	CG	TYR	B	150	38.643	89.480	-0.407	1.00	148.24
	4268	CD1	TYR	B	150	39.713	89.864	-1.214	1.00	148.24
	4269	CE1	TYR	B	150	39.871	91.204	-1.645	1.00	148.24
5	4270	CD2	TYR	B	150	37.724	90.461	-0.031	1.00	148.24
	4271	CE2	TYR	B	150	37.867	91.803	-0.454	1.00	148.24
	4272	CZ	TYR	B	150	38.946	92.168	-1.268	1.00	148.24
	4273	OH	TYR	B	150	39.096	93.473	-1.715	1.00	148.24
	4274	C	TYR	B	150	40.836	88.014	0.809	1.00	105.13
10	4275	O	TYR	B	150	41.228	89.015	1.414	1.00	105.13
	4276	N	CYS	B	151	41.612	87.372	-0.057	1.00	132.14
	4277	CA	CYS	B	151	42.986	87.840	-0.332	1.00	132.14
	4278	C	CYS	B	151	43.242	88.046	-1.822	1.00	132.14
	4279	O	CYS	B	151	42.511	87.547	-2.671	1.00	132.14
15	4280	CB	CYS	B	151	44.018	86.847	0.236	1.00	149.67
	4281	SG	CYS	B	151	43.926	85.150	-0.462	1.00	149.67
	4282	N	THR	B	152	44.288	88.798	-2.129	1.00	118.50
	4283	CA	THR	B	152	44.661	89.083	-3.516	1.00	118.50
	4284	CB	THR	B	152	44.403	90.547	-3.887	1.00	151.99
20	4285	OG1	THR	B	152	45.395	91.385	-3.266	1.00	151.99
	4286	CG2	THR	B	152	43.014	90.976	-3.430	1.00	151.99
	4287	C	THR	B	152	46.154	88.854	-3.689	1.00	118.50
	4288	O	THR	B	152	46.951	89.115	-2.768	1.00	118.50
	4289	N	GLY	B	153	46.544	88.378	-4.864	1.00	134.78
25	4290	CA	GLY	B	153	47.956	88.132	-5.089	1.00	134.78
	4291	C	GLY	B	153	48.309	87.906	-6.545	1.00	134.78
	4292	O	GLY	B	153	47.419	87.747	-7.387	1.00	134.78
	4293	N	LYS	B	154	49.605	87.885	-6.842	1.00	183.95
	4294	CA	LYS	B	154	50.077	87.673	-8.199	1.00	183.95
30	4295	CB	LYS	B	154	51.115	88.730	-8.542	1.00	202.68
	4296	CG	LYS	B	154	51.611	88.679	-9.971	1.00	202.68
	4297	CD	LYS	B	154	52.591	89.815	-10.237	1.00	202.68
	4298	CE	LYS	B	154	53.158	89.756	-11.649	1.00	202.68
	4299	NZ	LYS	B	154	54.131	90.860	-11.921	1.00	183.95
35	4300	C	LYS	B	154	50.672	86.268	-8.377	1.00	183.95
	4301	O	LYS	B	154	51.657	85.900	-7.729	1.00	214.72
	4302	N	VAL	B	155	50.048	85.484	-9.253	1.00	214.72
	4303	CA	VAL	B	155	50.480	84.117	-9.558	1.00	214.72
	4304	CB	VAL	B	155	49.275	83.155	-9.620	1.00	178.34
40	4305	CG1	VAL	B	155	49.717	81.766	-10.018	1.00	178.34
	4306	CG2	VAL	B	155	48.581	83.118	-8.276	1.00	178.34
	4307	C	VAL	B	155	51.122	84.193	-10.931	1.00	214.72
	4308	O	VAL	B	155	50.530	84.738	-11.865	1.00	214.72
	4309	N	TRP	B	156	52.321	83.636	-11.061	1.00	210.74
45	4310	CA	TRP	B	156	53.050	83.695	-12.334	1.00	210.74
	4311	CB	TRP	B	156	52.245	83.105	-13.514	1.00	249.69
	4312	CG	TRP	B	156	51.997	81.615	-13.504	1.00	249.69
	4313	CD2	TRP	B	156	52.972	80.576	-13.670	1.00	249.69
	4314	CE2	TRP	B	156	52.277	79.346	-13.606	1.00	249.69
50	4315	CE3	TRP	B	156	54.358	80.563	-13.864	1.00	249.69
	4316	CD1	TRP	B	156	50.790	80.988	-13.351	1.00	249.69
	4317	NE1	TRP	B	156	50.950	79.628	-13.414	1.00	249.69
	4318	CZ2	TRP	B	156	52.925	78.114	-13.729	1.00	249.69
	4319	CZ3	TRP	B	156	55.003	79.336	-13.990	1.00	249.69
55	4320	CH2	TRP	B	156	54.285	78.129	-13.915	1.00	210.74
	4321	C	TRP	B	156	53.249	85.183	-12.595	1.00	210.74
	4322	O	TRP	B	156	54.162	85.808	-12.059	1.00	156.28
	4323	N	GLN	B	157	52.355	85.739	-13.408	1.00	156.28
	4324	CA	GLN	B	157	52.406	87.144	-13.767	1.00	249.69
60	4325	CB	GLN	B	157	53.203	87.338	-15.074	1.00	249.69
	4326	CG	GLN	B	157	54.719	87.195	-14.910	1.00	249.69
	4327	CD	GLN	B	157	55.327	88.274	-14.019	1.00	249.69
	4328	OE1	GLN	B	157	55.277	89.465	-14.340	1.00	249.69
	4329	NE2	GLN	B	157	55.906	87.860	-12.893	1.00	156.28
65	4330	C	GLN	B	157	51.035	87.808	-13.891	1.00	156.28
	4331	O	GLN	B	157	50.893	88.830	-14.565	1.00	204.79
	4332	N	LEU	B	158	50.028	87.237	-13.243	1.00	204.79
	4333	CA	LEU	B	158	48.698	87.836	-13.267	1.00	162.40
	4334	CB	LEU	B	158	47.745	87.025	-14.156	1.00	162.40
70	4335	CG	LEU	B	158	47.849	87.176	-15.669	1.00	162.40

	4336	CD1	LEU	B	158	46.441	87.082	-16.258	1.00	162.40
	4337	CD2	LEU	B	158	48.464	88.518	-16.037	1.00	162.40
	4338	C	LEU	B	158	48.124	87.959	-11.852	1.00	204.79
	4339	O	LEU	B	158	48.450	87.172	-10.964	1.00	204.79
5	4340	N	ASP	B	159	47.277	88.961	-11.648	1.00	211.13
	4341	CA	ASP	B	159	46.669	89.179	-10.351	1.00	211.13
	4342	CB	ASP	B	159	46.316	90.659	-10.178	1.00	203.85
	4343	CG	ASP	B	159	47.491	91.574	-10.416	1.00	203.85
	4344	OD1	ASP	B	159	48.489	91.461	-9.680	1.00	203.85
10	4345	OD2	ASP	B	159	47.413	92.407	-11.342	1.00	203.85
	4346	C	ASP	B	159	45.397	88.344	-10.208	1.00	211.13
	4347	O	ASP	B	159	44.695	88.096	-11.193	1.00	211.13
	4348	N	TYR	B	160	45.101	87.907	-8.984	1.00	157.46
	4349	CA	TYR	B	160	43.891	87.129	-8.729	1.00	157.46
15	4350	CB	TYR	B	160	44.174	85.638	-8.836	1.00	182.37
	4351	CG	TYR	B	160	44.781	85.232	-10.147	1.00	182.37
	4352	CD1	TYR	B	160	46.161	85.213	-10.315	1.00	182.37
	4353	CE1	TYR	B	160	46.733	84.810	-11.517	1.00	182.37
	4354	CD2	TYR	B	160	43.977	84.849	-11.217	1.00	182.37
20	4355	CE2	TYR	B	160	44.537	84.446	-12.433	1.00	182.37
	4356	CZ	TYR	B	160	45.917	84.423	-12.578	1.00	182.37
	4357	OH	TYR	B	160	46.481	83.987	-13.765	1.00	182.37
	4358	C	TYR	B	160	43.275	87.423	-7.372	1.00	157.46
	4359	O	TYR	B	160	43.977	87.686	-6.377	1.00	157.46
25	4360	N	GLU	B	161	41.947	87.358	-7.357	1.00	159.09
	4361	CA	GLU	B	161	41.161	87.625	-6.168	1.00	159.09
	4362	CB	GLU	B	161	40.085	88.664	-6.527	1.00	208.73
	4363	CG	GLU	B	161	39.125	89.081	-5.420	1.00	208.73
	4364	CD	GLU	B	161	38.358	90.353	-5.769	1.00	208.73
30	4365	OE1	GLU	B	161	37.289	90.587	-5.169	1.00	208.73
	4366	OE2	GLU	B	161	38.829	91.125	-6.633	1.00	208.73
	4367	C	GLU	B	161	40.553	86.311	-5.703	1.00	159.09
	4368	O	GLU	B	161	40.167	85.483	-6.531	1.00	159.09
	4369	N	SER	B	162	40.491	86.120	-4.386	1.00	135.59
35	4370	CA	SER	B	162	39.945	84.894	-3.798	1.00	135.59
	4371	CB	SER	B	162	40.698	84.552	-2.508	1.00	156.53
	4372	OG	SER	B	162	40.507	85.561	-1.523	1.00	156.53
	4373	C	SER	B	162	38.467	85.022	-3.475	1.00	135.59
	4374	O	SER	B	162	37.948	86.125	-3.362	1.00	135.59
40	4375	N	GLU	B	163	37.785	83.891	-3.332	1.00	183.98
	4376	CA	GLU	B	163	36.382	83.933	-2.974	1.00	183.98
	4377	CB	GLU	B	163	35.794	82.514	-2.941	1.00	249.53
	4378	CG	GLU	B	163	35.543	81.880	-4.311	1.00	249.53
	4379	CD	GLU	B	163	34.339	82.475	-5.030	1.00	249.53
45	4380	OE1	GLU	B	163	33.229	82.464	-4.456	1.00	249.53
	4381	OE2	GLU	B	163	34.498	82.945	-6.173	1.00	249.53
	4382	C	GLU	B	163	36.369	84.544	-1.569	1.00	183.98
	4383	O	GLU	B	163	37.334	84.379	-0.818	1.00	183.98
	4384	N	PRO	B	164	35.304	85.273	-1.199	1.00	111.61
50	4385	CD	PRO	B	164	34.138	85.647	-2.030	1.00	194.84
	4386	CA	PRO	B	164	35.206	85.903	0.122	1.00	111.61
	4387	CB	PRO	B	164	34.171	86.986	-0.090	1.00	194.84
	4388	CG	PRO	B	164	33.217	86.310	-1.015	1.00	194.84
	4389	C	PRO	B	164	34.778	84.904	1.197	1.00	111.61
55	4390	O	PRO	B	164	33.894	83.997	0.926	1.00	111.61
	4391	N	LEU	B	165	35.268	85.078	2.417	1.00	125.70
	4392	CA	LEU	B	165	34.918	84.150	3.482	1.00	125.70
	4393	CB	LEU	B	165	36.104	83.241	3.771	1.00	110.19
	4394	CG	LEU	B	165	35.906	82.190	4.868	1.00	110.19
60	4395	CD1	LEU	B	165	34.494	81.640	4.805	1.00	110.19
	4396	CD2	LEU	B	165	36.944	81.076	4.711	1.00	110.19
	4397	C	LEU	B	165	34.468	84.800	4.775	1.00	125.70
	4398	O	LEU	B	165	35.127	85.716	5.274	1.00	125.70
	4399	N	ASN	B	166	33.348	84.317	5.319	1.00	120.14
65	4400	CA	ASN	B	166	32.809	84.855	6.577	1.00	120.14
	4401	CB	ASN	B	166	31.283	84.695	6.635	1.00	189.75
	4402	CG	ASN	B	166	30.537	85.923	6.141	1.00	189.75
	4403	OD1	ASN	B	166	31.053	87.039	6.184	1.00	189.75
	4404	ND2	ASN	B	166	29.303	85.713	5.694	1.00	189.75
70	4405	C	ASN	B	166	33.420	84.164	7.793	1.00	120.14

	Serial	Atom	Residue	Chain	ResNum	X	Y	Z	Occ	B
	4406	O	ASN	B	166	33.718	82.978	7.752	1.00	120.14
	4407	N	ILE	B	167	33.594	84.911	8.875	1.00	133.16
	4408	CA	ILE	B	167	34.163	84.359	10.087	1.00	133.16
	4409	CB	ILE	B	167	35.634	84.660	10.178	1.00	105.73
5	4410	CG2	ILE	B	167	36.159	84.179	11.513	1.00	105.73
	4411	CG1	ILE	B	167	36.355	83.972	9.038	1.00	105.73
	4412	CD1	ILE	B	167	37.820	84.256	9.039	1.00	105.73
	4413	C	ILE	B	167	33.510	84.926	11.319	1.00	133.16
	4414	O	ILE	B	167	33.451	86.140	11.480	1.00	133.16
10	4415	N	THR	B	168	33.058	84.057	12.213	1.00	113.92
	4416	CA	THR	B	168	32.409	84.557	13.402	1.00	113.92
	4417	CB	THR	B	168	30.931	84.189	13.377	1.00	138.53
	4418	OG1	THR	B	168	30.347	84.678	12.163	1.00	138.53
	4419	CG2	THR	B	168	30.214	84.810	14.563	1.00	138.53
15	4420	C	THR	B	168	33.018	84.135	14.728	1.00	113.92
	4421	O	THR	B	168	33.161	82.955	15.019	1.00	113.92
	4422	N	VAL	B	169	33.381	85.129	15.526	1.00	134.74
	4423	CA	VAL	B	169	33.953	84.905	16.840	1.00	134.74
	4424	CB	VAL	B	169	35.207	85.795	17.049	1.00	119.12
20	4425	CG1	VAL	B	169	35.482	85.994	18.518	1.00	119.12
	4426	CG2	VAL	B	169	36.403	85.141	16.397	1.00	119.12
	4427	C	VAL	B	169	32.864	85.249	17.868	1.00	134.74
	4428	O	VAL	B	169	32.511	86.415	18.047	1.00	134.74
	4429	N	ILE	B	170	32.326	84.222	18.527	1.00	162.52
25	4430	CA	ILE	B	170	31.270	84.383	19.532	1.00	162.52
	4431	CB	ILE	B	170	30.271	83.207	19.449	1.00	162.30
	4432	CG2	ILE	B	170	29.809	83.021	18.010	1.00	162.30
	4433	CG1	ILE	B	170	30.946	81.906	19.881	1.00	162.30
	4434	CD1	ILE	B	170	30.029	80.693	19.859	1.00	162.30
30	4435	C	ILE	B	170	31.881	84.444	20.932	1.00	162.52
	4436	O	ILE	B	170	33.039	84.092	21.122	1.00	162.52
	4437	N	LYS	B	171	31.114	84.869	21.923	1.00	183.47
	4438	CA	LYS	B	171	31.659	84.966	23.278	1.00	183.47
	4439	CB	LYS	B	171	31.632	86.425	23.716	1.00	228.46
35	4440	CG	LYS	B	171	30.255	87.040	23.602	1.00	228.46
	4441	CD	LYS	B	171	30.316	88.539	23.398	1.00	228.46
	4442	CE	LYS	B	171	31.046	89.232	24.538	1.00	228.46
	4443	NZ	LYS	B	171	31.040	90.714	24.377	1.00	228.46
	4444	C	LYS	B	171	30.941	84.101	24.319	1.00	183.47
40	4445	O	LYS	B	171	31.193	84.218	25.525	1.00	183.47
	4446	C1	NAG	B	221	48.145	62.916	-2.146	1.00	249.69
	4447	C2	NAG	B	221	49.283	63.891	-2.430	1.00	249.69
	4448	N2	NAG	B	221	48.728	65.201	-2.707	1.00	249.69
	4449	C7	NAG	B	221	49.464	66.290	-2.515	1.00	249.69
45	4450	O7	NAG	B	221	50.628	66.249	-2.115	1.00	249.69
	4451	C8	NAG	B	221	48.813	67.630	-2.819	1.00	249.69
	4452	C3	NAG	B	221	50.117	63.412	-3.614	1.00	249.69
	4453	O3	NAG	B	221	51.258	64.240	-3.757	1.00	249.69
	4454	C4	NAG	B	221	50.568	61.956	-3.448	1.00	249.69
50	4455	O4	NAG	B	221	51.118	61.532	-4.713	1.00	249.69
	4456	C5	NAG	B	221	49.362	61.063	-3.063	1.00	249.69
	4457	O5	NAG	B	221	48.675	61.604	-1.912	1.00	249.69
	4458	C6	NAG	B	221	49.751	59.637	-2.698	1.00	249.69
	4459	O6	NAG	B	221	50.700	59.612	-1.642	1.00	249.69
55	4460	C1	NAG	B	222	51.927	60.395	-4.782	1.00	249.69
	4461	C2	NAG	B	222	53.144	60.683	-5.692	1.00	249.69
	4462	N2	NAG	B	222	53.932	61.775	-5.134	1.00	249.69
	4463	C7	NAG	B	222	55.211	61.597	-4.802	1.00	249.69
	4464	O7	NAG	B	222	55.800	60.524	-4.944	1.00	249.69
60	4465	C8	NAG	B	222	55.954	62.796	-4.227	1.00	249.69
	4466	C3	NAG	B	222	52.654	61.043	-7.123	1.00	249.69
	4467	O3	NAG	B	222	53.784	61.185	-8.006	1.00	249.69
	4468	C4	NAG	B	222	51.697	59.861	-7.668	1.00	249.69
	4469	O4	NAG	B	222	51.134	60.393	-8.900	1.00	249.69
65	4470	C5	NAG	B	222	50.571	59.682	-6.652	1.00	249.69
	4471	O5	NAG	B	222	51.140	59.328	-5.356	1.00	249.69
	4472	C6	NAG	B	222	49.642	58.551	-7.073	1.00	249.69
	4473	O6	NAG	B	222	48.276	58.935	-6.979	1.00	249.69
	4474	C1	NAG	B	242	27.093	65.374	-0.289	1.00	220.33
70	4475	C2	NAG	B	242	27.619	64.790	-1.606	1.00	220.33

	4476	N2	NAG B	242	28.439	63.617	-1.372	1.00	220.33
	4477	C7	NAG B	242	28.079	62.446	-1.890	1.00	220.33
	4478	O7	NAG B	242	27.061	62.304	-2.564	1.00	220.33
	4479	C8	NAG B	242	28.977	61.252	-1.616	1.00	220.33
5	4480	C3	NAG B	242	28.417	65.869	-2.342	1.00	220.33
	4481	O3	NAG B	242	28.893	65.358	-3.579	1.00	220.33
	4482	C4	NAG B	242	27.524	67.092	-2.588	1.00	220.33
	4483	O4	NAG B	242	28.320	68.165	-3.127	1.00	220.33
	4484	C5	NAG B	242	26.849	67.565	-1.278	1.00	220.33
10	4485	O5	NAG B	242	26.201	66.460	-0.583	1.00	220.33
	4486	C6	NAG B	242	25.764	68.596	-1.552	1.00	220.33
	4487	O6	NAG B	242	26.133	69.886	-1.090	1.00	233.97
	4488	C1	NAG B	243	27.960	68.648	-4.371	1.00	233.97
	4489	C2	NAG B	243	28.552	70.043	-4.570	1.00	233.97
15	4490	N2	NAG B	243	28.067	70.964	-3.561	1.00	233.97
	4491	C7	NAG B	243	28.929	71.745	-2.911	1.00	233.97
	4492	O7	NAG B	243	30.147	71.719	-3.114	1.00	233.97
	4493	C8	NAG B	243	28.358	72.696	-1.871	1.00	233.97
	4494	C3	NAG B	243	28.185	70.544	-5.960	1.00	233.97
20	4495	O3	NAG B	243	28.726	71.840	-6.174	1.00	233.97
	4496	C4	NAG B	243	28.751	69.586	-6.984	1.00	233.97
	4497	O4	NAG B	243	28.443	70.118	-8.263	1.00	233.97
	4498	C5	NAG B	243	28.175	68.165	-6.727	1.00	233.97
	4499	O5	NAG B	243	28.488	67.756	-5.361	1.00	233.97
25	4500	C6	NAG B	243	28.776	67.113	-7.637	1.00	233.97
	4501	O6	NAG B	243	30.175	66.991	-7.430	1.00	229.91
	4502	C1	MAN B	244	29.240	69.821	-9.345	1.00	229.91
	4503	C2	MAN B	244	28.260	69.705	-10.400	1.00	229.91
	4504	O2	MAN B	244	27.196	70.659	-10.238	1.00	229.91
30	4505	C3	MAN B	244	28.928	69.691	-11.752	1.00	229.91
	4506	O3	MAN B	244	28.001	69.355	-12.770	1.00	229.91
	4507	C4	MAN B	244	29.658	70.989	-12.013	1.00	229.91
	4508	O4	MAN B	244	30.237	70.964	-13.307	1.00	229.91
	4509	C5	MAN B	244	30.732	71.128	-10.933	1.00	229.91
35	4510	O5	MAN B	244	30.062	71.170	-9.601	1.00	229.91
	4511	C6	MAN B	244	31.699	72.322	-11.158	1.00	229.91
	4512	O6	MAN B	244	31.180	73.559	-10.690	1.00	249.69
	4513	C1	NAG B	250	44.268	53.492	9.707	1.00	249.69
	4514	C2	NAG B	250	45.671	53.603	10.328	1.00	249.69
40	4515	N2	NAG B	250	45.573	53.779	11.763	1.00	249.69
	4516	C7	NAG B	250	45.937	52.792	12.578	1.00	249.69
	4517	O7	NAG B	250	46.363	51.706	12.172	1.00	249.69
	4518	C8	NAG B	250	45.811	53.044	14.074	1.00	249.69
	4519	C3	NAG B	250	46.415	54.790	9.702	1.00	249.69
45	4520	O3	NAG B	250	47.749	54.843	10.194	1.00	249.69
	4521	C4	NAG B	250	46.432	54.657	8.172	1.00	249.69
	4522	O4	NAG B	250	47.008	55.826	7.602	1.00	249.69
	4523	C5	NAG B	250	44.994	54.460	7.640	1.00	249.69
	4524	O5	NAG B	250	44.369	53.324	8.287	1.00	249.69
50	4525	C6	NAG B	250	44.929	54.206	6.139	1.00	249.69
	4526	O6	NAG B	250	43.668	53.664	5.761	1.00	249.69
	4527	C1	NAG B	274	23.582	59.809	24.027	1.00	249.69
	4528	C2	NAG B	274	23.459	61.065	24.903	1.00	249.69
	4529	N2	NAG B	274	24.613	61.181	25.777	1.00	249.69
55	4530	C7	NAG B	274	24.999	62.374	26.223	1.00	249.69
	4531	O7	NAG B	274	24.418	63.422	25.934	1.00	249.69
	4532	C8	NAG B	274	26.218	62.415	27.133	1.00	249.69
	4533	C3	NAG B	274	22.167	60.997	25.741	1.00	249.69
	4534	O3	NAG B	274	21.983	62.216	26.451	1.00	249.69
60	4535	C4	NAG B	274	20.951	60.745	24.836	1.00	249.69
	4536	O4	NAG B	274	19.788	60.553	25.637	1.00	249.69
	4537	C5	NAG B	274	21.198	59.506	23.958	1.00	249.69
	4538	O5	NAG B	274	22.418	59.674	23.192	1.00	249.69
	4539	C6	NAG B	274	20.073	59.255	22.962	1.00	249.69
65	4540	O6	NAG B	274	20.404	58.209	22.054	1.00	249.69
	4541	C1	NAG B	335	50.936	78.660	5.286	1.00	249.69
	4542	C2	NAG B	335	51.372	77.658	6.389	1.00	249.69
	4543	N2	NAG B	335	51.470	78.372	7.651	1.00	249.69
	4544	C7	NAG B	335	50.669	78.063	8.668	1.00	249.69
70	4545	O7	NAG B	335	49.823	77.166	8.611	1.00	249.69

	4548	C8	NAG	B	335	50.837	78.865	9.950	1.00	249.69
	4547	C3	NAG	B	335	52.711	76.938	6.115	1.00	249.69
	4548	O3	NAG	B	335	52.790	75.759	6.909	1.00	249.69
	4549	C4	NAG	B	335	52.852	76.553	4.647	1.00	249.69
5	4550	O4	NAG	B	335	54.131	75.970	4.410	1.00	249.69
	4551	C5	NAG	B	335	52.678	77.814	3.812	1.00	249.69
	4552	O5	NAG	B	335	51.319	78.289	3.939	1.00	249.69
	4553	C6	NAG	B	335	52.935	77.564	2.334	1.00	249.69
	4554	O6	NAG	B	335	53.923	78.447	1.826	1.00	249.69
10	4555	C1	NAG	B	340	43.529	87.808	25.515	1.00	249.69
	4556	C2	NAG	B	340	42.252	87.842	26.379	1.00	249.69
	4557	N2	NAG	B	340	41.073	87.751	25.533	1.00	249.69
	4558	C7	NAG	B	340	40.086	86.909	25.835	1.00	249.69
	4559	O7	NAG	B	340	40.099	86.177	26.833	1.00	249.69
15	4560	C8	NAG	B	340	38.898	86.878	24.882	1.00	249.69
	4561	C3	NAG	B	340	42.235	89.153	27.182	1.00	249.69
	4562	O3	NAG	B	340	41.117	89.172	28.061	1.00	249.69
	4563	C4	NAG	B	340	43.537	89.304	27.991	1.00	249.69
	4564	O4	NAG	B	340	43.566	90.587	28.606	1.00	249.69
20	4565	C5	NAG	B	340	44.768	89.134	27.069	1.00	249.69
	4566	O5	NAG	B	340	44.691	87.877	26.352	1.00	249.69
	4567	C6	NAG	B	340	46.101	89.143	27.805	1.00	249.69
	4568	O6	NAG	B	340	47.172	88.783	26.936	1.00	249.69
	4569	C1	NAG	B	366	28.566	86.792	5.084	1.00	212.59
25	4570	C2	NAG	B	366	27.788	86.264	3.928	1.00	212.59
	4571	N2	NAG	B	366	28.623	85.657	2.952	1.00	212.59
	4572	C7	NAG	B	366	28.903	84.360	3.019	1.00	212.59
	4573	O7	NAG	B	366	28.430	83.623	3.883	1.00	212.59
	4574	C8	NAG	B	366	29.845	83.792	1.966	1.00	212.59
30	4575	C3	NAG	B	366	26.966	87.413	3.282	1.00	212.59
	4576	O3	NAG	B	366	26.061	86.895	2.319	1.00	212.59
	4577	C4	NAG	B	366	26.186	88.236	4.315	1.00	212.59
	4578	O4	NAG	B	366	25.698	89.443	3.682	1.00	212.59
	4579	C5	NAG	B	366	27.096	88.607	5.499	1.00	212.59
35	4580	O5	NAG	B	366	27.723	87.423	6.036	1.00	212.59
	4581	C6	NAG	B	366	26.361	89.288	6.648	1.00	212.59
	4582	O6	NAG	B	366	27.276	89.790	7.613	1.00	212.59
	4583	C1	NAG	B	367	24.341	89.710	3.786	1.00	243.26
	4584	C2	NAG	B	367	24.090	91.194	3.541	1.00	243.26
40	4585	N2	NAG	B	367	24.852	92.006	4.472	1.00	243.26
	4586	C7	NAG	B	367	25.846	92.768	4.025	1.00	243.26
	4587	O7	NAG	B	367	26.167	92.827	2.834	1.00	243.26
	4588	C8	NAG	B	367	26.602	93.591	5.058	1.00	243.26
	4589	C3	NAG	B	367	22.591	91.455	3.687	1.00	243.26
45	4590	O3	NAG	B	367	22.313	92.825	3.445	1.00	243.26
	4591	C4	NAG	B	367	21.820	90.586	2.689	1.00	243.26
	4592	O4	NAG	B	367	20.423	90.749	2.897	1.00	243.26
	4593	C5	NAG	B	367	22.208	89.105	2.859	1.00	243.26
	4594	O5	NAG	B	367	23.647	88.941	2.791	1.00	243.26
50	4595	C6	NAG	B	367	21.611	88.219	1.777	1.00	243.26
	4596	O6	NAG	B	367	22.614	87.692	0.915	1.00	243.26
	4597	CB	LYS	D	4	55.929	67.814	61.471	1.00	249.69
	4598	CG	LYS	D	4	55.569	66.389	61.069	1.00	249.69
	4599	CD	LYS	D	4	55.219	65.523	62.280	1.00	249.69
55	4600	CE	LYS	D	4	54.831	64.103	61.856	1.00	249.69
	4601	NZ	LYS	D	4	54.503	63.215	63.020	1.00	226.67
	4602	C	LYS	D	4	54.982	68.782	59.376	1.00	226.67
	4603	O	LYS	D	4	53.862	68.517	59.816	1.00	226.67
	4604	N	LYS	D	4	56.551	70.102	60.766	1.00	226.67
60	4605	CA	LYS	D	4	56.206	68.740	60.282	1.00	199.21
	4606	N	PRO	D	5	55.175	69.129	58.098	1.00	157.97
	4607	CD	PRO	D	5	56.399	69.692	57.504	1.00	199.21
	4608	CA	PRO	D	5	54.056	69.192	57.153	1.00	157.97
	4609	CB	PRO	D	5	54.551	70.184	56.106	1.00	157.97
65	4610	CG	PRO	D	5	56.009	69.877	56.038	1.00	199.21
	4611	C	PRO	D	5	53.742	67.819	56.558	1.00	199.21
	4612	O	PRO	D	5	54.592	66.931	56.558	1.00	205.80
	4613	N	LYS	D	6	52.523	67.641	56.064	1.00	205.80
	4614	CA	LYS	D	6	52.136	66.371	55.468	1.00	205.80
70	4615	CB	LYS	D	6	51.395	65.500	56.489	1.0C	249.69

	4616	CG	LYS	D	6	51.007	64.131	55.942	1.00	249.69
	4617	CD	LYS	D	6	50.433	63.220	57.018	1.00	249.69
	4618	CE	LYS	D	6	50.116	61.838	56.448	1.00	249.69
	4619	NZ	LYS	D	6	49.665	60.880	57.497	1.00	249.69
5	4620	C	LYS	D	6	51.263	66.599	54.246	1.00	205.80
	4621	O	LYS	D	6	50.132	67.075	54.362	1.00	205.80
	4622	N	VAL	D	7	51.797	66.245	53.080	1.00	180.35
	4623	CA	VAL	D	7	51.082	66.425	51.823	1.00	180.35
	4624	CB	VAL	D	7	52.002	66.148	50.636	1.00	112.97
10	4625	CG1	VAL	D	7	51.369	66.692	49.350	1.00	112.97
	4626	CG2	VAL	D	7	53.374	66.752	50.884	1.00	112.97
	4627	C	VAL	D	7	49.846	65.540	51.677	1.00	180.35
	4628	O	VAL	D	7	49.935	64.315	51.772	1.00	180.35
	4629	N	SER	D	8	48.699	66.171	51.443	1.00	191.62
15	4630	CA	SER	D	8	47.441	65.455	51.269	1.00	191.62
	4631	CB	SER	D	8	46.339	66.118	52.114	1.00	215.34
	4632	OG	SER	D	8	46.315	67.528	51.940	1.00	215.34
	4633	C	SER	D	8	47.066	65.475	49.790	1.00	191.62
	4634	O	SER	D	8	47.587	66.285	49.026	1.00	191.62
20	4635	N	LEU	D	9	46.175	64.579	49.374	1.00	183.49
	4636	CA	LEU	D	9	45.753	64.552	47.973	1.00	183.49
	4637	CB	LEU	D	9	46.289	63.316	47.250	1.00	153.82
	4638	CG	LEU	D	9	47.793	63.054	47.150	1.00	153.82
	4639	CD1	LEU	D	9	48.011	61.992	46.080	1.00	153.82
25	4640	CD2	LEU	D	9	48.557	64.312	46.800	1.00	153.82
	4641	C	LEU	D	9	44.243	64.561	47.836	1.00	183.49
	4642	O	LEU	D	9	43.522	64.243	48.781	1.00	183.49
	4643	N	ASN	D	10	43.769	64.929	46.650	1.00	161.08
	4644	CA	ASN	D	10	42.340	64.954	46.383	1.00	161.08
30	4645	CB	ASN	D	10	41.701	66.192	46.999	1.00	220.60
	4646	CG	ASN	D	10	40.195	66.089	47.052	1.00	220.60
	4647	OD1	ASN	D	10	39.645	65.222	47.732	1.00	220.60
	4648	ND2	ASN	D	10	39.515	66.966	46.328	1.00	220.60
	4649	C	ASN	D	10	42.077	64.931	44.883	1.00	161.08
35	4650	O	ASN	D	10	42.376	65.903	44.187	1.00	161.08
	4651	N	PRO	D	11	41.505	63.830	44.368	1.00	193.66
	4652	CD	PRO	D	11	41.212	63.723	42.927	1.00	148.22
	4653	CA	PRO	D	11	41.077	62.602	45.052	1.00	193.66
	4654	CB	PRO	D	11	40.656	61.698	43.905	1.00	148.22
40	4655	CG	PRO	D	11	40.146	62.658	42.901	1.00	148.22
	4656	C	PRO	D	11	42.161	61.959	45.924	1.00	193.66
	4657	O	PRO	D	11	43.336	62.325	45.849	1.00	193.66
	4658	N	PRO	D	12	41.772	60.982	46.769	1.00	193.56
	4659	CD	PRO	D	12	40.402	60.544	47.062	1.00	138.53
45	4660	CA	PRO	D	12	42.731	60.293	47.644	1.00	193.56
	4661	CB	PRO	D	12	41.824	59.503	48.588	1.00	138.53
	4662	CG	PRO	D	12	40.494	60.225	48.520	1.00	138.53
	4663	C	PRO	D	12	43.633	59.379	46.825	1.00	193.56
	4664	O	PRO	D	12	44.775	59.096	47.204	1.00	193.56
50	4665	N	TRP	D	13	43.081	58.919	45.700	1.00	115.99
	4666	CA	TRP	D	13	43.745	58.039	44.727	1.00	115.99
	4667	CB	TRP	D	13	42.854	57.917	43.495	1.00	155.11
	4668	CG	TRP	D	13	41.432	57.624	43.839	1.00	155.11
	4669	CD2	TRP	D	13	40.964	56.869	44.959	1.00	155.11
55	4670	CE2	TRP	D	13	39.560	56.822	44.873	1.00	155.11
	4671	CE3	TRP	D	13	41.596	56.233	46.022	1.00	155.11
	4672	CD1	TRP	D	13	40.330	57.988	43.138	1.00	155.11
	4673	NE1	TRP	D	13	39.192	57.509	43.751	1.00	155.11
	4674	CZ2	TRP	D	13	38.778	56.160	45.808	1.00	155.11
60	4675	CZ3	TRP	D	13	40.824	55.569	46.957	1.00	155.11
	4676	CH2	TRP	D	13	39.426	55.538	46.844	1.00	155.11
	4677	C	TRP	D	13	45.119	58.540	44.288	1.00	115.99
	4678	O	TRP	D	13	45.213	59.565	43.618	1.00	115.99
	4679	N	ASN	D	14	46.176	57.810	44.644	1.00	127.73
65	4680	CA	ASN	D	14	47.541	58.211	44.268	1.00	127.73
	4681	CB	ASN	D	14	48.472	58.128	45.485	1.00	164.43
	4682	CG	ASN	D	14	48.644	56.717	45.996	1.00	164.43
	4683	OD1	ASN	D	14	47.674	56.039	46.369	1.00	164.43
	4684	ND2	ASN	D	14	49.888	56.265	46.023	1.00	164.43
70	4685	C	ASN	D	14	48.124	57.395	43.094	1.00	127.73

	#	Atom	Res	Chain	Seq	X	Y	Z	Occ	B
	4686	O	ASN	D	14	49.361	57.291	42.929	1.00	127.73
	4687	N	ARG	D	15	47.202	56.825	42.304	1.00	124.12
	4688	CA	ARG	D	15	47.484	56.018	41.111	1.00	124.12
	4689	CB	ARG	D	15	47.249	54.517	41.374	1.00	138.52
5	4690	CG	ARG	D	15	47.935	53.919	42.607	1.00	138.52
	4691	CD	ARG	D	15	47.775	52.394	42.630	1.00	138.52
	4692	NE	ARG	D	15	48.696	51.717	41.716	1.00	138.52
	4693	CZ	ARG	D	15	48.387	50.631	41.012	1.00	138.52
	4694	NH1	ARG	D	15	47.175	50.091	41.111	1.00	138.52
10	4695	NH2	ARG	D	15	49.292	50.084	40.211	1.00	138.52
	4696	C	ARG	D	15	46.436	56.487	40.117	1.00	124.12
	4697	O	ARG	D	15	45.277	56.068	40.197	1.00	124.12
	4698	N	ILE	D	16	46.825	57.344	39.182	1.00	134.05
	4699	CA	ILE	D	16	45.853	57.861	38.222	1.00	134.05
15	4700	CB	ILE	D	16	45.666	59.359	38.405	1.00	185.30
	4701	CG2	ILE	D	16	44.824	59.635	39.645	1.00	185.30
	4702	CG1	ILE	D	16	47.047	60.016	38.464	1.00	185.30
	4703	CD1	ILE	D	16	47.030	61.514	38.379	1.00	185.30
	4704	C	ILE	D	16	46.150	57.638	36.740	1.00	134.05
20	4705	O	ILE	D	16	47.301	57.474	36.330	1.00	134.05
	4706	N	PHE	D	17	45.088	57.650	35.944	1.00	221.22
	4707	CA	PHE	D	17	45.198	57.475	34.508	1.00	221.22
	4708	CB	PHE	D	17	43.814	57.258	33.908	1.00	170.58
	4709	CG	PHE	D	17	43.398	55.818	33.833	1.00	170.58
25	4710	CD1	PHE	D	17	42.060	55.454	34.005	1.00	170.58
	4711	CD2	PHE	D	17	44.330	54.832	33.544	1.00	170.58
	4712	CE1	PHE	D	17	41.658	54.141	33.886	1.00	170.58
	4713	CE2	PHE	D	17	43.932	53.511	33.422	1.00	170.58
	4714	CZ	PHE	D	17	42.590	53.167	33.594	1.00	170.58
30	4715	C	PHE	D	17	45.825	58.706	33.880	1.00	221.22
	4716	O	PHE	D	17	46.106	59.689	34.562	1.00	221.22
	4717	N	LYS	D	18	46.023	58.646	32.569	1.00	189.75
	4718	CA	LYS	D	18	46.615	59.743	31.808	1.00	189.75
	4719	CB	LYS	D	18	47.255	59.178	30.538	1.00	249.69
35	4720	CG	LYS	D	18	47.978	60.189	29.663	1.00	249.69
	4721	CD	LYS	D	18	48.719	59.471	28.531	1.00	249.69
	4722	CE	LYS	D	18	49.392	60.449	27.572	1.00	249.69
	4723	NZ	LYS	D	18	48.405	61.242	26.779	1.00	249.69
	4724	C	LYS	D	18	45.573	60.806	31.450	1.00	189.75
40	4725	O	LYS	D	18	44.509	60.493	30.912	1.00	189.75
	4726	N	GLY	D	19	45.887	62.060	31.766	1.00	246.53
	4727	CA	GLY	D	19	44.979	63.151	31.467	1.00	246.53
	4728	C	GLY	D	19	44.072	63.582	32.607	1.00	246.53
	4729	O	GLY	D	19	43.415	64.620	32.512	1.00	246.53
45	4730	N	GLU	D	20	44.029	62.794	33.680	1.00	150.48
	4731	CA	GLU	D	20	43.189	63.103	34.849	1.00	150.48
	4732	CB	GLU	D	20	42.969	61.840	35.704	1.00	195.02
	4733	CG	GLU	D	20	42.534	60.576	34.943	1.00	195.02
	4734	CD	GLU	D	20	42.202	59.403	35.877	1.00	195.02
50	4735	OE1	GLU	D	20	43.045	59.054	36.735	1.00	195.02
	4736	OE2	GLU	D	20	41.093	58.831	35.748	1.00	195.02
	4737	C	GLU	D	20	43.844	64.181	35.717	1.00	150.48
	4738	O	GLU	D	20	45.062	64.375	35.641	1.00	150.48
	4739	N	ASN	D	21	43.054	64.870	36.545	1.00	166.05
55	4740	CA	ASN	D	21	43.621	65.916	37.407	1.00	166.05
	4741	CB	ASN	D	21	42.869	67.242	37.240	1.00	249.69
	4742	CG	ASN	D	21	42.390	67.487	35.822	1.00	249.69
	4743	OD1	ASN	D	21	43.129	67.337	34.850	1.00	249.69
	4744	ND2	ASN	D	21	41.130	67.891	35.723	1.00	166.05
60	4745	C	ASN	D	21	43.632	65.566	38.903	1.00	166.05
	4746	O	ASN	D	21	42.697	64.941	39.418	1.00	232.99
	4747	N	VAL	D	22	44.685	66.001	39.593	1.00	232.99
	4748	CA	VAL	D	22	44.836	65.753	41.022	1.00	144.01
	4749	CB	VAL	D	22	45.811	64.598	41.274	1.00	144.01
65	4750	CG1	VAL	D	22	47.232	65.032	40.844	1.00	144.01
	4751	CG2	VAL	D	22	45.711	64.149	42.718	1.00	232.99
	4752	C	VAL	D	22	45.367	67.003	41.726	1.00	232.99
	4753	O	VAL	D	22	46.132	67.762	41.135	1.00	149.70
	4754	N	THR	D	23	44.977	67.204	42.986	1.00	149.70
70	4755	CA	THR	D	23	45.409	68.376	43.760	1.00	149.70

4756	CB	THR	D	23	44.185	69.205	44.222	1.00	239.97
4757	OG1	THR	D	23	43.328	69.469	43.101	1.00	239.97
4758	CG2	THR	D	23	44.641	70.527	44.839	1.00	239.97
4759	C	THR	D	23	46.242	68.035	45.013	1.00	149.70
4760	O	THR	D	23	45.802	67.260	45.865	1.00	149.70
4761	N	LEU	D	24	47.426	68.633	45.130	1.00	183.97
4762	CA	LEU	D	24	48.291	68.390	46.282	1.00	183.97
4763	CB	LEU	D	24	49.736	68.117	45.847	1.00	149.27
4764	CG	LEU	D	24	50.067	67.414	44.528	1.00	149.27
4765	CD1	LEU	D	24	51.537	66.998	44.556	1.00	149.27
4766	CD2	LEU	D	24	49.182	66.203	44.315	1.00	149.27
4767	C	LEU	D	24	48.292	69.583	47.247	1.00	183.97
4768	O	LEU	D	24	48.884	70.627	46.961	1.00	183.97
4769	N	THR	D	25	47.642	69.414	48.394	1.00	179.50
4770	CA	THR	D	25	47.555	70.453	49.422	1.00	179.50
4771	CB	THR	D	25	46.149	70.455	50.074	1.00	206.28
4772	OG1	THR	D	25	45.152	70.641	49.059	1.00	206.28
4773	CG2	THR	D	25	46.035	71.567	51.109	1.00	206.28
4774	C	THR	D	25	48.608	70.207	50.510	1.00	179.50
4775	O	THR	D	25	48.762	69.083	50.983	1.00	179.50
4776	N	CYS	D	26	49.321	71.258	50.907	1.00	232.65
4777	CA	CYS	D	26	50.349	71.137	51.941	1.00	232.65
4778	C	CYS	D	26	49.723	71.185	53.337	1.00	232.65
4779	O	CYS	D	26	48.767	71.928	53.562	1.00	232.65
4780	CB	CYS	D	26	51.377	72.252	51.784	1.00	181.06
4781	SG	CYS	D	26	52.866	72.078	52.815	1.00	181.06
4782	N	ASN	D	27	50.274	70.400	54.266	1.00	211.42
4783	CA	ASN	D	27	49.762	70.299	55.633	1.00	211.42
4784	CB	ASN	D	27	50.909	70.245	56.640	1.00	249.69
4785	CG	ASN	D	27	50.435	69.883	58.041	1.00	249.69
4786	OD1	ASN	D	27	49.691	68.915	58.228	1.00	249.69
4787	ND2	ASN	D	27	50.866	70.658	59.035	1.00	249.69
4788	C	ASN	D	27	48.782	71.397	56.027	1.00	211.42
4789	O	ASN	D	27	49.176	72.473	56.478	1.00	211.42
4790	N	GLY	D	28	47.499	71.096	55.848	1.00	232.09
4791	CA	GLY	D	28	46.428	72.024	56.166	1.00	232.09
4792	C	GLY	D	28	45.145	71.413	55.640	1.00	232.09
4793	O	GLY	D	28	45.028	71.150	54.442	1.00	232.09
4794	N	ASN	D	29	44.183	71.179	56.527	1.00	249.69
4795	CA	ASN	D	29	42.916	70.564	56.138	1.00	249.69
4796	CB	ASN	D	29	42.185	70.041	57.392	1.00	249.66
4797	CG	ASN	D	29	40.997	69.139	57.060	1.00	249.66
4798	OD1	ASN	D	29	40.786	68.758	55.903	1.00	249.66
4799	ND2	ASN	D	29	40.223	68.786	58.082	1.00	249.66
4800	C	ASN	D	29	41.992	71.490	55.331	1.00	249.69
4801	O	ASN	D	29	41.536	71.122	54.239	1.00	249.69
4802	N	ASN	D	30	41.730	72.692	55.843	1.00	249.69
4803	CA	ASN	D	30	40.830	73.606	55.146	1.00	249.69
4804	CB	ASN	D	30	39.518	73.728	55.941	1.00	249.69
4805	CG	ASN	D	30	38.761	72.406	56.039	1.00	249.69
4806	OD1	ASN	D	30	38.314	72.011	57.123	1.00	249.69
4807	ND2	ASN	D	30	38.607	71.718	54.903	1.00	249.69
4808	C	ASN	D	30	41.378	75.001	54.827	1.00	249.69
4809	O	ASN	D	30	41.596	75.328	53.656	1.00	249.69
4810	N	PHE	D	31	41.599	75.820	55.856	1.00	244.83
4811	CA	PHE	D	31	42.085	77.179	55.639	1.00	244.83
4812	CB	PHE	D	31	41.091	78.191	56.235	1.00	249.48
4813	CG	PHE	D	31	39.675	78.021	55.735	1.00	249.48
4814	CD1	PHE	D	31	38.843	77.036	56.268	1.00	249.48
4815	CD2	PHE	D	31	39.182	78.824	54.704	1.00	249.48
4816	CE1	PHE	D	31	37.543	76.849	55.782	1.00	249.48
4817	CE2	PHE	D	31	37.880	78.644	54.208	1.00	249.48
4818	CZ	PHE	D	31	37.061	77.654	54.750	1.00	249.48
4819	C	PHE	D	31	43.496	77.454	56.169	1.00	244.83
4820	O	PHE	D	31	43.773	77.287	57.358	1.00	244.83
4821	N	PHE	D	32	44.378	77.888	55.265	1.00	249.69
4822	CA	PHE	D	32	45.775	78.197	55.591	1.00	249.69
4823	CB	PHE	D	32	46.711	77.304	54.761	1.00	249.69
4824	CG	PHE	D	32	48.130	77.274	55.266	1.00	249.69
4825	CD1	PHE	D	32	48.435	76.713	56.514	1.00	249.69

	4826	CD2	PHE	D	32-	49.164	77.800	54.494	1.00	249.69
	4827	CE1	PHE	D	32	49.752	76.678	56.983	1.00	249.69
	4828	CE2	PHE	D	32	50.487	77.770	54.954	1.00	249.69
	4829	CZ	PHE	D	32	50.779	77.207	56.198	1.00	249.69
5	4830	C	PHE	D	32	46.086	79.681	55.325	1.00	249.69
	4831	O	PHE	D	32	45.300	80.381	54.671	1.00	249.69
	4832	N	GLU	D	33	47.241	80.150	55.802	1.00	237.86
	4833	CA	GLU	D	33	47.603	81.555	55.640	1.00	237.86
	4834	CB	GLU	D	33	47.766	82.184	57.029	1.00	249.69
10	4835	CG	GLU	D	33	47.688	83.708	57.034	1.00	249.69
	4836	CD	GLU	D	33	46.478	84.238	56.256	1.00	249.69
	4837	OE1	GLU	D	33	45.351	83.734	56.476	1.00	249.69
	4838	OE2	GLU	D	33	46.656	85.163	55.429	1.00	237.86
	4839	C	GLU	D	33	48.821	81.908	54.779	1.00	237.86
15	4840	O	GLU	D	33	48.729	82.759	53.896	1.00	249.69
	4841	N	VAL	D	34	49.957	81.269	55.041	1.00	249.69
	4842	CA	VAL	D	34	51.188	81.553	54.302	1.00	249.69
	4843	CB	VAL	D	34	52.357	80.686	54.850	1.00	245.39
	4844	CG1	VAL	D	34	53.648	81.015	54.126	1.00	245.39
20	4845	CG2	VAL	D	34	52.522	80.928	56.343	1.00	245.39
	4846	C	VAL	D	34	51.103	81.386	52.773	1.00	249.69
	4847	O	VAL	D	34	50.330	80.567	52.254	1.00	249.69
	4848	N	SER	D	35	51.900	82.188	52.065	1.00	249.69
	4849	CA	SER	D	35	51.963	82.160	50.603	1.00	249.69
25	4850	CB	SER	D	35	51.850	83.577	50.033	1.00	241.64
	4851	OG	SER	D	35	53.028	84.324	50.300	1.00	241.64
	4852	C	SER	D	35	53.307	81.559	50.188	1.00	249.69
	4853	O	SER	D	35	53.587	81.400	48.997	1.00	249.69
	4854	N	SER	D	36	54.137	81.243	51.184	1.00	249.69
30	4855	CA	SER	D	36	55.455	80.654	50.953	1.00	249.69
	4856	CB	SER	D	36	56.516	81.325	51.841	1.00	249.69
	4857	OG	SER	D	36	56.379	80.950	53.201	1.00	249.69
	4858	C	SER	D	36	55.430	79.150	51.227	1.00	249.69
	4859	O	SER	D	36	55.650	78.692	52.354	1.00	216.36
35	4860	N	THR	D	37	55.147	78.389	50.176	1.00	216.36
	4861	CA	THR	D	37	55.091	76.944	50.267	1.00	218.49
	4862	CB	THR	D	37	53.651	76.439	50.029	1.00	218.49
	4863	OG1	THR	D	37	52.773	77.009	51.009	1.00	218.49
	4864	CG2	THR	D	37	53.595	74.930	50.138	1.00	216.36
40	4865	C	THR	D	37	56.027	76.399	49.193	1.00	216.36
	4866	O	THR	D	37	56.067	76.908	48.070	1.00	249.68
	4867	N	LYS	D	38	56.792	75.372	49.539	1.00	249.68
	4868	CA	LYS	D	38	57.737	74.790	48.591	1.00	248.74
	4869	CB	LYS	D	38	59.115	74.638	49.265	1.00	248.74
45	4870	CG	LYS	D	38	59.701	75.962	49.786	1.00	248.74
	4871	CD	LYS	D	38	61.060	75.782	50.467	1.00	248.74
	4872	CE	LYS	D	38	61.627	77.123	50.933	1.00	248.74
	4873	NZ	LYS	D	38	62.953	76.993	51.599	1.00	249.68
	4874	C	LYS	D	38	57.259	73.445	48.044	1.00	249.68
50	4875	O	LYS	D	38	56.626	72.660	48.747	1.00	200.98
	4876	N	TRP	D	39	57.552	73.197	46.775	1.00	200.98
	4877	CA	TRP	D	39	57.178	71.944	46.137	1.00	193.49
	4878	CB	TRP	D	39	56.085	72.188	45.096	1.00	193.49
	4879	CG	TRP	D	39	54.754	72.634	45.638	1.00	193.49
55	4880	CD2	TRP	D	39	53.910	71.924	46.562	1.00	193.49
	4881	CE2	TRP	D	39	52.708	72.649	46.669	1.00	193.49
	4882	CE3	TRP	D	39	54.053	70.747	47.307	1.00	193.49
	4883	CD1	TRP	D	39	54.051	73.727	45.247	1.00	193.49
	4884	NE1	TRP	D	39	52.822	73.745	45.854	1.00	193.49
60	4885	CZ2	TRP	D	39	51.648	72.242	47.487	1.00	193.49
	4886	CZ3	TRP	D	39	52.994	70.335	48.124	1.00	193.49
	4887	CH2	TRP	D	39	51.807	71.084	48.204	1.00	200.98
	4888	C	TRP	D	39	58.428	71.393	45.451	1.00	200.98
	4889	O	TRP	D	39	59.127	72.127	44.763	1.00	160.00
65	4890	N	PHE	D	40	58.712	70.108	45.635	1.00	160.00
	4891	CA	PHE	D	40	59.896	69.514	45.027	1.00	228.90
	4892	CB	PHE	D	40	60.943	69.163	46.100	1.00	228.90
	4893	CG	PHE	D	40	61.397	70.336	46.936	1.00	228.90
	4894	CD1	PHE	D	40	60.620	70.798	47.999	1.00	228.90
70	4895	CD2	PHE	D	40	62.611	70.962	46.677	1.00	228.90

	4896	CE1	PHE	D	40.	61.049	71.862	48.794	1.00	228.90
	4897	CE2	PHE	D	40	63.046	72.028	47.465	1.00	228.90
	4898	CZ	PHE	D	40	62.263	72.477	48.526	1.00	228.90
	4899	C	PHE	D	40	59.620	68.266	44.183	1.00	160.00
5	4900	O	PHE	D	40	59.908	67.142	44.615	1.00	160.00
	4901	N	HIS	D	41	59.088	68.469	42.976	1.00	161.00
	4902	CA	HIS	D	41	58.786	67.371	42.052	1.00	161.00
	4903	CB	HIS	D	41	58.044	67.915	40.844	1.00	195.26
	4904	CG	HIS	D	41	57.679	66.868	39.847	1.00	195.26
10	4905	CD2	HIS	D	41	57.680	66.881	38.493	1.00	195.26
	4906	ND1	HIS	D	41	57.205	65.626	40.216	1.00	195.26
	4907	CE1	HIS	D	41	56.928	64.923	39.133	1.00	195.26
	4908	NE2	HIS	D	41	57.207	65.660	38.073	1.00	195.26
	4909	C	HIS	D	41	60.056	66.641	41.588	1.00	161.00
15	4910	O	HIS	D	41	60.798	67.153	40.751	1.00	161.00
	4911	N	ASN	D	42	60.280	65.437	42.118	1.00	193.10
	4912	CA	ASN	D	42	61.464	64.633	41.801	1.00	193.10
	4913	CB	ASN	D	42	61.638	64.471	40.281	1.00	195.59
	4914	CG	ASN	D	42	60.700	63.415	39.686	1.00	195.59
20	4915	OD1	ASN	D	42	59.501	63.435	39.953	1.00	195.59
	4916	ND2	ASN	D	42	61.240	62.506	38.873	1.00	195.59
	4917	C	ASN	D	42	62.690	65.318	42.397	1.00	193.10
	4918	O	ASN	D	42	63.810	65.146	41.919	1.00	193.10
	4919	N	GLY	D	43	62.462	66.092	43.456	1.00	217.79
25	4920	CA	GLY	D	43	63.540	66.809	44.120	1.00	217.79
	4921	C	GLY	D	43	63.681	68.227	43.596	1.00	217.79
	4922	O	GLY	D	43	63.883	69.166	44.372	1.00	217.79
	4923	N	SER	D	44	63.567	68.373	42.275	1.00	249.69
	4924	CA	SER	D	44	63.675	69.669	41.598	1.00	249.69
30	4925	CB	SER	D	44	63.508	69.497	40.083	1.00	225.92
	4926	OG	SER	D	44	64.485	68.631	39.546	1.00	225.92
	4927	C	SER	D	44	62.620	70.652	42.085	1.00	249.69
	4928	O	SER	D	44	61.423	70.374	41.997	1.00	249.69
	4929	N	LEU	D	45	63.056	71.806	42.579	1.00	241.20
35	4930	CA	LEU	D	45	62.110	72.805	43.063	1.00	241.20
	4931	CB	LEU	D	45	62.841	74.084	43.488	1.00	237.73
	4932	CG	LEU	D	45	61.948	75.186	44.070	1.00	237.73
	4933	CD1	LEU	D	45	61.151	74.631	45.239	1.00	237.73
	4934	CD2	LEU	D	45	62.798	76.363	44.515	1.00	237.73
40	4935	C	LEU	D	45	61.074	73.125	41.980	1.00	241.20
	4936	O	LEU	D	45	61.365	73.051	40.783	1.00	241.20
	4937	N	SER	D	46	59.865	73.470	42.416	1.00	233.99
	4938	CA	SER	D	46	58.772	73.787	41.503	1.00	233.99
	4939	CB	SER	D	46	57.494	73.050	41.932	1.00	249.22
45	4940	OG	SER	D	46	56.444	73.250	40.995	1.00	249.22
	4941	C	SER	D	46	58.506	75.285	41.441	1.00	233.99
	4942	O	SER	D	46	59.042	76.064	42.232	1.00	233.99
	4943	N	GLU	D	47	57.648	75.671	40.502	1.00	249.69
	4944	CA	GLU	D	47	57.306	77.074	40.285	1.00	249.69
50	4945	CB	GLU	D	47	57.093	77.311	38.786	1.00	249.69
	4946	CG	GLU	D	47	58.330	77.026	37.945	1.00	249.69
	4947	CD	GLU	D	47	58.089	77.248	36.471	1.00	249.69
	4948	OE1	GLU	D	47	57.260	76.516	35.888	1.00	249.69
	4949	OE2	GLU	D	47	58.728	78.156	35.899	1.00	249.69
55	4950	C	GLU	D	47	56.102	77.618	41.063	1.00	249.69
	4951	O	GLU	D	47	55.889	78.827	41.111	1.00	249.69
	4952	N	GLU	D	48	55.306	76.740	41.661	1.00	194.51
	4953	CA	GLU	D	48	54.159	77.204	42.424	1.00	194.51
	4954	CB	GLU	D	48	53.081	76.117	42.492	1.00	249.69
60	4955	CG	GLU	D	48	51.885	76.488	43.366	1.00	249.69
	4956	CD	GLU	D	48	51.102	77.675	42.836	1.00	249.69
	4957	OE1	GLU	D	48	50.401	77.515	41.814	1.00	249.69
	4958	OE2	GLU	D	48	51.189	78.768	43.437	1.00	249.69
	4959	C	GLU	D	48	54.611	77.576	43.826	1.00	194.51
65	4960	O	GLU	D	48	55.645	77.100	44.311	1.00	194.51
	4961	N	THR	D	49	53.834	78.438	44.472	1.00	208.13
	4962	CA	THR	D	49	54.134	78.889	45.831	1.00	208.13
	4963	CB	THR	D	49	54.570	80.363	45.826	1.00	249.69
	4964	OG1	THR	D	49	53.575	81.153	45.159	1.00	249.69
70	4965	CG2	THR	D	49	55.902	80.516	45.103	1.00	249.69

						x	y	z	occ	B
	4966	C	THR	D	49	52.905	78.729	46.737	1.00	208.13
	4967	O	THR	D	49	53.022	78.579	47.958	1.00	208.13
	4968	N	ASN	D	50	51.725	78.765	46.127	1.00	217.97
	4969	CA	ASN	D	50	50.477	78.601	46.861	1.00	217.97
5	4970	CB	ASN	D	50	49.294	78.643	45.885	1.00	202.82
	4971	CG	ASN	D	50	47.963	78.742	46.592	1.00	202.82
	4972	OD1	ASN	D	50	47.874	78.441	47.781	1.00	202.82
	4973	ND2	ASN	D	50	46.924	79.156	45.865	1.00	202.82
	4974	C	ASN	D	50	50.539	77.236	47.545	1.00	217.97
10	4975	O	ASN	D	50	51.219	76.338	47.072	1.00	198.36
	4976	N	SER	D	51	49.834	77.071	48.653	1.00	198.36
	4977	CA	SER	D	51	49.854	75.790	49.352	1.00	249.69
	4978	CB	SER	D	51	49.201	75.920	50.738	1.00	249.69
	4979	OG	SER	D	51	47.794	76.051	50.640	1.00	198.36
15	4980	C	SER	D	51	49.166	74.663	48.566	1.00	198.36
	4981	O	SER	D	51	49.350	73.484	48.876	1.00	249.63
	4982	N	SER	D	52	48.375	75.019	47.555	1.00	249.63
	4983	CA	SER	D	52	47.679	74.019	46.739	1.00	163.31
	4984	CB	SER	D	52	46.187	74.334	46.625	1.00	163.31
20	4985	OG	SER	D	52	45.563	74.298	47.891	1.00	249.63
	4986	C	SER	D	52	48.258	73.922	45.336	1.00	249.63
	4987	O	SER	D	52	48.011	74.780	44.489	1.00	224.52
	4988	N	LEU	D	53	49.024	72.867	45.096	1.00	224.52
	4989	CA	LEU	D	53	49.637	72.642	43.799	1.00	138.37
25	4990	CB	LEU	D	53	51.016	72.017	43.989	1.00	138.37
	4991	CG	LEU	D	53	51.627	71.271	42.806	1.00	138.37
	4992	CD1	LEU	D	53	51.483	72.075	41.504	1.00	138.37
	4993	CD2	LEU	D	53	53.089	70.983	43.128	1.00	224.52
	4994	C	LEU	D	53	48.761	71.740	42.951	1.00	224.52
30	4995	O	LEU	D	53	48.703	70.536	43.177	1.00	200.53
	4996	N	ASN	D	54	48.080	72.325	41.973	1.00	200.53
	4997	CA	ASN	D	54	47.219	71.538	41.115	1.00	228.73
	4998	CB	ASN	D	54	46.121	72.402	40.513	1.00	228.73
	4999	CG	ASN	D	54	45.105	72.817	41.535	1.00	228.73
35	5000	OD1	ASN	D	54	44.559	71.982	42.255	1.00	228.73
	5001	ND2	ASN	D	54	44.839	74.111	41.608	1.00	200.53
	5002	C	ASN	D	54	47.977	70.834	40.003	1.00	200.53
	5003	O	ASN	D	54	49.102	71.221	39.639	1.00	249.24
	5004	N	ILE	D	55	47.341	69.785	39.482	1.00	249.24
40	5005	CA	ILE	D	55	47.874	68.962	38.403	1.00	185.84
	5006	CB	ILE	D	55	48.369	67.589	38.934	1.00	185.84
	5007	CG2	ILE	D	55	48.373	66.564	37.819	1.00	185.84
	5008	CG1	ILE	D	55	49.764	67.751	39.564	1.00	185.84
	5009	CD1	ILE	D	55	50.346	66.474	40.129	1.00	249.24
45	5010	C	ILE	D	55	46.742	68.738	37.416	1.00	249.24
	5011	O	ILE	D	55	45.735	68.117	37.750	1.00	249.05
	5012	N	VAL	D	56	46.903	69.251	36.205	1.00	249.05
	5013	CA	VAL	D	56	45.870	69.090	35.198	1.00	249.53
	5014	CB	VAL	D	56	45.719	70.362	34.349	1.00	249.53
50	5015	CG1	VAL	D	56	44.353	70.370	33.664	1.00	249.53
	5016	CG2	VAL	D	56	45.886	71.589	35.230	1.00	249.05
	5017	C	VAL	D	56	46.211	67.906	34.301	1.00	249.05
	5018	O	VAL	D	56	46.980	67.034	34.704	1.00	232.44
	5019	N	ASN	D	57	45.641	67.879	33.094	1.00	232.44
55	5020	CA	ASN	D	57	45.859	66.786	32.143	1.00	224.76
	5021	CB	ASN	D	57	45.815	67.311	30.708	1.00	224.76
	5022	CG	ASN	D	57	44.410	67.743	30.292	1.00	224.76
	5023	OD1	ASN	D	57	43.446	66.989	30.437	1.00	224.76
	5024	ND2	ASN	D	57	44.292	68.958	29.772	1.00	232.44
60	5025	C	ASN	D	57	47.149	66.031	32.410	1.00	232.44
	5026	O	ASN	D	57	48.227	66.398	31.940	1.00	180.25
	5027	N	ALA	D	58	46.988	64.963	33.186	1.00	180.25
	5028	CA	ALA	D	58	48.062	64.086	33.631	1.00	155.06
	5029	CB	ALA	D	58	47.470	62.956	34.453	1.00	180.25
65	5030	C	ALA	D	58	48.976	63.508	32.559	1.00	180.25
	5031	O	ALA	D	58	48.587	62.620	31.794	1.00	167.78
	5032	N	LYS	D	59	50.209	64.009	32.531	1.00	167.78
	5033	CA	LYS	D	59	51.224	63.558	31.585	1.00	249.69
	5034	CB	LYS	D	59	51.992	64.761	31.017	1.00	249.69
70	5035	CG	LYS	D	59	51.110	65.772	30.290		

	5036	CD	LYS D	59	51.889	67.003	29.845	1.00	249.69
	5037	CE	LYS D	59	50.965	68.013	29.165	1.00	249.69
	5038	NZ	LYS D	59	51.690	69.228	28.694	1.00	249.69
	5039	C	LYS D	59	52.159	62.654	32.356	1.00	167.78
5	5040	O	LYS D	59	52.494	62.936	33.500	1.00	167.78
	5041	N	PHE D	60	52.566	61.564	31.727	1.00	220.31
	5042	CA	PHE D	60	53...	60.608	32.364	1.00	220.31
	5043	CB	PHE D	60	54.062	59.699	31.294	1.00	243.71
	5044	CG	PHE D	60	53.053	58.843	30.590	1.00	243.71
10	5045	CD1	PHE D	60	53.280	58.409	29.293	1.00	243.71
	5046	CD2	PHE D	60	51.881	58.454	31.232	1.00	243.71
	5047	CE1	PHE D	60	52.357	57.600	28.639	1.00	243.71
	5048	CE2	PHE D	60	50.954	57.647	30.589	1.00	243.71
	5049	CZ	PHE D	60	51.194	57.217	29.287	1.00	243.71
15	5050	C	PHE D	60	54.571	61.240	33.202	1.00	220.31
	5051	O	PHE D	60	55.007	60.671	34.207	1.00	220.31
	5052	N	GLU D	61	55.025	62.417	32.789	1.00	201.05
	5053	CA	GLU D	61	56.101	63.125	33.487	1.00	201.05
	5054	CB	GLU D	61	56.5..	64.332	32.653	1.00	249.69
20	5055	CG	GLU D	61	57.065	63.987	31.251	1.00	249.69
	5056	CD	GLU D	61	56.045	63.244	30.385	1.00	249.69
	5057	OE1	GLU D	61	54.897	63.728	30.245	1.00	249.69
	5058	OE2	GLU D	61	56.395	62.176	29.835	1.00	249.69
	5059	C	GLU D	61	55.671	63.588	34.884	1.00	201.05
25	5060	O	GLU D	61	56.512	63.803	35.757	1.00	201.05
	5061	N	ASP D	62	54.359	63.735	35.086	1.00	185.73
	5062	CA	ASP D	62	53.815	64.165	36.371	1.00	185.73
	5063	CB	ASP D	62	52.334	64.502	36.245	1.00	180.28
	5064	CG	ASP D	62	52.063	65.480	35.132	1.00	180.28
30	5065	OD1	ASP D	62	52.924	66.360	34.882	1.00	180.28
	5066	OD2	ASP D	62	50.985	65.379	34.514	1.00	180.28
	5067	C	ASP D	62	53.982	63.078	37.414	1.00	185.73
	5068	O	ASP D	62	53.979	63.353	38.606	1.00	185.73
	5069	N	SER D	63	54.106	61.837	36.960	1.00	159.27
35	5070	CA	SER D	63	54.292	60.711	37.864	1.00	159.27
	5071	CB	SER D	63	54.380	59.390	37.086	1.00	168.15
	5072	OG	SER D	63	53.226	59.160	36.318	1.00	168.15
	5073	C	SER D	63	55.608	60.949	38.595	1.00	159.27
	5074	O	SER D	63	56.640	61.192	37.968	1.00	159.27
40	5075	N	GLY D	64	55.584	60.889	39.918	1.00	167.46
	5076	CA	GLY D	64	56.818	61.106	40.647	1.00	167.46
	5077	C	GLY D	64	56.687	61.299	42.144	1.00	167.46
	5078	O	GLY D	64	55.643	61.035	42.741	1.00	167.46
	5079	N	GLU D	65	57.772	61.788	42.737	1.00	249.05
45	5080	CA	GLU D	65	57.882	62.037	44.170	1.00	249.05
	5081	CB	GLU D	65	59.223	61.476	44.640	1.00	248.88
	5082	CG	GLU D	65	59.604	61.791	46.061	1.00	248.88
	5083	CD	GLU D	65	61.083	61.571	46.298	1.00	248.88
	5084	OE1	GLU D	65	61.892	62.265	45.646	1.00	248.88
50	5085	OE2	GLU D	65	61.439	60.704	47.125	1.00	248.88
	5086	C	GLU D	65	57.794	63.533	44.486	1.00	249.05
	5087	O	GLU D	65	58.598	64.318	43.989	1.00	249.05
	5088	N	TYR D	66	56.828	63.924	45.319	1.00	212.16
	5089	CA	TYR D	66	56.652	65.335	45.686	1.00	212.16
55	5090	CB	TYR D	66	55.264	65.835	45.288	1.00	195.47
	5091	CG	TYR D	66	54.953	65.854	43.813	1.00	195.47
	5092	CD1	TYR D	66	54.636	64.683	43.131	1.00	195.47
	5093	CE1	TYR D	66	54.241	64.715	41.795	1.00	195.47
	5094	CD2	TYR D	66	54.885	67.060	43.118	1.00	195.47
60	5095	CE2	TYR D	66	54.493	67.105	41.789	1.00	195.47
	5096	CZ	TYR D	66	54.169	65.932	41.131	1.00	195.47
	5097	OH	TYR D	66	53.738	65.982	39.822	1.00	195.47
	5098	C	TYR D	66	56.819	65.617	47.183	1.00	212.16
	5099	O	TYR D	66	56.894	64.694	47.993	1.00	212.16
65	5100	N	LYS D	67	56.848	66.906	47.534	1.00	190.15
	5101	CA	LYS D	67	56.984	67.355	48.926	1.00	190.15
	5102	CB	LYS D	67	58.310	66.886	49.512	1.00	181.22
	5103	CG	LYS D	67	59.513	67.251	48.669	1.00	181.22
	5104	CD	LYS D	67	60.788	66.691	49.285	1.00	181.22
70	5105	CE	LYS D	67	61.948	66.688	48.285	1.00	181.22

	5106	NZ	LYS	D	67·	63.216	66.167	48.871	1.00	181.22
	5107	C	LYS	D	67	56.878	68.876	49.119	1.00	190.15
	5108	O	LYS	D	67	57.155	69.660	48.209	1.00	190.15
	5109	N	CYS	D	68	56.473	69.282	50.320	1.00	199.06
5	5110	CA	CYS	D	68	56.346	70.695	50.654	1.00	199.06
	5111	C	CYS	D	68	57.039	71.004	51.975	1.00	199.06
	5112	O	CYS	D	68	57.153	70.155	52.861	1.00	199.06
	5113	CB	CYS	D	68	54.871	71.135	50.708	1.00	219.86
	5114	SG	CYS	D	68	53.830	70.461	52.050	1.00	219.86
10	5115	N	GLN	D	69	57.505	72.240	52.083	1.00	249.17
	5116	CA	GLN	D	69	58.212	72.728	53.257	1.00	249.17
	5117	CB	GLN	D	69	59.714	72.495	53.072	1.00	249.69
	5118	CG	GLN	D	69	60.606	73.364	53.942	1.00	249.69
	5119	CD	GLN	D	69	62.082	73.199	53.613	1.00	249.69
15	5120	OE1	GLN	D	69	62.491	73.322	52.452	1.00	249.69
	5121	NE2	GLN	D	69	62.892	72.925	54.634	1.00	249.69
	5122	C	GLN	D	69	57.925	74.222	53.407	1.00	249.17
	5123	O	GLN	D	69	57.726	74.927	52.418	1.00	249.17
	5124	N	HIS	D	70	57.896	74.706	54.642	1.00	249.69
20	5125	CA	HIS	D	70	57.642	76.122	54.874	1.00	249.69
	5126	CB	HIS	D	70	56.693	76.309	56.060	1.00	249.61
	5127	CG	HIS	D	70	55.290	75.881	55.773	1.00	249.61
	5128	CD2	HIS	D	70	54.464	75.035	56.426	1.00	249.61
	5129	ND1	HIS	D	70	54.583	76.348	54.683	1.00	249.61
25	5130	CE1	HIS	D	70	53.382	75.805	54.680	1.00	249.61
	5131	NE2	HIS	D	70	53.280	75.003	55.727	1.00	249.61
	5132	C	HIS	D	70	58.936	76.887	55.115	1.00	249.69
	5133	O	HIS	D	70	60.031	76.352	54.920	1.00	249.69
	5134	N	GLN	D	71	58.803	78.140	55.540	1.00	249.69
30	5135	CA	GLN	D	71	59.955	79.008	55.802	1.00	249.69
	5136	CB	GLN	D	71	59.459	80.374	56.307	1.00	249.69
	5137	CG	GLN	D	71	60.461	81.539	56.197	1.00	249.69
	5138	CD	GLN	D	71	60.863	81.861	54.754	1.00	249.69
	5139	OE1	GLN	D	71	60.016	81.976	53.858	1.00	249.69
35	5140	NE2	GLN	D	71	62.163	82.021	54.530	1.00	249.69
	5141	C	GLN	D	71	60.929	78.392	56.816	1.00	249.69
	5142	O	GLN	D	71	62.143	78.352	56.581	1.00	249.69
	5143	N	GLN	D	72	60.389	77.905	57.932	1.00	249.69
	5144	CA	GLN	D	72	61.203	77.301	58.984	1.00	249.69
40	5145	CB	GLN	D	72	61.267	78.257	60.181	1.00	247.95
	5146	CG	GLN	D	72	62.117	77.792	61.354	1.00	247.95
	5147	CD	GLN	D	72	61.994	78.719	62.551	1.00	247.95
	5148	OE1	GLN	D	72	62.253	79.917	62.449	1.00	247.95
	5149	NE2	GLN	D	72	61.591	78.168	63.693	1.00	247.95
45	5150	C	GLN	D	72	60.624	75.947	59.409	1.00	249.69
	5151	O	GLN	D	72	60.335	75.721	60.584	1.00	249.69
	5152	N	VAL	D	73	60.449	75.052	58.443	1.00	248.81
	5153	CA	VAL	D	73	59.911	73.726	58.720	1.00	248.81
	5154	CB	VAL	D	73	58.396	73.640	58.398	1.00	224.12
50	5155	CG1	VAL	D	73	57.822	72.365	58.991	1.00	224.12
	5156	CG2	VAL	D	73	57.664	74.863	58.936	1.00	224.12
	5157	C	VAL	D	73	60.641	72.704	57.858	1.00	248.81
	5158	O	VAL	D	73	60.991	72.985	56.717	1.00	248.81
	5159	N	ASN	D	74	60.869	71.519	58.404	1.00	237.91
55	5160	CA	ASN	D	74	61.552	70.475	57.660	1.00	237.91
	5161	CB	ASN	D	74	62.098	69.419	58.631	1.00	218.21
	5162	CG	ASN	D	74	63.003	70.022	59.699	1.00	218.21
	5163	OD1	ASN	D	74	63.818	70.893	59.398	1.00	218.21
	5164	ND2	ASN	D	74	62.865	69.553	60.940	1.00	218.21
60	5165	C	ASN	D	74	60.595	69.846	56.635	1.00	237.91
	5166	O	ASN	D	74	59.477	69.450	56.973	1.00	237.91
	5167	N	GLU	D	75	61.042	69.772	55.381	1.00	249.69
	5168	CA	GLU	D	75	60.252	69.219	54.276	1.00	249.69
	5169	CB	GLU	D	75	61.161	68.971	53.065	1.00	244.63
65	5170	CG	GLU	D	75	62.563	68.479	53.417	1.00	244.63
	5171	CD	GLU	D	75	63.503	68.477	52.223	1.00	244.63
	5172	OE1	GLU	D	75	63.579	69.508	51.523	1.00	244.63
	5173	OE2	GLU	D	75	64.172	67.448	51.989	1.00	244.63
	5174	C	GLU	D	75	59.463	67.954	54.609	1.00	249.69
70	5175	O	GLU	D	75	59.947	67.066	55.313	1.00	249.69

	5176	N	SER D	76	58.244	67.886	54.080	1.00	245.54
	5177	CA	SER D	76	57.338	66.759	54.313	1.00	245.54
	5178	CB	SER D	76	55.952	67.070	53.739	1.00	192.35
	5179	OG	SER D	76	55.961	66.977	52.328	1.00	192.35
5	5180	C	SER D	76	57.811	65.437	53.721	1.00	245.54
	5181	O	SER D	76	58.617	65.413	52.791	1.00	245.54
	5182	N	GLU D	77	57.289	64.340	54.268	1.00	239.60
	5183	CA	GLU D	77	57.628	63.013	53.788	1.00	239.60
	5184	CB	GLU D	77	56.972	61.938	54.663	1.00	249.69
10	5185	CG	GLU D	77	57.497	61.895	56.089	1.00	249.69
	5186	CD	GLU D	77	58.969	61.533	56.157	1.00	249.69
	5187	OE1	GLU D	77	59.621	61.453	55.090	1.00	249.69
	5188	OE2	GLU D	77	59.476	61.333	57.282	1.00	249.69
	5189	C	GLU D	77	57.106	62.902	52.366	1.00	239.60
15	5190	O	GLU D	77	55.898	62.905	52.139	1.00	239.60
	5191	N	PRO D	78	58.019	62.800	51.386	1.00	190.36
	5192	CD	PRO D	78	59.457	62.543	51.572	1.00	231.46
	5193	CA	PRO D	78	57.642	62.695	49.969	1.00	190.36
	5194	CB	PRO D	78	58.919	62.159	49.320	1.00	231.46
20	5195	CG	PRO D	78	60.002	62.732	50.179	1.00	231.46
	5196	C	PRO D	78	56.456	61.764	49.731	1.00	190.36
	5197	O	PRO D	78	56.163	60.897	50.553	1.00	190.36
	5198	N	VAL D	79	55.760	61.969	48.620	1.00	182.77
	5199	CA	VAL D	79	54.639	61.112	48.261	1.00	182.77
25	5200	CB	VAL D	79	53.272	61.804	48.426	1.00	114.23
	5201	CG1	VAL D	79	52.173	60.961	47.770	1.00	114.23
	5202	CG2	VAL D	79	52.957	61.977	49.909	1.00	114.23
	5203	C	VAL D	79	54.845	60.799	46.800	1.00	182.77
	5204	O	VAL D	79	55.292	61.663	46.043	1.00	182.77
30	5205	N	TYR D	80	54.538	59.570	46.397	1.00	172.05
	5206	CA	TYR D	80	54.726	59.204	45.004	1.00	172.05
	5207	CB	TYR D	80	55.475	57.870	44.888	1.00	249.30
	5208	CG	TYR D	80	56.087	57.651	43.518	1.00	249.30
	5209	CD1	TYR D	80	57.327	58.197	43.191	1.00	249.30
35	5210	CE1	TYR D	80	57.868	58.042	41.917	1.00	249.30
	5211	CD2	TYR D	80	55.403	56.940	42.531	1.00	249.30
	5212	CE2	TYR D	80	55.937	56.780	41.254	1.00	249.30
	5213	CZ	TYR D	80	57.167	57.335	40.956	1.00	249.30
	5214	OH	TYR D	80	57.689	57.191	39.696	1.00	249.30
40	5215	C	TYR D	80	53.407	59.120	44.238	1.00	172.05
	5216	O	TYR D	80	52.419	58.550	44.701	1.00	172.05
	5217	N	LEU D	81	53.407	59.702	43.054	1.00	138.80
	5218	CA	LEU D	81	52.239	59.681	42.207	1.00	138.80
	5219	CB	LEU D	81	51.837	61.099	41.821	1.00	163.84
45	5220	CG	LEU D	81	50.683	61.126	40.812	1.00	163.84
	5221	CD1	LEU D	81	49.462	60.512	41.463	1.00	163.84
	5222	CD2	LEU D	81	50.394	62.539	40.357	1.00	163.84
	5223	C	LEU D	81	52.560	58.907	40.932	1.00	138.80
	5224	O	LEU D	81	53.554	59.196	40.251	1.00	138.80
50	5225	N	GLU D	82	51.728	57.924	40.598	1.00	140.95
	5226	CA	GLU D	82	51.964	57.149	39.380	1.00	140.95
	5227	CB	GLU D	82	52.148	55.662	39.716	1.00	249.69
	5228	CG	GLU D	82	52.985	54.915	38.685	1.00	249.69
	5229	CD	GLU D	82	53.177	53.447	39.028	1.00	249.69
55	5230	OE1	GLU D	82	53.282	53.118	40.233	1.00	249.69
	5231	OE2	GLU D	82	53.238	52.623	38.088	1.00	249.69
	5232	C	GLU D	82	50.798	57.324	38.415	1.00	140.95
	5233	O	GLU D	82	49.629	57.287	38.824	1.00	140.95
	5234	N	VAL D	83	51.121	57.533	37.139	1.00	204.94
60	5235	CA	VAL D	83	50.098	57.704	36.106	1.00	204.94
	5236	CB	VAL D	83	50.307	58.985	35.282	1.00	154.41
	5237	CG1	VAL D	83	49.194	59.119	34.248	1.00	154.41
	5238	CG2	VAL D	83	50.333	60.203	36.207	1.00	154.41
	5239	C	VAL D	83	50.072	56.510	35.159	1.00	204.94
65	5240	O	VAL D	83	51.125	55.962	34.781	1.00	204.94
	5241	N	PHE D	84	48.858	56.137	34.755	1.00	140.70
	5242	CA	PHE D	84	48.655	54.961	33.916	1.00	140.70
	5243	CB	PHE D	84	48.013	53.843	34.738	1.00	172.63
	5244	CG	PHE D	84	48.828	53.387	35.905	1.00	172.63
70	5245	CD1	PHE D	84	48.823	54.095	37.102	1.00	172.63

	5246	CD2	PHE	D	84	49.579	52.229	35.815	1.00	172.63
	5247	CE1	PHE	D	84	49.553	53.648	38.187	1.00	172.63
	5248	CE2	PHE	D	84	50.310	51.776	36.892	1.00	172.63
	5249	CZ	PHE	D	84	50.298	52.483	38.084	1.00	172.63
5	5250	C	PHE	D	84	47.811	55.075	32.669	1.00	140.70
	5251	O	PHE	D	84	46.952	55.941	32.546	1.00	140.70
	5252	N	SER	D	85	48.057	54.127	31.773	1.00	187.78
	5253	CA	SER	D	85	47.318	53.999	30.534	1.00	187.78
	5254	CB	SER	D	85	48.163	54.364	29.322	1.00	228.86
10	5255	OG	SER	D	85	47.394	54.223	28.141	1.00	228.86
	5256	C	SER	D	85	46.957	52.522	30.461	1.00	187.78
	5257	O	SER	D	85	47.841	51.663	30.344	1.00	187.78
	5258	N	ASP	D	86	45.657	52.235	30.551	1.00	145.83
	5259	CA	ASP	D	86	45.141	50.864	30.508	1.00	145.83
15	5260	CB	ASP	D	86	45.692	50.069	31.690	1.00	155.62
	5261	CG	ASP	D	86	45.997	48.650	31.328	1.00	155.62
	5262	OD1	ASP	D	86	45.107	47.971	30.755	1.00	155.62
	5263	OD2	ASP	D	86	47.133	48.214	31.610	1.00	155.62
	5264	C	ASP	D	86	43.621	50.885	30.580	1.00	145.83
20	5265	O	ASP	D	86	43.019	51.914	30.878	1.00	145.83
	5266	N	TRP	D	87	42.997	49.749	30.315	1.00	152.62
	5267	CA	TRP	D	87	41.544	49.688	30.387	1.00	152.62
	5268	CB	TRP	D	87	41.038	48.369	29.817	1.00	249.69
	5269	CG	TRP	D	87	40.784	48.449	28.349	1.00	249.69
25	5270	CD2	TRP	D	87	41.700	48.112	27.306	1.00	249.69
	5271	CE2	TRP	D	87	41.058	48.385	26.079	1.00	249.69
	5272	CE3	TRP	D	87	43.010	47.599	27.285	1.00	249.69
	5273	CD1	TRP	D	87	39.649	48.907	27.735	1.00	249.69
	5274	NE1	TRP	D	87	39.807	48.868	26.373	1.00	249.69
30	5275	CZ2	TRP	D	87	41.674	48.164	24.845	1.00	249.69
	5276	CZ3	TRP	D	87	43.623	47.377	26.056	1.00	249.69
	5277	CH2	TRP	D	87	42.955	47.666	24.854	1.00	249.69
	5278	C	TRP	D	87	41.058	49.854	31.821	1.00	152.62
	5279	O	TRP	D	87	40.220	50.708	32.092	1.00	152.62
35	5280	N	LEU	D	88	41.578	49.041	32.739	1.00	136.73
	5281	CA	LEU	D	88	41.190	49.161	34.137	1.00	136.73
	5282	CB	LEU	D	88	40.415	47.933	34.574	1.00	120.19
	5283	CG	LEU	D	88	39.068	47.722	33.876	1.00	120.19
	5284	CD1	LEU	D	88	38.314	46.521	34.481	1.00	120.19
40	5285	CD2	LEU	D	88	38.232	48.972	34.012	1.00	136.73
	5286	C	LEU	D	88	42.405	49.364	35.043	1.00	136.73
	5287	O	LEU	D	88	43.486	48.794	34.806	1.00	129.46
	5288	N	LEU	D	89	42.238	50.206	36.063	1.00	129.46
	5289	CA	LEU	D	89	43.315	50.483	37.021	1.00	166.27
45	5290	CB	LEU	D	89	43.867	51.888	36.838	1.00	166.27
	5291	CG	LEU	D	89	44.935	52.257	37.864	1.00	166.27
	5292	CD1	LEU	D	89	46.034	51.209	37.875	1.00	166.27
	5293	CD2	LEU	D	89	45.502	53.621	37.532	1.00	129.46
	5294	C	LEU	D	89	42.751	50.361	38.425	1.00	129.46
50	5295	O	LEU	D	89	41.706	50.925	38.731	1.00	149.29
	5296	N	LEU	D	90	43.435	49.611	39.278	1.00	149.29
	5297	CA	LEU	D	90	42.966	49.415	40.640	1.00	119.67
	5298	CB	LEU	D	90	43.433	48.070	41.171	1.00	119.67
	5299	CG	LEU	D	90	43.122	47.859	42.640	1.00	119.67
55	5300	CD1	LEU	D	90	41.612	47.911	42.843	1.00	119.67
	5301	CD2	LEU	D	90	43.003	46.531	43.108	1.00	149.29
	5302	C	LEU	D	90	43.486	50.508	41.543	1.00	149.29
	5303	O	LEU	D	90	44.695	50.591	41.785	1.00	104.53
	5304	N	GLN	D	91	42.577	51.336	42.059	1.00	104.53
60	5305	CA	GLN	D	91	42.981	52.439	42.946	1.00	160.34
	5306	CB	GLN	D	91	42.241	53.716	42.566	1.00	160.34
	5307	CG	GLN	D	91	42.495	54.188	41.147	1.00	160.34
	5308	CD	GLN	D	91	41.751	55.470	40.843	1.00	160.34
	5309	OE1	GLN	D	91	40.527	55.541	40.995	1.00	160.34
65	5310	NE2	GLN	D	91	42.485	56.493	40.412	1.00	104.53
	5311	C	GLN	D	91	42.756	52.156	44.424	1.00	104.53
	5312	O	GLN	D	91	41.691	51.645	44.823	1.00	107.84
	5313	N	ALA	D	92	43.762	52.506	45.227	1.00	107.84
	5314	CA	ALA	D	92	43.673	52.285	46.657	1.00	189.20
70	5315	CB	ALA	D	92	44.731	51.297	47.102	1.00	

	5316	C	ALA	D	92	43.850	53.594	47.399	1.00	107.84
	5317	O	ALA	D	92	44.683	54.436	46.987	1.00	107.84
	5318	N	SER	D	93	43.062	53.754	48.477	1.00	115.75
	5319	CA	SER	D	93	43.108	54.947	49.319	1.00	115.75
5	5320	CB	SER	D	93	42.212	54.756	50.553	1.00	115.29
	5321	OG	SER	D	93	42.503	53.560	51.271	1.00	115.29
	5322	C	SER	D	93	44.559	55.177	49.730	1.00	115.75
	5323	O	SER	D	93	45.176	56.193	49.371	1.00	115.75
	5324	N	ALA	D	94	45.094	54.214	50.476	1.00	146.78
10	5325	CA	ALA	D	94	46.481	54.242	50.924	1.00	146.78
	5326	CB	ALA	D	94	46.552	54.536	52.412	1.00	207.94
	5327	C	ALA	D	94	46.992	52.846	50.626	1.00	146.78
	5328	O	ALA	D	94	46.194	51.905	50.566	1.00	146.78
	5329	N	GLU	D	95	48.300	52.699	50.426	1.00	134.86
15	5330	CA	GLU	D	95	48.844	51.383	50.125	1.00	134.86
	5331	CB	GLU	D	95	49.967	51.498	49.101	1.00	220.03
	5332	CG	GLU	D	95	49.489	52.026	47.768	1.00	220.03
	5333	CD	GLU	D	95	50.535	51.898	46.687	1.00	220.03
	5334	OE1	GLU	D	95	50.271	52.341	45.547	1.00	220.03
20	5335	OE2	GLU	D	95	51.621	51.351	46.970	1.00	220.03
	5336	C	GLU	D	95	49.335	50.662	51.376	1.00	134.86
	5337	O	GLU	D	95	49.412	49.423	51.408	1.00	134.86
	5338	N	VAL	D	96	49.655	51.439	52.407	1.00	128.32
	5339	CA	VAL	D	96	50.122	50.876	53.668	1.00	128.32
25	5340	CB	VAL	D	96	51.561	51.292	53.949	1.00	128.30
	5341	CG1	VAL	D	96	52.157	50.377	55.003	1.00	128.30
	5342	CG2	VAL	D	96	52.372	51.260	52.675	1.00	128.30
	5343	C	VAL	D	96	49.242	51.383	54.816	1.00	128.32
	5344	O	VAL	D	96	49.010	52.588	54.932	1.00	128.32
30	5345	N	VAL	D	97	48.775	50.480	55.678	1.00	152.31
	5346	CA	VAL	D	97	47.890	50.898	56.756	1.00	152.31
	5347	CB	VAL	D	97	46.438	50.575	56.406	1.00	113.44
	5348	CG1	VAL	D	97	45.533	51.442	57.216	1.00	113.44
	5349	CG2	VAL	D	97	46.185	50.774	54.941	1.00	113.44
35	5350	C	VAL	D	97	48.135	50.330	58.152	1.00	152.31
	5351	O	VAL	D	97	48.616	49.193	58.305	1.00	152.31
	5352	N	MET	D	98	47.765	51.133	59.160	1.00	133.53
	5353	CA	MET	D	98	47.880	50.784	60.590	1.00	133.53
	5354	CB	MET	D	98	47.836	52.058	61.440	1.00	228.89
40	5355	CG	MET	D	98	49.145	52.951	61.220	1.00	228.89
	5356	SD	MET	D	98	50.627	52.296	62.005	1.00	228.89
	5357	CE	MET	D	98	50.300	52.679	63.720	1.00	228.89
	5358	C	MET	D	98	46.651	49.985	61.010	1.00	133.53
	5359	O	MET	D	98	45.535	50.470	60.868	1.00	133.53
45	5360	N	GLU	D	99	46.849	48.786	61.547	1.00	198.14
	5361	CA	GLU	D	99	45.726	47.954	61.963	1.00	198.14
	5362	CB	GLU	D	99	46.179	46.922	63.001	1.00	249.68
	5363	CG	GLU	D	99	45.303	45.675	63.049	1.00	249.68
	5364	CD	GLU	D	99	45.586	44.809	64.259	1.00	249.68
50	5365	OE1	GLU	D	99	46.770	44.698	64.645	1.00	249.68
	5366	OE2	GLU	D	99	44.627	44.233	64.816	1.00	249.68
	5367	C	GLU	D	99	44.614	48.812	62.563	1.00	198.14
	5368	O	GLU	D	99	44.852	49.583	63.489	1.00	198.14
	5369	N	GLY	D	100	43.402	48.692	62.031	1.00	166.74
55	5370	CA	GLY	D	100	42.296	49.467	62.569	1.00	166.74
	5371	C	GLY	D	100	41.812	50.625	61.718	1.00	166.74
	5372	O	GLY	D	100	40.670	51.053	61.861	1.00	166.74
	5373	N	GLN	D	101	42.669	51.133	60.842	1.00	134.36
	5374	CA	GLN	D	101	42.317	52.250	59.961	1.00	134.36
60	5375	CB	GLN	D	101	43.571	52.882	59.372	1.00	207.44
	5376	CG	GLN	D	101	44.392	53.630	60.387	1.00	207.44
	5377	CD	GLN	D	101	43.524	54.494	61.269	1.00	207.44
	5378	OE1	GLN	D	101	42.774	53.987	62.103	1.00	207.44
	5379	NE2	GLN	D	101	43.607	55.807	61.083	1.00	207.44
65	5380	C	GLN	D	101	41.345	51.862	58.841	1.00	134.36
	5381	O	GLN	D	101	41.004	50.693	58.670	1.00	134.36
	5382	N	PRO	D	102	40.894	52.871	58.051	1.00	115.73
	5383	CD	PRO	D	102	40.996	54.307	58.285	1.00	176.17
	5384	CA	PRO	D	102	39.973	52.569	56.946	1.00	115.73
70	5385	CB	PRO	D	102	39.138	53.843	56.890	1.00	176.17

	5386	CG	PRO	D	102	40.181	54.884	57.136	1.00	176.17
	5387	C	PRO	D	102	40.678	52.280	55.630	1.00	115.73
	5388	O	PRO	D	102	41.771	52.810	55.342	1.00	115.73
	5389	N	LEU	D	103	40.042	51.439	54.818	1.00	118.65
5	5390	CA	LEU	D	103	40.610	51.062	53.547	1.00	118.65
	5391	CB	LEU	D	103	41.185	49.671	53.652	1.00	120.76
	5392	CG	LEU	D	103	42.003	49.394	52.400	1.00	120.76
	5393	CD1	LEU	D	103	43.228	50.310	52.430	1.00	120.76
	5394	CD2	LEU	D	103	42.399	47.938	52.323	1.00	120.76
10	5395	C	LEU	D	103	39.597	51.065	52.413	1.00	118.65
	5396	O	LEU	D	103	38.575	50.389	52.508	1.00	118.65
	5397	N	PHE	D	104	39.875	51.798	51.332	1.00	129.85
	5398	CA	PHE	D	104	38.955	51.830	50.187	1.00	129.85
	5399	CB	PHE	D	104	38.327	53.199	50.024	1.00	234.23
15	5400	CG	PHE	D	104	37.655	53.699	51.249	1.00	234.23
	5401	CD1	PHE	D	104	38.402	54.218	52.300	1.00	234.23
	5402	CD2	PHE	D	104	36.273	53.651	51.365	1.00	234.23
	5403	CE1	PHE	D	104	37.779	54.688	53.457	1.00	234.23
	5404	CE2	PHE	D	104	35.638	54.116	52.517	1.00	234.23
20	5405	CZ	PHE	D	104	36.393	54.637	53.567	1.00	234.23
	5406	C	PHE	D	104	39.651	51.480	48.881	1.00	129.85
	5407	O	PHE	D	104	40.632	52.139	48.499	1.00	129.85
	5408	N	LEU	D	105	39.152	50.446	48.198	1.00	126.08
	5409	CA	LEU	D	105	39.725	50.039	46.914	1.00	126.08
25	5410	CB	LEU	D	105	40.031	48.548	46.910	1.00	130.08
	5411	CG	LEU	D	105	41.013	48.106	47.993	1.00	130.08
	5412	CD1	LEU	D	105	41.358	46.640	47.803	1.00	130.08
	5413	CD2	LEU	D	105	42.266	48.976	47.919	1.00	130.08
	5414	C	LEU	D	105	38.719	50.360	45.832	1.00	126.08
30	5415	O	LEU	D	105	37.510	50.328	46.061	1.00	126.08
	5416	N	ARG	D	106	39.203	50.658	44.641	1.00	133.86
	5417	CA	ARG	D	106	38.288	51.013	43.581	1.00	133.86
	5418	CB	ARG	D	106	38.213	52.537	43.522	1.00	170.25
	5419	CG	ARG	D	106	37.267	53.090	42.509	1.00	170.25
35	5420	CD	ARG	D	106	37.416	54.594	42.401	1.00	170.25
	5421	NE	ARG	D	106	36.634	55.086	41.272	1.00	170.25
	5422	CZ	ARG	D	106	36.946	56.155	40.553	1.00	170.25
	5423	NH1	ARG	D	106	38.031	56.855	40.841	1.00	170.25
	5424	NH2	ARG	D	106	36.181	56.503	39.529	1.00	170.25
40	5425	C	ARG	D	106	38.732	50.439	42.239	1.00	133.86
	5426	O	ARG	D	106	39.882	50.624	41.824	1.00	133.86
	5427	N	CYS	D	107	37.833	49.718	41.572	1.00	163.35
	5428	CA	CYS	D	107	38.144	49.158	40.256	1.00	163.35
	5429	C	CYS	D	107	37.800	50.290	39.316	1.00	163.35
45	5430	O	CYS	D	107	36.621	50.528	39.043	1.00	163.35
	5431	CB	CYS	D	107	37.250	47.960	39.954	1.00	164.16
	5432	SG	CYS	D	107	37.777	46.984	38.529	1.00	164.16
	5433	N	HIS	D	108	38.824	50.991	38.834	1.00	196.08
	5434	CA	HIS	D	108	38.626	52.153	37.962	1.00	196.08
50	5435	CB	HIS	D	108	39.641	53.252	38.313	1.00	199.66
	5436	CG	HIS	D	108	39.354	54.579	37.678	1.00	199.66
	5437	CD2	HIS	D	108	40.151	55.424	36.978	1.00	199.66
	5438	ND1	HIS	D	108	38.135	55.214	37.796	1.00	199.66
	5439	CE1	HIS	D	108	38.197	56.390	37.202	1.00	199.66
55	5440	NE2	HIS	D	108	39.411	56.543	36.699	1.00	199.66
	5441	C	HIS	D	108	38.691	51.885	36.473	1.00	196.08
	5442	O	HIS	D	108	39.670	51.330	35.965	1.00	196.08
	5443	N	GLY	D	109	37.636	52.310	35.785	1.00	171.21
	5444	CA	GLY	D	109	37.566	52.139	34.354	1.00	171.21
60	5445	C	GLY	D	109	38.291	53.283	33.690	1.00	171.21
	5446	O	GLY	D	109	38.608	54.272	34.344	1.00	171.21
	5447	N	TRP	D	110	38.566	53.141	32.395	1.00	191.90
	5448	CA	TRP	D	110	39.258	54.181	31.637	1.00	191.90
	5449	CB	TRP	D	110	40.029	53.562	30.453	1.00	203.94
65	5450	CG	TRP	D	110	40.592	54.575	29.502	1.00	203.94
	5451	CD2	TRP	D	110	41.946	55.053	29.444	1.00	203.94
	5452	CE2	TRP	D	110	41.995	56.035	28.434	1.00	203.94
	5453	CE3	TRP	D	110	43.117	54.754	30.151	1.00	203.94
	5454	CD1	TRP	D	110	39.904	55.256	28.549	1.00	203.94
70	5455	NE1	TRP	D	110	40.740	56.136	27.907	1.00	203.94

	5456	CZ2	TRP	D	110	43.173	56.718	28.110	1.00	203.94
	5457	CZ3	TRP	D	110	44.291	55.439	29.823	1.00	203.94
	5458	CH2	TRP	D	110	44.305	56.406	28.809	1.00	203.94
	5459	C	TRP	D	110	38.245	55.224	31.155	1.00	191.80
5	5460	O	TRP	D	110	37.070	54.922	30.950	1.00	191.90
	5461	N	ARG	D	111	38.715	56.454	30.987	1.00	162.83
	5462	CA	ARG	D	111	37.866	57.551	30.568	1.00	162.83
	5463	CB	ARG	D	111	37.487	57.418	29.098	1.00	249.69
	5464	CG	ARG	D	111	38.456	58.111	28.158	1.00	249.69
10	5465	CD	ARG	D	111	37.865	58.254	26.769	1.00	249.69
	5466	NE	ARG	D	111	38.203	59.544	26.175	1.00	249.69
	5467	CZ	ARG	D	111	37.865	60.717	26.705	1.00	249.69
	5468	NH1	ARG	D	111	37.178	60.769	27.840	1.00	249.69
	5469	NH2	ARG	D	111	38.209	61.844	26.098	1.00	249.69
15	5470	C	ARG	D	111	36.612	57.597	31.415	1.00	162.83
	5471	O	ARG	D	111	35.552	58.005	30.954	1.00	162.83
	5472	N	ASN	D	112	36.744	57.175	32.663	1.00	190.45
	5473	CA	ASN	D	112	35.632	57.162	33.585	1.00	190.45
	5474	CB	ASN	D	112	35.305	53.593	34.044	1.00	228.54
20	5475	CG	ASN	D	112	34.442	58.632	35.296	1.00	228.54
	5476	OD1	ASN	D	112	33.860	57.622	35.701	1.00	228.54
	5477	ND2	ASN	D	112	34.352	59.805	35.914	1.00	228.54
	5478	C	ASN	D	112	34.389	56.509	32.982	1.00	190.45
	5479	O	ASN	D	112	33.263	56.879	33.318	1.00	190.45
25	5480	N	TRP	D	113	34.582	55.549	32.078	1.00	238.93
	5481	CA	TRP	D	113	33.437	54.868	31.475	1.00	238.93
	5482	CB	TRP	D	113	33.872	53.936	30.353	1.00	249.51
	5483	CG	TRP	D	113	34.087	54.608	29.061	1.00	249.51
	5484	CD2	TRP	D	113	35.060	54.251	28.071	1.00	249.51
30	5485	CE2	TRP	D	113	34.860	55.110	26.973	1.00	249.51
	5486	CE3	TRP	D	113	36.079	53.296	28.013	1.00	249.51
	5487	CD1	TRP	D	113	33.360	55.626	28.538	1.00	249.51
	5488	NE1	TRP	D	113	33.817	55.940	27.283	1.00	249.51
	5489	CZ2	TRP	D	113	35.648	55.038	25.816	1.00	249.51
35	5490	CZ3	TRP	D	113	36.862	53.222	26.864	1.00	249.51
	5491	CH2	TRP	D	113	36.637	54.088	25.779	1.00	249.51
	5492	C	TRP	D	113	32.733	54.037	32.530	1.00	238.93
	5493	O	TRP	D	113	33.007	54.178	33.719	1.00	238.93
	5494	N	ASP	D	114	31.831	53.167	32.096	1.00	249.69
40	5495	CA	ASP	D	114	31.117	52.312	33.034	1.00	249.69
	5496	CB	ASP	D	114	29.600	52.451	32.843	1.00	249.69
	5497	CG	ASP	D	114	29.025	53.672	33.560	1.00	249.69
	5498	OD1	ASP	D	114	29.189	53.780	34.798	1.00	249.69
	5499	OD2	ASP	D	114	28.401	54.522	32.887	1.00	249.69
45	5500	C	ASP	D	114	31.538	50.845	32.895	1.00	249.69
	5501	O	ASP	D	114	31.612	50.312	31.778	1.00	198.18
	5502	N	VAL	D	115	31.825	50.203	34.032	1.00	198.18
	5503	CA	VAL	D	115	32.232	48.800	34.043	1.00	157.60
	5504	CB	VAL	D	115	33.535	48.596	34.828	1.00	157.60
50	5505	CG1	VAL	D	115	34.102	47.220	34.521	1.00	157.60
	5506	CG2	VAL	D	115	34.539	49.673	34.470	1.00	198.18
	5507	C	VAL	D	115	31.149	47.938	34.683	1.00	198.18
	5508	O	VAL	D	115	30.530	48.329	35.681	1.00	134.91
	5509	N	TYR	D	116	30.933	46.764	34.099	1.00	134.91
55	5510	CA	TYR	D	116	29.922	45.824	34.578	1.00	249.45
	5511	CB	TYR	D	116	28.849	45.620	33.503	1.00	249.45
	5512	CG	TYR	D	116	28.064	46.874	33.197	1.00	249.45
	5513	CD1	TYR	D	116	28.381	47.679	32.099	1.00	249.45
	5514	CE1	TYR	D	116	27.673	48.861	31.844	1.00	249.45
60	5515	CD2	TYR	D	116	27.023	47.278	34.031	1.00	249.45
	5516	CE2	TYR	D	116	26.312	48.452	33.787	1.00	249.45
	5517	CZ	TYR	D	116	26.638	49.240	32.696	1.00	249.45
	5518	OH	TYR	D	116	25.933	50.399	32.462	1.00	134.91
	5519	C	TYR	D	116	30.536	44.468	34.960	1.00	134.91
65	5520	O	TYR	D	116	31.706	44.205	34.670	1.00	179.36
	5521	N	LYS	D	117	29.739	43.615	35.611	1.00	179.36
	5522	CA	LYS	D	117	30.185	42.289	36.054	1.00	249.69
	5523	CB	LYS	D	117	30.277	41.324	34.871	1.00	249.69
	5524	CG	LYS	D	117	28.960	40.651	34.494	1.00	249.69
70	5525	CD	LYS	D	117	29.202	39.387	33.661	1.00	249.69

	5526	CE	LYS	D	117	30.074	38.376	34.424	1.00	249.69
	5527	NZ	LYS	D	117	30.356	37.108	33.677	1.00	249.69
	5528	C	LYS	D	117	31.531	42.338	36.769	1.00	179.36
	5529	O	LYS	D	117	32.463	41.608	36.425	1.00	179.36
5	5530	N	VAL	D	118	31.611	43.189	37.783	1.00	143.78
	5531	CA	VAL	D	118	32.837	43.356	38.531	1.00	143.78
	5532	CB	VAL	D	118	32.928	44.783	39.076	1.00	119.69
	5533	CG1	VAL	D	118	33.829	44.851	40.289	1.00	119.69
	5534	CG2	VAL	D	118	33.481	45.684	37.995	1.00	119.69
10	5535	C	VAL	D	118	33.071	42.366	39.664	1.00	143.78
	5536	O	VAL	D	118	32.142	41.998	40.411	1.00	143.78
	5537	N	ILE	D	119	34.341	41.948	39.775	1.00	115.37
	5538	CA	ILE	D	119	34.809	41.005	40.796	1.00	115.37
	5539	CB	ILE	D	119	34.981	39.618	40.220	1.00	109.20
15	5540	CG2	ILE	D	119	35.367	38.649	41.306	1.00	109.20
	5541	CG1	ILE	D	119	33.691	39.187	39.545	1.00	109.20
	5542	CD1	ILE	D	119	33.917	38.153	38.481	1.00	109.20
	5543	C	ILE	D	119	36.184	41.446	41.260	1.00	115.37
	5544	O	ILE	D	119	37.068	41.721	40.429	1.00	115.37
20	5545	N	TYR	D	120	36.364	41.538	42.573	1.00	120.82
	5546	CA	TYR	D	120	37.664	41.913	43.089	1.00	120.82
	5547	CB	TYR	D	120	37.537	42.814	44.308	1.00	123.48
	5548	CG	TYR	D	120	37.016	44.181	44.008	1.00	123.48
	5549	CD1	TYR	D	120	35.652	44.419	43.958	1.00	123.48
25	5550	CE1	TYR	D	120	35.154	45.696	43.664	1.00	123.48
	5551	CD2	TYR	D	120	37.889	45.246	43.758	1.00	123.48
	5552	CE2	TYR	D	120	37.408	46.518	43.464	1.00	123.48
	5553	CZ	TYR	D	120	36.036	46.742	43.419	1.00	123.48
	5554	OH	TYR	D	120	35.552	48.010	43.132	1.00	123.48
30	5555	C	TYR	D	120	38.340	40.613	43.500	1.00	120.82
	5556	O	TYR	D	120	37.656	39.656	43.881	1.00	120.82
	5557	N	TYR	D	121	39.672	40.567	43.420	1.00	108.96
	5558	CA	TYR	D	121	40.412	39.364	43.803	1.00	108.96
	5559	CB	TYR	D	121	41.007	38.672	42.579	1.00	127.51
35	5560	CG	TYR	D	121	40.034	38.043	41.600	1.00	127.51
	5561	CD1	TYR	D	121	39.097	38.813	40.928	1.00	127.51
	5562	CE1	TYR	D	121	38.263	38.256	39.947	1.00	127.51
	5563	CD2	TYR	D	121	40.116	36.690	41.277	1.00	127.51
	5564	CE2	TYR	D	121	39.298	36.123	40.302	1.00	127.51
40	5565	CZ	TYR	D	121	38.371	36.912	39.635	1.00	127.51
	5566	OH	TYR	D	121	37.566	36.374	38.642	1.00	127.51
	5567	C	TYR	D	121	41.557	39.682	44.755	1.00	108.96
	5568	O	TYR	D	121	42.328	40.624	44.539	1.00	108.96
	5569	N	LYS	D	122	41.666	38.885	45.807	1.00	150.86
45	5570	CA	LYS	D	122	42.741	39.060	46.762	1.00	150.86
	5571	CB	LYS	D	122	42.199	39.419	48.145	1.00	185.53
	5572	CG	LYS	D	122	43.292	39.629	49.176	1.00	185.53
	5573	CD	LYS	D	122	42.724	39.656	50.576	1.00	185.53
	5574	CE	LYS	D	122	43.826	39.686	51.615	1.00	185.53
50	5575	NZ	LYS	D	122	43.245	39.553	52.970	1.00	185.53
	5576	C	LYS	D	122	43.496	37.738	46.834	1.00	150.86
	5577	O	LYS	D	122	42.928	36.707	47.210	1.00	150.86
	5578	N	ASP	D	123	44.771	37.771	46.463	1.00	129.20
	5579	CA	ASP	D	123	45.601	36.577	46.485	1.00	129.20
55	5580	CB	ASP	D	123	45.857	36.104	47.924	1.00	160.45
	5581	CG	ASP	D	123	46.852	36.986	48.661	1.00	160.45
	5582	OD1	ASP	D	123	47.927	37.268	48.096	1.00	160.45
	5583	OD2	ASP	D	123	46.572	37.390	49.808	1.00	160.45
	5584	C	ASP	D	123	44.999	35.441	45.687	1.00	129.20
60	5585	O	ASP	D	123	44.855	34.331	46.205	1.00	129.20
	5586	N	GLY	D	124	44.643	35.729	44.434	1.00	131.93
	5587	CA	GLY	D	124	44.085	34.715	43.547	1.00	131.93
	5588	C	GLY	D	124	42.682	34.206	43.837	1.00	131.93
	5589	O	GLY	D	124	42.137	33.416	43.058	1.00	141.53
65	5590	N	GLU	D	125	42.093	34.656	44.942	1.00	141.53
	5591	CA	GLU	D	125	40.751	34.229	45.321	1.00	249.69
	5592	CB	GLU	D	125	40.682	34.033	46.840	1.00	249.69
	5593	CG	GLU	D	125	41.469	32.842	47.372	1.00	249.69
	5594	CD	GLU	D	125	40.788	31.512	47.074	1.00	249.69
70	5595	OE1	GLU	D	125	39.664	31.297	47.571	1.00	249.69

	5596	OE2	GLU	D	125	41.373	30.682	46.346	1.00	249.69
	5597	C	GLU	D	125	39.673	35.224	44.897	1.00	141.53
	5598	O	GLU	D	125	39.903	36.441	44.907	1.00	141.53
	5599	N	ALA	D	126	38.503	34.707	44.520	1.00	148.59
5	5600	CA	ALA	D	126	37.393	35.570	44.136	1.00	148.59
	5601	CB	ALA	D	126	36.274	34.743	43.560	1.00	144.26
	5602	C	ALA	D	126	36.961	36.205	45.453	1.00	148.59
	5603	O	ALA	D	126	36.909	35.516	46.481	1.00	148.59
	5604	N	LEU	D	127	36.652	37.501	45.448	1.00	169.46
10	5605	CA	LEU	D	127	36.274	38.153	46.700	1.00	169.46
	5606	CB	LEU	D	127	37.294	39.224	47.040	1.00	146.34
	5607	CG	LEU	D	127	37.368	39.389	48.547	1.00	146.34
	5608	CD1	LEU	D	127	37.671	38.030	49.183	1.00	146.34
	5609	CD2	LEU	D	127	38.440	40.394	48.897	1.00	146.34
15	5610	C	LEU	D	127	34.880	38.750	46.796	1.00	169.46
	5611	O	LEU	D	127	34.081	38.350	47.640	1.00	169.46
	5612	N	LYS	D	128	34.609	39.738	45.957	1.00	129.34
	5613	CA	LYS	D	128	33.302	40.371	45.930	1.00	129.34
	5614	CB	LYS	D	128	33.390	41.784	46.505	1.00	216.92
20	5615	CG	LYS	D	128	33.863	41.849	47.952	1.00	216.92
	5616	CD	LYS	D	128	32.806	41.345	48.935	1.00	216.92
	5617	CE	LYS	D	128	33.279	41.519	50.376	1.00	216.92
	5618	NZ	LYS	D	128	32.194	41.270	51.366	1.00	216.92
	5619	C	LYS	D	128	32.834	40.419	44.475	1.00	129.34
25	5620	O	LYS	D	128	33.645	40.314	43.556	1.00	129.34
	5621	N	TYR	D	129	31.532	40.581	44.261	1.00	159.52
	5622	CA	TYR	D	129	31.000	40.642	42.907	1.00	159.52
	5623	CB	TYR	D	129	30.682	39.239	42.432	1.00	146.13
	5624	CG	TYR	D	129	29.763	39.234	41.246	1.00	146.13
30	5625	CD1	TYR	D	129	30.255	39.420	39.958	1.00	146.13
	5626	CE1	TYR	D	129	29.395	39.478	38.859	1.00	146.13
	5627	CD2	TYR	D	129	28.380	39.103	41.419	1.00	146.13
	5628	CE2	TYR	D	129	27.507	39.162	40.337	1.00	146.13
	5629	CZ	TYR	D	129	28.021	39.350	39.055	1.00	146.13
35	5630	OH	TYR	D	129	27.158	39.406	37.976	1.00	146.13
	5631	C	TYR	D	129	29.747	41.516	42.767	1.00	159.52
	5632	O	TYR	D	129	28.858	41.489	43.622	1.00	159.52
	5633	N	TRP	D	130	29.676	42.283	41.678	1.00	181.39
	5634	CA	TRP	D	130	28.519	43.144	41.418	1.00	181.39
40	5635	CB	TRP	D	130	28.703	44.540	42.021	1.00	248.73
	5636	CG	TRP	D	130	29.193	44.604	43.436	1.00	248.73
	5637	CD2	TRP	D	130	28.426	44.935	44.598	1.00	248.73
	5638	CE2	TRP	D	130	29.302	44.930	45.703	1.00	248.73
	5639	CE3	TRP	D	130	27.074	45.246	44.816	1.00	248.73
45	5640	CD1	TRP	D	130	30.471	44.405	43.872	1.00	248.73
	5641	NE1	TRP	D	130	30.551	44.606	45.229	1.00	248.73
	5642	CZ2	TRP	D	130	28.883	45.219	47.005	1.00	248.73
	5643	CZ3	TRP	D	130	26.651	45.532	46.116	1.00	248.73
	5644	CH2	TRP	D	130	27.555	45.511	47.192	1.00	248.73
50	5645	C	TRP	D	130	28.281	43.326	39.916	1.00	181.39
	5646	O	TRP	D	130	29.126	42.952	39.090	1.00	181.39
	5647	N	TYR	D	131	27.129	43.907	39.576	1.00	195.20
	5648	CA	TYR	D	131	26.776	44.183	38.185	1.00	195.20
	5649	CB	TYR	D	131	25.263	44.162	38.020	1.00	249.67
55	5650	CG	TYR	D	131	24.831	44.143	36.579	1.00	249.67
	5651	CD1	TYR	D	131	24.974	42.992	35.806	1.00	249.67
	5652	CE1	TYR	D	131	24.612	42.979	34.465	1.00	249.67
	5653	CD2	TYR	D	131	24.311	45.285	35.973	1.00	249.67
	5654	CE2	TYR	D	131	23.949	45.285	34.632	1.00	249.67
60	5655	CZ	TYR	D	131	24.101	44.131	33.884	1.00	249.67
	5656	OH	TYR	D	131	23.751	44.140	32.553	1.00	249.67
	5657	C	TYR	D	131	27.319	45.591	37.904	1.00	195.20
	5658	O	TYR	D	131	28.458	45.746	37.468	1.00	195.20
	5659	N	GLU	D	132	26.492	46.614	38.131	1.00	246.45
65	5660	CA	GLU	D	132	26.949	47.894	37.982	1.00	246.45
	5661	CB	GLU	D	132	25.841	48.983	38.357	1.00	249.69
	5662	CG	GLU	D	132	24.774	49.219	37.292	1.00	249.69
	5663	CD	GLU	D	132	24.782	50.658	36.806	1.00	249.69
	5664	OE1	GLU	D	132	25.408	51.508	37.461	1.00	249.69
70	5665	OE2	GLU	D	132	24.106	50.945	35.777	1.00	249.69

	5666	C	GLU	D	132	27.976	47.829	39.090	1.00	246.45
	5667	O	GLU	D	132	27.639	47.527	40.210	1.00	246.45
	5668	N	ASN	D	133	29.219	48.320	38.821	1.00	125.13
	5669	CA	ASN	D	133	30.220	48.146	39.877	1.00	125.13
5	5670	CB	ASN	D	133	31.670	48.261	39.299	1.00	124.76
	5671	CG	ASN	D	133	32.189	49.671	39.168	1.00	124.76
	5672	OD1	ASN	D	133	31.488	50.569	38.725	1.00	124.76
	5673	ND2	ASN	D	133	33.462	49.855	39.512	1.00	124.76
	5674	C	ASN	D	133	30.069	48.859	41.223	1.00	125.13
10	5675	O	ASN	D	133	29.046	49.479	41.527	1.00	125.13
	5676	N	HIS	D	134	31.077	48.688	42.057	1.00	175.64
	5677	CA	HIS	D	134	31.054	49.259	43.375	1.00	175.64
	5678	CB	HIS	D	134	30.511	48.218	44.358	1.00	249.69
	5679	CG	HIS	D	134	30.264	48.759	45.738	1.00	249.69
15	5680	CD2	HIS	D	134	30.834	48.440	46.925	1.00	249.69
	5681	ND1	HIS	D	134	29.361	49.759	45.988	1.00	249.69
	5682	CE1	HIS	D	134	29.377	50.048	47.287	1.00	249.69
	5683	NE2	HIS	D	134	30.260	49.263	47.870	1.00	249.69
	5684	C	HIS	D	134	32.481	49.650	43.733	1.00	175.64
20	5685	O	HIS	D	134	33.352	49.738	42.862	1.00	175.64
	5686	N	ASN	D	135	32.714	49.878	45.020	1.00	171.27
	5687	CA	ASN	D	135	34.020	50.269	45.510	1.00	171.27
	5688	CB	ASN	D	135	34.116	51.799	45.567	1.00	249.69
	5689	CG	ASN	D	135	34.113	52.439	44.180	1.00	249.69
25	5690	OD1	ASN	D	135	34.830	51.972	43.295	1.00	249.69
	5691	ND2	ASN	D	135	33.336	53.512	43.992	1.00	249.69
	5692	C	ASN	D	135	34.237	49.660	46.894	1.00	171.27
	5693	O	ASN	D	135	34.009	50.303	47.907	1.00	171.27
	5694	N	ILE	D	136	34.670	48.405	46.916	1.00	141.21
30	5695	CA	ILE	D	136	34.953	47.636	48.143	1.00	141.21
	5696	CB	ILE	D	136	35.894	46.432	47.813	1.00	122.14
	5697	CG2	ILE	D	136	37.169	46.918	47.141	1.00	122.14
	5698	CG1	ILE	D	136	36.246	45.665	49.068	1.00	122.14
	5699	CD1	ILE	D	136	37.202	44.530	48.789	1.00	122.14
35	5700	C	ILE	D	136	35.571	48.458	49.276	1.00	141.21
	5701	O	ILE	D	136	36.769	48.809	49.257	1.00	141.21
	5702	N	SER	D	137	34.751	48.728	50.282	1.00	155.34
	5703	CA	SER	D	137	35.189	49.539	51.415	1.00	155.34
	5704	CB	SER	D	137	34.179	50.648	51.662	1.00	178.90
40	5705	OG	SER	D	137	34.452	51.311	52.884	1.00	178.90
	5706	C	SER	D	137	35.447	48.817	52.739	1.00	155.34
	5707	O	SER	D	137	34.804	47.815	53.067	1.00	155.34
	5708	N	ILE	D	138	36.378	49.372	53.509	1.00	165.15
	5709	CA	ILE	D	138	36.770	48.823	54.792	1.00	165.15
45	5710	CB	ILE	D	138	38.095	48.075	54.654	1.00	128.87
	5711	CG2	ILE	D	138	38.690	47.804	56.022	1.00	128.87
	5712	CG1	ILE	D	138	37.861	46.780	53.894	1.00	128.87
	5713	CD1	ILE	D	138	39.131	46.098	53.483	1.00	128.87
	5714	C	ILE	D	138	36.919	49.901	55.863	1.00	165.15
50	5715	O	ILE	D	138	37.703	50.849	55.720	1.00	165.15
	5716	N	THR	D	139	36.167	49.733	56.944	1.00	191.18
	5717	CA	THR	D	139	36.186	50.663	58.065	1.00	191.18
	5718	CB	THR	D	139	34.891	50.533	58.855	1.00	246.32
	5719	OG1	THR	D	139	34.694	49.160	59.210	1.00	246.32
55	5720	CG2	THR	D	139	33.713	50.988	58.006	1.00	246.32
	5721	C	THR	D	139	37.364	50.342	58.976	1.00	191.18
	5722	O	THR	D	139	38.413	50.981	58.911	1.00	191.18
	5723	N	ASN	D	140	37.173	49.343	59.827	1.00	193.50
	5724	CA	ASN	D	140	38.211	48.887	60.742	1.00	193.50
60	5725	CB	ASN	D	140	37.561	48.246	61.967	1.00	183.46
	5726	CG	ASN	D	140	38.567	47.701	62.943	1.00	183.46
	5727	OD1	ASN	D	140	39.474	46.972	62.554	1.00	183.46
	5728	ND2	ASN	D	140	38.403	48.038	64.218	1.00	183.46
	5729	C	ASN	D	140	39.022	47.849	59.960	1.00	193.50
65	5730	O	ASN	D	140	38.472	46.846	59.482	1.00	183.50
	5731	N	ALA	D	141	40.324	48.088	59.822	1.00	163.85
	5732	CA	ALA	D	141	41.190	47.179	59.061	1.00	163.85
	5733	CB	ALA	D	141	42.181	48.002	58.187	1.00	57.61
	5734	C	ALA	D	141	41.956	46.131	59.872	1.00	163.85
70	5735	O	ALA	D	141	42.669	46.446	60.823	1.00	163.85

	5736	N	THR	D	142	41.794	44.880	59.470	1.00	158.30
	5737	CA	THR	D	142	42.464	43.765	60.113	1.00	158.30
	5738	CB	THR	D	142	41.654	42.703	59.957	1.00	191.01
	5739	OG1	THR	D	142	40.299	42.703	60.352	1.00	191.01
5	5740	CG2	THR	D	142	42.248	41.370	60.813	1.00	191.01
	5741	C	THR	D	142	43.798	43.568	59.407	1.00	158.30
	5742	O	THR	D	142	43.992	44.042	58.282	1.00	158.30
	5743	N	VAL	D	143	44.723	42.867	60.052	1.00	168.28
	5744	CA	VAL	D	143	46.017	42.637	59.430	1.00	168.28
10	5745	CB	VAL	D	143	47.063	42.169	60.441	1.00	249.69
	5746	CG1	VAL	D	143	46.777	40.734	60.851	1.00	249.69
	5747	CG2	VAL	D	143	48.453	42.298	59.830	1.00	249.69
	5748	C	VAL	D	143	45.893	41.580	58.357	1.00	168.28
	5749	O	VAL	D	143	46.711	41.521	57.446	1.00	168.28
15	5750	N	GLU	D	144	44.874	40.737	58.469	1.00	197.52
	5751	CA	GLU	D	144	44.671	39.694	57.475	1.00	197.52
	5752	CB	GLU	D	144	43.667	38.654	57.965	1.00	249.69
	5753	CG	GLU	D	144	44.088	37.957	59.232	1.00	249.69
	5754	CD	GLU	D	144	43.210	38.332	60.397	1.00	249.69
20	5755	OE1	GLU	D	144	41.994	38.051	60.329	1.00	249.69
	5756	OE2	GLU	D	144	43.729	38.910	61.376	1.00	249.69
	5757	C	GLU	D	144	44.186	40.286	56.154	1.00	197.52
	5758	O	GLU	D	144	44.159	39.591	55.137	1.00	197.52
	5759	N	ASP	D	145	43.805	41.565	56.173	1.00	135.76
25	5760	CA	ASP	D	145	43.346	42.243	54.965	1.00	135.76
	5761	CB	ASP	D	145	42.617	43.538	55.311	1.00	217.88
	5762	CG	ASP	D	145	41.206	43.293	55.813	1.00	217.88
	5763	OD1	ASP	D	145	40.415	42.658	55.081	1.00	217.88
	5764	OD2	ASP	D	145	40.881	43.737	56.938	1.00	217.88
30	5765	C	ASP	D	145	44.512	42.549	54.030	1.00	135.76
	5766	O	ASP	D	145	44.319	42.840	52.851	1.00	135.76
	5767	N	SER	D	146	45.728	42.478	54.559	1.00	129.49
	5768	CA	SER	D	146	46.945	42.736	53.778	1.00	129.49
	5769	CB	SER	D	146	48.185	42.741	54.696	1.00	138.30
35	5770	OG	SER	D	146	48.092	43.709	55.730	1.00	138.30
	5771	C	SER	D	146	47.128	41.662	52.709	1.00	129.49
	5772	O	SER	D	146	47.094	40.471	53.005	1.00	129.49
	5773	N	GLY	D	147	47.335	42.079	51.466	1.00	156.91
	5774	CA	GLY	D	147	47.534	41.109	50.400	1.00	156.91
40	5775	C	GLY	D	147	47.729	41.750	49.041	1.00	156.91
	5776	O	GLY	D	147	48.071	42.922	48.948	1.00	156.91
	5777	N	THR	D	148	47.514	40.983	47.980	1.00	120.73
	5778	CA	THR	D	148	47.663	41.506	46.626	1.00	120.73
	5779	CB	THR	D	148	48.770	40.742	45.861	1.00	132.18
45	5780	OG1	THR	D	148	48.194	39.716	45.043	1.00	132.18
	5781	CG2	THR	D	148	49.728	40.096	46.837	1.00	132.18
	5782	C	THR	D	148	46.320	41.438	45.848	1.00	120.73
	5783	O	THR	D	148	45.808	40.338	45.526	1.00	120.73
	5784	N	TYR	D	149	45.757	42.618	45.545	1.00	89.32
50	5785	CA	TYR	D	149	44.471	42.706	44.849	1.00	89.32
	5786	CB	TYR	D	149	43.573	43.748	45.540	1.00	105.54
	5787	CG	TYR	D	149	43.303	43.551	47.020	1.00	105.54
	5788	CD1	TYR	D	149	44.281	43.842	47.984	1.00	105.54
	5789	CE1	TYR	D	149	44.016	43.690	49.350	1.00	105.54
55	5790	CD2	TYR	D	149	42.056	43.098	47.460	1.00	105.54
	5791	CE2	TYR	D	149	41.781	42.942	48.812	1.00	105.54
	5792	CZ	TYR	D	149	42.761	43.237	49.747	1.00	105.54
	5793	OH	TYR	D	149	42.470	43.085	51.077	1.00	105.54
	5794	C	TYR	D	149	44.565	43.068	43.360	1.00	89.32
60	5795	O	TYR	D	149	45.586	43.579	42.877	1.00	89.32
	5796	N	TYR	D	150	43.462	42.806	42.662	1.00	127.86
	5797	CA	TYR	D	150	43.278	43.117	41.246	1.00	127.86
	5798	CB	TYR	D	150	44.146	42.218	40.355	1.00	148.19
	5799	CG	TYR	D	150	43.643	40.801	40.109	1.00	148.19
65	5800	CD1	TYR	D	150	42.539	40.554	39.296	1.00	148.19
	5801	CE1	TYR	D	150	42.105	39.243	39.025	1.00	148.19
	5802	CD2	TYR	D	150	44.308	39.701	40.649	1.00	148.19
	5803	CE2	TYR	D	150	43.888	38.381	40.378	1.00	148.19
	5804	CZ	TYR	D	150	42.785	38.163	39.563	1.00	148.19
70	5805	OH	TYR	D	150	42.376	36.876	39.273	1.00	148.19

	5806	C	TYR	D	150	41.790	42.882	40.976	1.00	127.86
	5807	O	TYR	D	150	41.157	42.091	41.681	1.00	127.86
	5808	N	CYS	D	151	41.218	43.567	39.987	1.00	122.94
	5809	CA	CYS	D	151	39.793	43.385	39.685	1.00	122.94
5	5810	C	CYS	D	151	39.559	43.047	38.224	1.00	122.94
	5811	O	CYS	D	151	40.438	43.275	37.379	1.00	122.94
	5812	CB	CYS	D	151	39.010	44.640	40.049	1.00	183.39
	5813	SG	CYS	D	151	39.522	46.144	39.169	1.00	183.39
	5814	N	THR	D	152	38.379	42.494	37.935	1.00	139.21
10	5815	CA	THR	D	152	38.013	42.119	36.565	1.00	139.21
	5816	CB	THR	D	152	37.955	40.598	36.383	1.00	172.57
	5817	OG1	THR	D	152	36.776	40.090	37.025	1.00	172.57
	5818	CG2	THR	D	152	39.185	39.945	36.985	1.00	172.57
	5819	C	THR	D	152	36.627	42.660	36.247	1.00	139.21
15	5820	O	THR	D	152	35.765	42.721	37.124	1.00	139.21
	5821	N	GLY	D	153	36.411	43.037	34.993	1.00	182.81
	5822	CA	GLY	D	153	35.115	43.562	34.620	1.00	182.81
	5823	C	GLY	D	153	34.905	43.665	33.126	1.00	182.81
	5824	O	GLY	D	153	35.844	43.520	32.350	1.00	182.81
20	5825	N	LYS	D	154	33.662	43.917	32.730	1.00	140.36
	5826	CA	LYS	D	154	33.307	44.047	31.327	1.00	140.36
	5827	CB	LYS	D	154	32.064	43.211	31.040	1.00	249.69
	5828	CG	LYS	D	154	31.649	43.177	29.581	1.00	249.69
	5829	CD	LYS	D	154	30.442	42.266	29.384	1.00	249.69
25	5830	CE	LYS	D	154	29.973	42.264	27.938	1.00	249.69
	5831	NZ	LYS	D	154	28.786	41.385	27.740	1.00	249.69
	5832	C	LYS	D	154	33.055	45.519	30.936	1.00	140.36
	5833	O	LYS	D	154	32.150	46.184	31.458	1.00	140.36
	5834	N	VAL	D	155	33.881	46.020	30.021	1.00	200.49
30	5835	CA	VAL	D	155	33.793	47.390	29.517	1.00	200.49
	5836	CB	VAL	D	155	35.198	48.038	29.434	1.00	172.58
	5837	CG1	VAL	D	155	35.116	49.415	28.834	1.00	172.58
	5838	CG2	VAL	D	155	35.811	48.111	30.820	1.00	172.58
	5839	C	VAL	D	155	33.211	47.276	28.116	1.00	200.49
35	5840	O	VAL	D	155	33.711	46.504	27.298	1.00	200.49
	5841	N	TRP	D	156	32.169	48.051	27.831	1.00	193.00
	5842	CA	TRP	D	156	31.502	47.986	26.522	1.00	193.00
	5843	CB	TRP	D	156	32.472	48.222	25.344	1.00	249.69
	5844	CG	TRP	D	156	33.061	49.610	25.206	1.00	249.69
40	5845	CD2	TRP	D	156	32.372	50.817	24.849	1.00	249.69
	5846	CE2	TRP	D	156	33.330	51.857	24.815	1.00	249.69
	5847	CE3	TRP	D	156	31.047	51.121	24.550	1.00	249.69
	5848	CD1	TRP	D	156	34.372	49.961	25.377	1.00	249.69
	5849	NE1	TRP	D	156	34.537	51.309	25.141	1.00	249.69
45	5850	CZ2	TRP	D	156	32.996	53.172	24.499	1.00	249.69
	5851	CZ3	TRP	D	156	30.729	52.433	24.235	1.00	249.69
	5852	CH2	TRP	D	156	31.692	53.438	24.219	1.00	249.69
	5853	C	TRP	D	156	30.980	46.564	26.418	1.00	193.00
	5854	O	TRP	D	156	29.921	46.232	26.957	1.00	193.00
50	5855	N	GLN	D	157	31.755	45.727	25.732	1.00	206.01
	5856	CA	GLN	D	157	31.402	44.330	25.555	1.00	206.01
	5857	CB	GLN	D	157	30.644	44.150	24.236	1.00	249.69
	5858	CG	GLN	D	157	29.201	44.650	24.285	1.00	249.69
	5859	CD	GLN	D	157	28.329	43.857	25.262	1.00	249.69
55	5860	OE1	GLN	D	157	28.115	42.651	25.090	1.00	249.69
	5861	NE2	GLN	D	157	27.820	44.535	26.291	1.00	249.69
	5862	C	GLN	D	157	32.585	43.353	25.631	1.00	206.01
	5863	O	GLN	D	157	32.508	42.233	25.122	1.00	206.01
	5864	N	LEU	D	158	33.674	43.773	26.269	1.00	203.26
60	5865	CA	LEU	D	158	34.833	42.900	26.427	1.00	203.26
	5866	CB	LEU	D	158	35.991	43.350	25.529	1.00	242.89
	5867	CG	LEU	D	158	35.914	43.035	24.033	1.00	242.89
	5868	CD1	LEU	D	158	37.324	42.735	23.537	1.00	242.89
	5869	CD2	LEU	D	158	35.015	41.829	23.772	1.00	242.89
65	5870	C	LEU	D	158	35.301	42.846	27.878	1.00	203.26
	5871	O	LEU	D	158	35.127	43.802	28.629	1.00	203.26
	5872	N	ASP	D	159	35.886	41.718	28.268	1.00	176.99
	5873	CA	ASP	D	159	36.376	41.545	29.629	1.00	176.99
	5874	CB	ASP	D	159	36.361	40.068	30.005	1.00	232.53
70	5875	CG	ASP	D	159	35.012	39.424	29.781	1.00	232.53

	5876	OD1	ASP	D	159	34.036	39.849	30.434	1.00	232.53
	5877	OD2	ASP	D	159	34.929	38.495	28.950	1.00	232.53
	5878	C	ASP	D	159	37.805	42.075	29.760	1.00	176.99
	5879	O	ASP	D	159	38.590	42.025	28.810	1.00	176.99
5	5880	N	TYR	D	160	38.143	42.588	30.938	1.00	175.60
	5881	CA	TYR	D	160	39.484	43.102	31.170	1.00	175.60
	5882	CB	TYR	D	160	39.559	44.592	30.873	1.00	205.83
	5883	CG	TYR	D	160	39.112	44.956	29.483	1.00	205.83
	5884	CD1	TYR	D	160	37.778	45.271	29.216	1.00	205.83
10	5885	CE1	TYR	D	160	37.361	45.636	27.939	1.00	205.83
	5886	CD2	TYR	D	160	40.022	45.009	28.435	1.00	205.83
	5887	CE2	TYR	D	160	39.614	45.373	27.148	1.00	205.83
	5888	CZ	TYR	D	160	38.284	45.687	26.912	1.00	205.83
	5889	OH	TYR	D	160	37.883	46.070	25.658	1.00	205.83
15	5890	C	TYR	D	160	39.941	42.855	32.593	1.00	175.60
	5891	O	TYR	D	160	39.151	42.853	33.545	1.00	175.60
	5892	N	GLU	D	161	41.243	42.653	32.718	1.00	144.68
	5893	CA	GLU	D	161	41.879	42.385	33.998	1.00	144.68
	5894	CB	GLU	D	161	42.697	41.094	33.859	1.00	232.05
20	5895	CG	GLU	D	161	43.497	40.642	35.071	1.00	232.05
	5896	CD	GLU	D	161	43.969	39.194	34.942	1.00	232.05
	5897	OE1	GLU	D	161	44.936	38.819	35.643	1.00	232.05
	5898	OE2	GLU	D	161	43.363	38.430	34.151	1.00	232.05
	5899	C	GLU	D	161	42.759	43.587	34.344	1.00	144.68
25	5900	O	GLU	D	161	43.353	44.206	33.459	1.00	144.68
	5901	N	SER	D	162	42.814	43.922	35.628	1.00	134.82
	5902	CA	SER	D	162	43.594	45.064	36.101	1.00	134.82
	5903	CB	SER	D	162	42.881	45.712	37.288	1.00	129.75
	5904	OG	SER	D	162	42.767	44.801	38.381	1.00	129.75
30	5905	C	SER	D	162	44.983	44.669	36.541	1.00	134.82
	5906	O	SER	D	162	45.221	43.504	36.838	1.00	134.82
	5907	N	GLU	D	163	45.898	45.634	36.581	1.00	145.43
	5908	CA	GLU	D	163	47.238	45.334	37.050	1.00	145.43
'	5909	CB	GLU	D	163	48.133	46.575	36.964	1.00	249.69
35	5910	CG	GLU	D	163	48.587	46.949	35.552	1.00	249.69
	5911	CD	GLU	D	163	49.651	46.008	35.001	1.00	249.69
	5912	OE1	GLU	D	163	50.709	45.850	35.650	1.00	249.69
	5913	OE2	GLU	D	163	49.433	45.429	33.917	1.00	249.69
	5914	C	GLU	D	163	47.047	44.921	38.519	1.00	145.43
40	5915	O	GLU	D	163	46.101	45.384	39.168	1.00	145.43
	5916	N	PRO	D	164	47.906	44.037	39.057	1.00	113.31
	5917	CD	PRO	D	164	48.999	43.317	38.369	1.00	144.09
	5918	CA	PRO	D	164	47.794	43.578	40.447	1.00	113.31
	5919	CB	PRO	D	164	48.555	42.277	40.434	1.00	144.09
45	5920	CG	PRO	D	164	49.685	42.607	39.519	1.00	144.09
	5921	C	PRO	D	164	48.395	44.576	41.422	1.00	113.31
	5922	O	PRO	D	164	49.399	45.229	41.095	1.00	113.31
	5923	N	LEU	D	165	47.807	44.679	42.613	1.00	104.79
	5924	CA	LEU	D	165	48.305	45.642	43.591	1.00	104.79
50	5925	CB	LEU	D	165	47.329	46.816	43.687	1.00	127.61
	5926	CG	LEU	D	165	47.719	47.920	44.665	1.00	127.61
	5927	CD1	LEU	D	165	49.250	48.130	44.649	1.00	127.61
	5928	CD2	LEU	D	165	46.959	49.193	44.283	1.00	127.61
	5929	C	LEU	D	165	48.560	45.097	44.980	1.00	104.79
55	5930	O	LEU	D	165	47.691	44.427	45.545	1.00	104.79
	5931	N	ASN	D	166	49.739	45.405	45.533	1.00	129.66
	5932	CA	ASN	D	166	50.090	44.944	46.878	1.00	129.66
	5933	CB	ASN	D	166	51.594	44.769	47.024	1.00	189.08
	5934	CG	ASN	D	166	52.050	43.354	46.741	1.00	189.08
60	5935	OD1	ASN	D	166	51.275	42.407	46.867	1.00	189.08
	5936	ND2	ASN	D	166	53.324	43.209	46.381	1.00	189.08
	5937	C	ASN	D	166	49.612	45.924	47.955	1.00	129.66
	5938	O	ASN	D	166	49.610	47.138	47.755	1.00	129.66
	5939	N	ILE	D	167	49.221	45.387	49.105	1.00	126.98
65	5940	CA	ILE	D	167	48.731	46.196	50.211	1.00	126.98
	5941	CB	ILE	D	167	47.211	46.242	50.220	1.00	113.09
	5942	CG2	ILE	D	167	46.740	46.998	51.438	1.00	113.09
	5943	CG1	ILE	D	167	46.716	46.889	48.940	1.00	113.09
	5944	CD1	ILE	D	167	45.225	46.900	48.843	1.00	113.09
70	5945	C	ILE	D	167	49.185	45.645	51.555	1.00	126.98

	5946	O	ILE	D	167	48.978	44.480	51.875	1.00	126.98
	5947	N	THR	D	168	49.769	46.499	52.369	1.00	123.13
	5948	CA	THR	D	168	50.238	46.029	53.647	1.00	123.13
	5949	CB	THR	D	168	51.761	46.052	53.678	1.00	145.39
5	5950	OG1	THR	D	168	52.253	45.258	52.593	1.00	145.39
	5951	CG2	THR	D	168	52.281	45.490	54.987	1.00	145.39
	5952	C	THR	D	168	49.695	46.766	54.864	1.00	123.13
	5953	O	THR	D	168	49.839	47.983	55.000	1.00	123.13
	5954	N	VAL	D	169	49.061	46.004	55.748	1.00	129.26
10	5955	CA	VAL	D	169	48.501	46.536	56.981	1.00	129.26
	5956	CB	VAL	D	169	47.067	45.982	57.209	1.00	119.28
	5957	CG1	VAL	D	169	46.683	46.096	58.653	1.00	119.28
	5958	CG2	VAL	D	169	46.065	46.769	56.377	1.00	119.28
	5959	C	VAL	D	169	49.439	46.104	58.098	1.00	129.26
15	5960	O	VAL	D	169	49.525	44.914	58.419	1.00	129.26
	5961	N	ILE	D	170	50.162	47.069	58.664	1.00	108.63
	5962	CA	ILE	D	170	51.111	46.798	59.750	1.00	108.63
	5963	CB	ILE	D	170	52.340	47.687	59.607	1.00	169.72
	5964	CG2	ILE	D	170	52.891	47.560	58.200	1.00	169.72
20	5965	CG1	ILE	D	170	51.963	49.148	59.833	1.00	169.72
	5966	CD1	ILE	D	170	53.138	50.116	59.741	1.00	169.72
	5967	C	ILE	D	170	50.448	47.058	61.111	1.00	108.63
	5968	O	ILE	D	170	49.389	47.687	61.170	1.00	108.63
	5969	N	LYS	D	171	51.044	46.600	62.206	1.00	180.64
25	5970	CA	LYS	D	171	50.427	46.811	63.518	1.00	180.64
	5971	CB	LYS	D	171	50.095	45.460	64.130	1.00	216.97
	5972	CG	LYS	D	171	51.300	44.550	64.204	1.00	216.97
	5973	CD	LYS	D	171	50.911	43.084	64.180	1.00	216.97
	5974	CE	LYS	D	171	49.997	42.721	65.338	1.00	216.97
30	5975	NZ	LYS	D	171	49.677	41.265	65.351	1.00	216.97
	5976	C	LYS	D	171	51.277	47.623	64.496	1.00	180.64
	5977	O	LYS	D	171	50.952	47.715	65.686	1.00	180.64
	5978	C1	NAG	D	221	40.588	68.345	34.460	1.00	249.69
	5979	C2	NAG	D	221	39.263	67.620	34.228	1.00	249.69
35	5980	N2	NAG	D	221	39.503	66.190	34.156	1.00	249.69
	5981	C7	NAG	D	221	38.524	65.328	34.426	1.00	249.69
	5982	O7	NAG	D	221	37.379	65.680	34.734	1.00	249.69
	5983	C8	NAG	D	221	38.865	63.847	34.336	1.00	249.69
	5984	C3	NAG	D	221	38.607	68.107	32.935	1.00	249.69
40	5985	O3	NAG	D	221	37.303	67.542	32.815	1.00	249.69
	5986	C4	NAG	D	221	38.508	69.645	32.882	1.00	249.69
	5987	O4	NAG	D	221	38.122	70.004	31.534	1.00	249.69
	5988	C5	NAG	D	221	39.874	70.288	33.238	1.00	249.69
	5989	O5	NAG	D	221	40.374	69.764	34.489	1.00	2 ·9.69
45	5990	C6	NAG	D	221	39.806	71.797	33.398	1.00	249.69
	5991	O6	NAG	D	221	38.830	72.175	34.359	1.00	249.69
	5992	C1	NAG	D	222	37.598	71.265	31.271	1.00	249.69
	5993	C2	NAG	D	222	36.393	71.128	30.316	1.00	249.69
	5994	N2	NAG	D	222	35.353	70.322	30.940	1.00	249.69
50	5995	C7	NAG	D	222	34.138	70.826	31.159	1.00	249.69
	5996	O7	NAG	D	222	33.821	71.980	30.854	1.00	249.69
	5997	C8	NAG	D	222	33.115	69.911	31.816	1.00	249.69
	5998	C3	NAG	D	222	36.853	70.476	28.991	1.00	249.69
	5999	O3	NAG	D	222	35.784	70.461	28.055	1.00	249.69
55	6000	C4	NAG	D	222	38.047	71.236	28.392	1.00	249.69
	6001	O4	NAG	D	222	38.552	70.527	27.265	1.00	249.69
	6002	C5	NAG	D	222	39.161	71.402	29.445	1.00	249.69
	6003	O5	NAG	D	222	38.632	72.044	30.639	1.00	249.69
	6004	C6	NAG	D	222	40.342	72.235	28.961	1.00	249.69
60	6005	O6	NAG	D	222	41.578	71.582	29.216	1.00	249.69
	6006	C1	NAG	D	242	60.393	61.563	38.161	1.00	217.32
	6007	C2	NAG	D	242	60.080	62.065	36.753	1.00	217.32
	6008	N2	NAG	D	242	59.542	63.410	36.776	1.00	217.32
	6009	C7	NAG	D	242	60.185	64.390	36.140	1.00	217.32
65	6010	O7	NAG	D	242	61.243	64.215	35.527	1.00	217.32
	6011	C8	NAG	D	242	59.572	65.781	36.193	1.00	217.32
	6012	C3	NAG	D	242	59.090	61.109	36.102	1.00	217.32
	6013	O3	NAG	D	242	58.789	61.543	34.778	1.00	217.32
	6014	C4	NAG	D	242	59.683	59.697	36.072	1.00	217.32
70	6015	O4	NAG	D	242	58.682	58.764	35.604	1.00	217.32

	6016	C5	NAG	D	242	60.173	59.270	37.475	1.00	217.32
	6017	O5	NAG	D	242	61.023	60.283	38.071	1.00	217.32
	6018	C6	NAG	D	242	61.001	57.999	37.419	1.00	217.32
	6019	O6	NAG	D	242	60.329	56.906	38.029	1.00	217.32
5	6020	C1	NAG	D	243	58.975	58.047	34.449	1.00	249.32
	6021	C2	NAG	D	243	58.093	56.797	34.373	1.00	249.32
	6022	N2	NAG	D	243	58.304	55.934	35.517	1.00	249.32
	6023	C7	NAG	D	243	57.260	55.458	36.184	1.00	249.32
	6024	O7	NAG	D	243	56.095	55.727	35.887	1.00	249.32
10	6025	C8	NAG	D	243	57.553	54.550	37.368	1.00	249.32
	6026	C3	NAG	D	243	58.410	56.048	33.091	1.00	249.32
	6027	O3	NAG	D	243	57.609	54.878	32.999	1.00	249.32
	6028	C4	NAG	D	243	58.125	56.960	31.920	1.00	249.32
	6029	O4	NAG	D	243	58.387	56.198	30.758	1.00	249.32
15	6030	C5	NAG	D	243	58.994	58.245	32.040	1.00	249.32
	6031	O5	NAG	D	243	58.710	58.893	33.315	1.00	249.32
	6032	C6	NAG	D	243	58.695	59.274	30.969	1.00	249.32
	6033	O6	NAG	D	243	57.361	59.747	31.063	1.00	249.32
	6034	C1	MAN	D	244	57.701	56.400	29.591	1.00	249.69
20	6035	C2	MAN	D	244	58.764	56.236	28.599	1.00	249.69
	6036	O2	MAN	D	244	59.572	55.101	28.964	1.00	249.69
	6037	C3	MAN	D	244	58.183	56.214	27.213	1.00	249.69
	6038	O3	MAN	D	244	59.205	56.198	26.236	1.00	249.69
	6039	C4	MAN	D	244	57.187	55.086	27.057	1.00	249.69
25	6040	O4	MAN	D	244	56.690	55.063	25.730	1.00	249.69
	6041	C5	MAN	D	244	56.059	55.334	28.066	1.00	249.69
	6042	O5	MAN	D	244	56.637	55.331	29.433	1.00	249.69
	6043	C6	MAN	D	244	54.855	54.371	27.914	1.00	249.69
	6044	O6	MAN	D	244	55.056	53.129	28.567	1.00	249.69
30	6045	C1	NAG	D	250	45.970	78.192	45.348	1.00	249.69
	6046	C2	NAG	D	250	44.549	78.482	45.867	1.00	249.69
	6047	N2	NAG	D	250	44.538	78.485	47.317	1.00	249.69
	6048	C7	NAG	D	250	44.384	79.627	47.981	1.00	249.69
	6049	O7	NAG	D	250	44.241	80.713	47.415	1.00	249.69
35	6050	C8	NAG	D	250	44.386	79.553	49.506	1.00	249.69
	6051	C3	NAG	D	250	43.581	77.413	45.337	1.00	249.69
	6052	O3	NAG	D	250	42.249	77.716	45.732	1.00	249.69
	6053	C4	NAG	D	250	43.666	77.341	43.807	1.00	249.69
	6054	O4	NAG	D	250	42.863	76.265	43.339	1.00	249.69
40	6055	C5	NAG	D	250	45.136	77.138	43.368	1.00	249.69
	6056	O5	NAG	D	250	45.975	78.187	43.916	1.00	249.69
	6057	C6	NAG	D	250	45.334	77.155	41.856	1.00	249.69
	6058	O6	NAG	D	250	46.706	77.343	41.513	1.00	249.69
	6059	C1	NAG	D	274	64.018	69.436	61.817	1.00	249.69
45	6060	C2	NAG	D	274	63.805	68.308	62.845	1.00	249.69
	6061	N2	NAG	D	274	62.614	68.567	63.639	1.00	249.69
	6062	C7	NAG	D	274	61.945	67.559	64.201	1.00	249.69
	6063	O7	NAG	D	274	62.289	66.377	64.093	1.00	249.69
	6064	C8	NAG	D	274	60.707	67.911	65.011	1.00	249.69
50	6065	C3	NAG	D	274	65.040	68.194	63.760	1.00	249.69
	6066	O3	NAG	D	274	64.908	67.066	64.619	1.00	249.69
	6067	C4	NAG	D	274	66.321	68.053	62.922	1.00	249.69
	6068	O4	NAG	D	274	67.463	68.083	63.776	1.00	249.69
	6069	C5	NAG	D	274	66.405	69.191	61.890	1.00	249.69
55	6070	O5	NAG	D	274	65.217	69.199	61.060	1.00	249.69
	6071	C6	NAG	D	274	67.605	69.054	60.964	1.00	249.69
	6072	O6	NAG	D	274	67.558	70.006	59.911	1.00	249.69
	6073	C1	NAG	D	335	33.933	54.753	43.517	1.00	249.69
	6074	C2	NAG	D	335	33.681	55.966	44.462	1.00	249.69
60	6075	N2	NAG	D	335	33.369	55.476	45.797	1.00	249.69
	6076	C7	NAG	D	335	34.175	55.736	46.826	1.00	249.69
	6077	O7	NAG	D	335	35.208	56.398	46.727	1.00	249.69
	6078	C8	NAG	D	335	33.768	55.178	48.177	1.00	249.69
	6079	C3	NAG	D	335	32.547	56.909	44.003	1.00	249.69
65	6080	O3	NAG	D	335	32.693	58.170	44.644	1.00	249.69
	6081	C4	NAG	D	335	32.568	57.114	42.494	1.00	249.69
	6082	O4	NAG	D	335	31.469	57.925	42.098	1.00	249.69
	6083	C5	NAG	D	335	32.490	55.747	41.830	1.00	249.69
	6084	O5	NAG	D	335	33.699	55.014	42.109	1.00	249.69
70	6085	C6	NAG	D	335	32.365	55.844	40.319	1.00	249.69

	6086	O6	NAG D	335	31.232	55.131	39.850	1.00	249.69
	6087	C1	NAG D	340	38.129	47.005	65.199	1.00	249.69
	6088	C2	NAG D	340	39.319	46.805	66.150	1.00	249.69
	6089	N2	NAG D	340	40.524	46.521	65.388	1.00	249.69
5	6090	C7	NAG D	340	41.665	47.160	65.655	1.00	249.69
	6091	O7	NAG D	340	41.779	48.007	66.549	1.00	249.69
	6092	C8	NAG D	340	42.871	46.799	64.801	1.00	249.69
	6093	C3	NAG D	340	39.000	45.640	67.106	1.00	249.69
	6094	O3	NAG D	340	40.042	45.482	68.064	1.00	249.69
10	6095	C4	NAG D	340	37.670	45.894	67.828	1.00	249.69
	6096	O4	NAG D	340	37.324	44.743	68.593	1.00	249.69
	6097	C5	NAG D	340	36.556	46.207	66.801	1.00	249.69
	6098	O5	NAG D	340	36.949	47.307	65.948	1.00	249.69
	6099	C6	NAG D	340	35.226	46.591	67.427	1.00	249.69
15	6100	O6	NAG D	340	34.319	47.067	66.440	1.00	249.69
	6101	C1	NAG D	366	53.829	41.917	45.964	1.00	214.56
	6102	C2	NAG D	366	54.811	42.093	44.812	1.00	214.56
	6103	N2	NAG D	366	54.141	42.757	43.705	1.00	214.56
	6104	C7	NAG D	366	54.172	44.086	43.595	1.00	214.56
20	6105	O7	NAG D	366	54.769	44.819	44.396	1.00	214.56
	6106	C8	NAG D	366	53.436	44.705	42.413	1.00	214.56
	6107	C3	NAG D	366	55.328	40.725	44.367	1.00	214.56
	6108	O3	NAG D	366	56.374	40.896	43.416	1.00	214.56
	6109	C4	NAG D	366	55.847	39.896	45.553	1.00	214.56
25	6110	O4	NAG D	366	56.067	38.537	45.104	1.00	214.56
	6111	C5	NAG D	366	54.830	39.900	46.709	1.00	214.56
	6112	O5	NAG D	366	54.471	41.245	47.050	1.00	214.56
	6113	C6	NAG D	366	55.334	39.248	47.980	1.00	214.56
	6114	O6	NAG D	366	54.292	39.118	48.934	1.00	214.56
30	6115	C1	NAG D	367	57.323	37.987	45.329	1.00	231.83
	6116	C2	NAG D	367	57.238	36.462	45.283	1.00	231.83
	6117	N2	NAG D	367	56.271	35.974	46.246	1.00	231.83
	6118	C7	NAG D	367	55.141	35.410	45.821	1.00	231.83
	6119	O7	NAG D	367	54.861	35.279	44.620	1.00	231.83
35	6120	C8	NAG D	367	54.169	34.918	46.887	1.00	231.83
	6121	C3	NAG D	367	58.627	35.898	45.572	1.00	231.83
	6122	O3	NAG D	367	58.601	34.478	45.528	1.00	231.83
	6123	C4	NAG D	367	59.611	36.433	44.526	1.00	231.83
	6124	O4	NAG D	367	60.922	35.989	44.845	1.00	231.83
40	6125	C5	NAG D	367	59.572	37.974	44.486	1.00	231.83
	6126	O5	NAG D	367	58.216	38.443	44.296	1.00	231.83
	6127	C6	NAG D	367	60.403	38.550	43.358	1.00	231.83
	6128	O6	NAG D	367	59.584	39.177	42.385	1.00	231.83
	6129	CB	LYS E	4	8.883	64.586	0.000	1.00	249.69
45	6130	CG	LYS E	4	7.510	64.141	-0.503	1.00	249.69
	6131	CD	LYS E	4	6.532	63.873	0.645	1.00	249.69
	6132	CE	LYS E	4	5.149	63.459	0.123	1.00	249.69
	6133	NZ	LYS E	··	4.173	63.179	1.220	1.00	249.69
	6134	C	LYS E	4	9.271	66.045	-1.989	1.00	232.34
50	6135	O	LYS E	4	8.420	66.812	-1.537	1.00	232.34
	6136	N	LYS E	4	11.173	65.351	-0.540	1.00	232.34
	6137	CA	LYS E	4	9.865	64.939	-1.121	1.00	232.34
	6138	N	PRO E	5	9.723	66.150	-3.249	1.00	227.45
	6139	CD	PRO E	5	10.890	65.481	-3.843	1.00	124.73
55	6140	CA	PRO E	5	9.204	67.180	-4.150	1.00	227.45
	6141	CB	PRO E	5	10.351	67.382	-5.132	1.00	124.73
	6142	CG	PRO E	5	10.883	66.000	-5.275	1.00	124.73
	6143	C	PRO E	5	7.921	66.721	-4.845	1.00	227.45
	6144	O	PRO E	5	7.651	65.522	-4.954	1.00	227.45
60	6145	N	LYS E	6	7.125	67.679	-5.305	1.00	237.93
	6146	CA	LYS E	6	5.877	67.360	-5.987	1.00	237.93
	6147	CB	LYS E	6	4.702	67.440	-5.011	1.00	249.69
	6148	CG	LYS E	6	3.370	67.066	-5.640	1.00	249.69
	6149	CD	LYS E	6	2.244	66.893	-4.615	1.00	249.69
65	6150	CE	LYS E	6	0.935	66.562	-5.275	1.00	249.69
	6151	NZ	LYS E	6	-0.156	66.352	-4.287	1.00	249.69
	6152	C	LYS E	6	5.650	68.308	-7.153	1.00	237.93
	6153	O	LYS E	6	5.422	69.505	-6.970	1.00	237.93
	6154	N	VAL E	7	5.709	67.754	-8.356	1.00	162.26
70	6155	CA	VAL E	7	5.532	68.543	-9.567	1.00	162.26

	6156	CB	VAL	E	7	5.858	67.703	-10.821	1.00	205.67
	6157	CG1	VAL	E	7	6.017	68.614	-12.040	1.00	205.67
	6158	CG2	VAL	E	7	7.117	66.881	-10.577	1.00	205.67
	6159	C	VAL	E	7	4.118	69.111	-9.723	1.00	162.26
5	6160	O	VAL	E	7	3.134	68.364	-9.717	1.00	162.26
	6161	N	SER	E	8	4.022	70.433	-9.868	1.00	174.49
	6162	CA	SER	E	8	2.741	71.111	-10.048	1.00	174.49
	6163	CB	SER	E	8	2.672	72.324	-9.131	1.00	223.27
	6164	OG	SER	E	8	3.850	73.111	-9.231	1.00	223.27
10	6165	C	SER	E	8	2.616	71.551	-11.501	1.00	174.49
	6166	O	SER	E	8	3.624	71.640	-12.215	1.00	174.49
	6167	N	LEU	E	9	1.392	71.815	-11.949	1.00	138.24
	6168	CA	LEU	E	9	1.200	72.248	-13.338	1.00	138.24
	6169	CB	LEU	E	9	0.497	71.161	-14.181	1.00	151.07
15	6170	CG	LEU	E	9	1.092	69.761	-14.372	1.00	151.07
	6171	CD1	LEU	E	9	0.374	69.105	-15.529	1.00	151.07
	6172	CD2	LEU	E	9	2.578	69.816	-14.665	1.00	151.07
	6173	C	LEU	E	9	0.394	73.544	-13.447	1.00	138.24
	6174	O	LEU	E	9	-0.329	73.919	-12.519	1.00	138.24
20	6175	N	ASN	E	10	0.520	74.217	-14.589	1.00	163.51
	6176	CA	ASN	E	10	-0.215	75.436	-14.823	1.00	163.51
	6177	CB	ASN	E	10	0.444	76.592	-14.100	1.00	242.89
	6178	CG	ASN	E	10	-0.467	77.788	-14.008	1.00	242.89
	6179	OD1	ASN	E	10	-1.520	77.730	-13.369	1.00	242.89
25	6180	ND2	ASN	E	10	-0.077	78.881	-14.650	1.00	242.89
	6181	C	ASN	E	10	-0.303	75.748	-16.310	1.00	163.51
	6182	O	ASN	E	10	0.703	76.073	-16.942	1.00	163.51
	6183	N	PRO	E	11	-1.515	75.661	-16.902	1.00	167.75
	6184	CD	PRO	E	11	-1.686	75.947	-18.332	1.00	141.15
30	6185	CA	PRO	E	11	-2.807	75.308	-16.289	1.00	167.75
	6186	CB	PRO	E	11	-3.740	75.243	-17.494	1.00	141.15
	6187	CG	PRO	E	11	-3.151	76.257	-18.413	1.00	141.15
	6188	C	PRO	E	11	-2.804	73.994	-15.505	1.00	167.75
	6189	O	PRO	E	11	-1.861	73.210	-15.588	1.00	167.75
35	6190	N	PRO	E	12	-3.874	73.736	-14.729	1.00	129.01
	6191	CD	PRO	E	12	-5.008	74.630	-14.438	1.00	158.46
	6192	CA	PRO	E	12	-3.963	72.506	-13.934	1.00	129.01
	6193	CB	PRO	E	12	-5.164	72.766	-13.028	1.00	158.46
	6194	CG	PRO	E	12	-5.297	74.281	-13.015	1.00	158.46
40	6195	C	PRO	E	12	-4.198	71.307	-14.852	1.00	129.01
	6196	O	PRO	E	12	-3.823	70.178	-14.535	1.00	129.01
	6197	N	TRP	E	13	-4.829	71.590	-15.992	1.00	148.97
	6198	CA	TRP	E	13	-5.176	70.617	-17.041	1.00	148.97
	6199	CB	TRP	E	13	-5.707	71.376	-18.252	1.00	139.57
45	6200	CG	TRP	E	13	-6.745	72.405	-17.878	1.00	139.57
	6201	CD2	TRP	E	13	-7.685	72.310	-16.810	1.00	139.57
	6202	CE2	TRP	E	13	-8.485	73.479	-16.851	1.00	139.57
	6203	CE3	TRP	E	13	-7.934	71.351	-15.816	1.00	139.57
	6204	CD1	TRP	E	13	-7.006	73.598	-18.513	1.00	139.57
50	6205	NE1	TRP	E	13	-8.049	74.249	-17.900	1.00	139.57
	6206	CZ2	TRP	E	13	-9.511	73.707	-15.834	1.00	139.57
	6207	CZ3	TRP	E	13	-8.950	71.581	-14.909	1.00	139.57
	6208	CH2	TRP	E	13	-9.731	72.746	-14.975	1.00	139.57
	6209	C	TRP	E	13	-4.000	69.772	-17.478	1.00	148.97
55	6210	O	TRP	E	13	-3.050	70.294	-18.052	1.00	148.97
	6211	N	ASN	E	14	-4.069	68.465	-17.236	1.00	121.67
	6212	CA	ASN	E	14	-2.967	67.569	-17.623	1.00	121.67
	6213	CB	ASN	E	14	-2.569	66.659	-16.443	1.00	170.43
	6214	CG	ASN	E	14	-3.669	65.717	-16.039	1.00	170.43
60	6215	OD1	ASN	E	14	-4.785	66.134	-15.711	1.00	170.43
	6216	ND2	ASN	E	14	-3.382	64.432	-16.058	1.00	170.43
	6217	C	ASN	E	14	-3.273	66.730	-18.871	1.00	121.67
	6218	O	ASN	E	14	-2.662	65.684	-19.103	1.00	121.67
	6219	N	ARG	E	15	-4.227	67.225	-19.661	1.00	100.94
65	6220	CA	ARG	E	15	-4.675	66.616	-20.914	1.00	100.94
	6221	CB	ARG	E	15	-6.069	65.991	-20.773	1.00	110.25
	6222	CG	ARG	E	15	-6.278	65.052	-19.581	1.00	110.25
	6223	CD	ARG	E	15	-7.642	64.353	-19.673	1.00	110.25
	6224	NE	ARG	E	15	-7.673	63.268	-20.667	1.00	110.25
70	6225	CZ	ARG	E	15	-8.713	62.965	-21.449	1.00	110.25

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	6226	NH1	ARG	E	15	-9.818	63.665	-21.363	1.00	110.25
	6227	NH2	ARG	E	15	-8.654	61.949	-22.308	1.00	110.25
	6228	C	ARG	E	15	-4.797	67.800	-21.845	1.00	100.94
	6229	O	ARG	E	15	-5.779	68.526	-21.776	1.00	100.94
5	6230	N	ILE	E	16	-3.824	68.012	-22.720	1.00	114.46
	6231	CA	ILE	E	16	-3.875	69.182	-23.615	1.00	114.46
	6232	CB	ILE	E	16	-2.723	70.141	-23.315	1.00	133.29
	6233	CG2	ILE	E	16	-3.008	70.920	-22.025	1.00	133.29
	6234	CG1	ILE	E	16	-1.422	69.334	-23.257	1.00	133.29
10	6235	CD1	ILE	E	16	-0.187	70.169	-23.241	1.00	133.29
	6236	C	ILE	E	16	-3.835	68.931	-25.116	1.00	114.46
	6237	O	ILE	E	16	-3.314	67.920	-25.573	1.00	114.46
	6238	N	PHE	E	17	-4.371	69.884	-25.869	1.00	157.55
	6239	CA	PHE	E	17	-4.389	69.799	-27.315	1.00	157.55
15	6240	CB	PHE	E	17	-5.291	70.875	-27.896	1.00	134.86
	6241	CG	PHE	E	17	-6.708	70.444	-28.068	1.00	134.86
	6242	CD1	PHE	E	17	-7.747	71.354	-27.884	1.00	134.86
	6243	CD2	PHE	E	17	-7.016	:.142	-28.445	1.00	134.86
	6244	CE1	PHE	E	17	-9.085	70.974	-28.072	1.00	134.86
20	6245	CE2	PHE	E	17	-8.339	68.753	-28.636	1.00	134.86
	6246	CZ	PHE	E	17	-9.378	69.677	-28.448	1.00	134.86
	6247	C	PHE	E	17	-2.984	69.975	-27.873	1.00	157.55
	6248	O	PHE	E	17	-2.038	70.221	-27.122	1.00	157.55
	6249	N	LYS	E	18	-2.860	69.858	-29.196	1.00	136.71
25	6250	CA	LYS	E	18	-1.582	69.998	-29.892	1.00	136.71
	6251	CB	LYS	E	18	-1.660	69.250	-31.219	1.00	249.69
	6252	CG	LYS	E	18	-0.384	69.249	-32.033	1.00	249.69
	6253	CD	LYS	E	18	-0.530	68.316	-33.230	1.00	249.69
	6254	CE	LYS	E	18	0.701	68.337	-34.128	1.00	249.69
30	6255	NZ	LYS	E	18	0.855	69.643	-34.825	1.00	249.69
	6256	C	LYS	E	18	-1.243	71.471	-30.127	1.00	136.71
	6257	O	LYS	E	18	-2.056	72.237	-30.646	1.00	136.71
	6258	N	GLY	E	19	-0.042	71.866	-29.726	1.00	201.41
	6259	CA	GLY	E	19	0.380	73.242	-29.913	1.00	201.41
35	6260	C	GLY	E	19	0.195	74.161	-28.717	1.00	201.41
	6261	O	GLY	E	19	0.717	75.279	-28.708	1.00	201.41
	6262	N	GLU	E	20	-0.541	73.703	-27.709	1.00	148.40
	6263	CA	GLU	E	20	-0.787	74.499	-26.497	1.00	148.40
	6264	CB	GLU	E	20	-2.004	73.945	-25.733	1.00	165.83
40	6265	CG	GLU	E	20	-3.267	73.658	-26.577	1.00	165.83
	6266	CD	GLU	E	20	-4.479	73.233	-25.726	1.00	165.83
	6267	OE1	GLU	E	20	-4.358	72.282	-24.926	1.00	165.83
	6268	OE2	GLU	E	20	-5.555	73.855	-25.864	1.00	165.83
	6269	C	GLU	E	20	0.439	74.469	-25.564	1.00	148.40
45	6270	O	GLU	E	20	1.273	73.561	-25.663	1.00	148.40
	6271	N	ASN	E	21	0.552	75.440	-24.653	1.00	156.11
	6272	CA	ASN	E	21	1.704	75.474	-23.731	1.00	156.11
	6273	CB	ASN	E	21	2.412	76.835	-23.774	1.00	249.69
	6274	CG	ASN	E	21	2.414	77.468	-25.153	1.00	249.69
50	6275	OD1	ASN	E	21	2.734	76.825	-26.157	1.00	249.69
	6276	ND2	ASN	E	21	2.070	78.754	-25.179	1.00	249.69
	6277	C	ASN	E	21	1.342	75.182	-22.267	1.00	156.11
	6278	O	ASN	E	21	0.288	75.589	-21.769	1.00	156.11
	6279	N	VAL	E	22	2.245	74.493	-21.580	1.00	182.17
55	6280	CA	VAL	E	22	2.049	74.137	-20.177	1.00	182.17
	6281	CB	VAL	E	22	1.601	72.669	-20.028	1.00	148.81
	6282	CG1	VAL	E	22	2.757	71.742	-20.356	1.00	148.81
	6283	CG2	VAL	E	22	1.109	72.404	-18.627	1.00	148.81
	6284	C	VAL	E	22	3.360	74.313	-19.407	1.00	182.17
60	6285	O	VAL	E	22	4.443	74.124	-19.965	1.00	182.17
	6286	N	THR	E	23	3.261	74.650	-18.120	1.00	131.37
	6287	CA	THR	E	23	4.447	74.874	-17.281	1.00	131.37
	6288	CB	THR	E	23	4.448	76.320	-16.723	1.00	249.69
	6289	OG1	THR	E	23	4.251	77.255	-17.794	1.00	249.69
65	6290	CG2	THR	E	23	5.773	76.619	-16.027	1.00	249.69
	6291	C	THR	E	23	4.559	73.928	-16.088	1.00	131.37
	6292	O	THR	E	23	3.643	73.866	-15.266	1.00	131.37
	6293	N	LEU	E	24	5.694	73.234	-15.974	1.00	247.08
	6294	CA	LEU	E	24	5.909	72.305	-14.862	1.00	247.08
70	6295	CB	LEU	E	24	6.490	70.972	-15.357	1.00	141.93

	6296	CG	LEU	E	24	6.154	70.407	-16.745	1.00	141.83
	6297	CD1	LEU	E	24	6.601	68.946	-16.814	1.00	141.83
	6298	CD2	LEU	E	24	4.668	70.513	-17.025	1.00	141.83
	6299	C	LEU	E	24	6.857	72.886	-13.807	1.00	247.08
5	6300	O	LEU	E	24	8.064	72.988	-14.032	1.00	247.08
	6301	N	THR	E	25	6.302	73.254	-12.653	1.00	187.47
	6302	CA	THR	E	25	7.075	73.824	-11.547	1.00	187.47
	6303	CB	THR	E	25	6.280	74.957	-10.847	1.00	161.19
	6304	OG1	THR	E	25	5.936	75.964	-11.806	1.00	161.19
10	6305	CG2	THR	E	25	7.100	75.590	-9.725	1.00	161.19
	6306	C	THR	E	25	7.391	72.739	-10.512	1.00	187.47
	6307	O	THR	E	25	6.513	71.981	-10.121	1.00	187.47
	6308	N	CYS	E	26	8.642	72.673	-10.069	1.00	208.94
	6309	CA	CYS	E	26	9.057	71.677	-9.078	1.00	208.94
15	6310	C	CYS	E	26	8.680	72.137	-7.667	1.00	208.94
	6311	O	CYS	E	26	8.738	73.326	-7.364	1.00	208.94
	6312	CB	CYS	E	26	10.562	71.439	-9.179	1.00	205.14
	6313	SG	CYS	E	26	11.190	70.046	-8.197	1.00	205.14
	6314	N	ASN	E	27	8.303	71.189	-6.812	1.00	249.69
20	6315	CA	ASN	E	27	7.875	71.478	-5.439	1.00	249.69
	6316	CB	ASN	E	27	8.415	70.418	-4.468	1.00	249.69
	6317	CG	ASN	E	27	7.792	70.526	-3.076	1.00	249.69
	6318	OD1	ASN	E	27	6.569	70.623	-2.936	1.00	249.69
	6319	ND2	ASN	E	27	8.632	70.505	-2.043	1.00	249.69
25	6320	C	ASN	E	27	8.241	72.870	-4.930	1.00	249.69
	6321	O	ASN	E	27	9.333	73.095	-4.401	1.00	249.69
	6322	N	GLY	E	28	7.301	73.795	-5.095	1.00	249.69
	6323	CA	GLY	E	28	7.486	75.172	-4.669	1.00	249.69
	6324	C	GLY	E	28	6.306	75.960	-5.202	1.00	249.69
30	6325	O	GLY	E	28	6.092	76.005	-6.419	1.00	249.69
	6326	N	ASN	E	29	5.537	76.576	-4.305	1.00	249.69
	6327	CA	ASN	E	29	4.349	77.334	-4.702	1.00	249.69
	6328	CB	ASN	E	29	3.447	77.573	-3.470	1.00	249.69
	6329	CG	ASN	E	29	2.043	78.092	-3.837	1.00	249.69
35	6330	OD1	ASN	E	29	1.664	78.143	-5.013	1.00	249.69
	6331	ND2	ASN	E	29	1.268	78.469	-2.821	1.00	249.69
	6332	C	ASN	E	29	4.659	78.665	-5.406	1.00	249.69
	6333	O	ASN	E	29	4.147	78.925	-6.509	1.00	249.69
	6334	N	ASN	E	30	5.502	79.498	-4.796	1.00	249.69
40	6335	CA	ASN	E	30	5.807	80.792	-5.395	1.00	249.69
	6336	CB	ASN	E	30	5.157	81.904	-4.559	1.00	249.69
	6337	CG	ASN	E	30	3.636	81.814	-4.543	1.00	249.69
	6338	OD1	ASN	E	30	3.012	81.900	-3.481	1.00	249.69
	6339	ND2	ASN	E	30	3.030	81.646	-5.721	1.00	249.69
45	6340	C	ASN	E	30	7.288	81.109	-5.624	1.00	249.69
	6341	O	ASN	E	30	7.734	81.191	-6.773	1.00	249.69
	6342	N	PHE	E	31	8.047	81.290	-4.544	1.00	249.25
	6343	CA	PHE	E	31	9.464	81.634	-4.672	1.00	249.25
	6344	CB	PHE	E	31	9.744	82.979	-3.973	1.00	249.69
50	6345	CG	PHE	E	31	8.853	84.109	-4.448	1.00	249.69
	6346	CD1	PHE	E	31	7.546	84.234	-3.971	1.00	249.69
	6347	CD2	PHE	E	31	9.307	85.030	-5.397	1.00	249.69
	6348	CE1	PHE	E	31	6.702	85.255	-4.433	1.00	249.69
	6349	CE2	PHE	E	31	8.470	86.054	-5.864	1.00	249.69
55	6350	CZ	PHE	E	31	7.167	86.166	-5.380	1.00	249.69
	6351	C	PHE	E	31	10.439	80.568	-4.166	1.00	249.25
	6352	O	PHE	E	31	10.399	80.170	-3.004	1.00	249.25
	6353	N	PHE	E	32	11.324	80.127	-5.061	1.00	241.74
	6354	CA	PHE	E	32	12.329	79.106	-4.757	1.00	241.74
60	6355	CB	PHE	E	32	12.131	77.894	-5.677	1.00	249.69
	6356	CG	PHE	E	32	12.858	76.648	-5.224	1.00	249.69
	6357	CD1	PHE	E	32	12.489	75.993	-4.048	1.00	249.69
	6358	CD2	PHE	E	32	13.905	76.121	-5.984	1.00	249.69
	6359	CE1	PHE	E	32	13.150	74.834	-3.639	1.00	249.69
65	6360	CE2	PHE	E	32	14.570	74.962	-5.582	1.00	249.69
	6361	CZ	PHE	E	32	14.191	74.320	-4.407	1.00	249.69
	6362	C	PHE	E	32	13.743	79.667	-4.926	1.00	241.74
	6363	O	PHE	E	32	13.927	80.745	-5.490	1.00	241.74
	6364	N	GLU	E	33	14.739	78.916	-4.465	1.00	249.60
70	6365	CA	GLU	E	33	16.114	79.383	-4.531	1.00	249.60

6366	CB	GLU	E	33	16.663	79.497	-3.101	1.00	249.49
6367	CG	GLU	E	33	17.893	80.382	-2.971	1.00	249.49
6368	CD	GLU	E	33	17.724	81.732	-3.659	1.00	249.49
6369	OE1	GLU	E	33	16.677	82.386	-3.446	1.00	249.49
6370	OE2	GLU	E	33	18.641	82.137	-4.409	1.00	249.49
6371	C	GLU	E	33	17.112	78.603	-5.404	1.00	249.60
6372	O	GLU	E	33	17.820	79.197	-6.225	1.00	249.60
6373	N	VAL	E	34	17.179	77.285	-5.229	1.00	249.69
6374	CA	VAL	E	34	18.123	76.456	-5.982	1.00	249.69
6375	CB	VAL	E	34	18.005	74.970	-5.541	1.00	249.69
6376	CG1	VAL	E	34	19.019	74.118	-6.281	1.00	249.69
6377	CG2	VAL	E	34	18.228	74.858	-4.032	1.00	249.69
6378	C	VAL	E	34	18.014	76.540	-7.511	1.00	249.69
6379	O	VAL	E	34	16.936	76.775	-8.062	1.00	249.69
6380	N	SER	E	35	19.152	76.355	-8.178	1.00	248.45
6381	CA	SER	E	35	19.231	76.387	-9.638	1.00	248.45
6382	CB	SER	E	35	20.377	77.287	-10.097	1.00	249.69
6383	OG	SER	E	35	21.627	76.682	-9.830	1.00	249.69
6384	C	SER	E	35	19.485	74.969	-10.140	1.00	248.45
6385	O	SER	E	35	19.572	74.732	-11.350	1.00	248.45
6386	N	SER	E	36	19.622	74.036	-9.196	1.00	249.69
6387	CA	SER	E	36	19.865	72.628	-9.516	1.00	249.69
6388	CB	SER	E	36	20.966	72.043	-8.614	1.00	244.12
6389	OG	SER	E	36	20.521	71.874	-7.278	1.00	244.12
6390	C	SER	E	36	18.578	71.819	-9.352	1.00	249.69
6391	O	SER	E	36	18.259	71.325	-8.266	1.00	249.69
6392	N	THR	E	37	17.836	71.701	-10.449	1.00	208.63
6393	CA	THR	E	37	16.589	70.958	-10.462	1.00	208.63
6394	CB	THR	E	37	15.388	71.911	-10.670	1.00	197.00
6395	OG1	THR	E	37	15.343	72.880	-9.604	1.00	197.00
6396	CG2	THR	E	37	14.089	71.128	-10.693	1.00	197.00
6397	C	THR	E	37	16.689	69.957	-11.608	1.00	208.63
6398	O	THR	E	37	17.186	70.277	-12.687	1.00	208.63
6399	N	LYS	E	38	16.236	68.739	-11.366	1.00	223.46
6400	CA	LYS	E	38	16.309	67.706	-12.384	1.00	223.46
6401	CB	LYS	E	38	16.899	66.425	-11.765	1.00	231.11
6402	CG	LYS	E	38	18.295	66.620	-11.158	1.00	231.11
6403	CD	LYS	E	38	18.852	65.344	-10.528	1.00	231.11
6404	CE	LYS	E	38	20.261	65.567	-9.976	1.00	231.11
6405	NZ	LYS	E	38	20.853	64.342	-9.367	1.00	231.11
6406	C	LYS	E	38	14.947	67.420	-13.018	1.00	223.46
6407	O	LYS	E	38	13.914	67.492	-12.361	1.00	223.46
6408	N	TRP	E	39	14.951	67.117	-14.308	1.00	249.08
6409	CA	TRP	E	39	13.721	66.798	-15.022	1.00	249.08
6410	CB	TRP	E	39	13.373	67.909	-16.006	1.00	173.34
6411	CG	TRP	E	39	12.996	69.216	-15.384	1.00	173.34
6412	CD2	TRP	E	39	11.899	69.476	-14.483	1.00	173.34
6413	CE2	TRP	E	39	11.857	70.869	-14.267	1.00	173.34
6414	CE3	TRP	E	39	10.957	68.673	-13.840	1.00	173.34
6415	CD1	TRP	E	39	13.550	70.422	-15.660	1.00	173.34
6416	NE1	TRP	E	39	12.871	71.424	-14.998	1.00	173.34
6417	CZ2	TRP	E	39	10.911	71.476	-13.440	1.00	173.34
6418	CZ3	TRP	E	39	10.011	69.281	-13.014	1.00	173.34
6419	CH2	TRP	E	39	9.995	70.668	-12.828	1.00	173.34
6420	C	TRP	E	39	13.964	65.501	-15.788	1.00	249.08
6421	O	TRP	E	39	14.993	65.363	-16.450	1.00	249.08
6422	N	PHE	E	40	13.032	64.553	-15.700	1.00	178.94
6423	CA	PHE	E	40	13.206	63.281	-16.394	1.00	178.94
6424	CB	PHE	E	40	13.435	62.145	-15.383	1.00	249.69
6425	CG	PHE	E	40	14.631	62.341	-14.475	1.00	249.69
6426	CD1	PHE	E	40	14.543	63.160	-13.347	1.00	249.69
6427	CD2	PHE	E	40	15.836	61.678	-14.729	1.00	249.69
6428	CE1	PHE	E	40	15.632	63.313	-12.484	1.00	249.69
6429	CE2	PHE	E	40	16.928	61.826	-13.873	1.00	249.69
6430	CZ	PHE	E	40	16.824	62.645	-12.748	1.00	249.69
6431	C	PHE	E	40	12.051	62.896	-17.323	1.00	178.94
6432	O	PHE	E	40	11.245	62.027	-16.988	1.00	178.94
6433	N	HIS	E	41	11.992	63.534	-18.488	1.00	163.57
6434	CA	HIS	E	41	10.961	63.256	-19.477	1.00	163.57
6435	CB	HIS	E	41	11.070	64.259	-20.627	1.00	157.46

6436	CG	HIS	E	41	10.025	64.069	-21.695	1.00	157.46
6437	CD2	HIS	E	41	10.104	64.164	-23.048	1.00	157.46
6438	ND1	HIS	E	41	8.710	63.777	-21.411	1.00	157.46
6439	CE1	HIS	E	41	8.018	63.698	-22.540	1.00	157.46
6440	NE2	HIS	E	41	8.840	63.930	-23.544	1.00	157.46
6441	C	HIS	E	41	11.067	61.816	-20.031	1.00	163.57
6442	O	HIS	E	41	11.955	61.520	-20.841	1.00	163.57
6443	N	ASN	E	42	10.149	60.937	-19.611	1.00	166.06
6444	CA	ASN	E	42	10.139	59.529	-20.031	1.00	166.06
6445	CB	ASN	E	42	10.165	59.393	-21.564	1.00	227.72
6446	CG	ASN	E	42	8.800	59.655	-22.205	1.00	227.72
6447	OD1	ASN	E	42	8.150	60.654	-21.900	1.00	227.72
6448	ND2	ASN	E	42	8.370	58.767	-23.101	1.00	227.72
6449	C	ASN	E	42	11.348	58.828	-19.424	1.00	166.06
6450	O	ASN	E	42	11.820	57.822	-19.950	1.00	166.06
6451	N	GLY	E	43	11.829	59.368	-18.305	1.00	222.62
6452	CA	GLY	E	43	12.985	58.804	-17.627	1.00	222.62
6453	C	GLY	E	43	14.272	59.493	-18.049	1.00	222.62
6454	O	GLY	E	43	15.139	59.780	-17.220	1.00	222.62
6455	N	SER	E	44	14.388	59.764	-19.346	1.00	232.48
6456	CA	SER	E	44	15.560	60.424	-19.919	1.00	232.48
6457	CB	SER	E	44	15.391	60.572	-21.435	1.00	196.92
6458	OG	SER	E	44	15.207	59.322	-22.064	1.00	196.92
6459	C	SER	E	44	15.788	61.806	-19.322	1.00	232.48
6460	O	SER	E	44	14.908	62.661	-19.386	1.00	232.48
6461	N	LEU	E	45	16.970	62.033	-18.759	1.00	247.61
6462	CA	LEU	E	45	17.273	63.331	-18.173	1.00	247.61
6463	CB	LEU	E	45	18.722	63.380	-17.682	1.00	238.67
6464	CG	LEU	E	45	19.128	64.690	-16.996	1.00	238.67
6465	CD1	LEU	E	45	18.176	64.989	-15.849	1.00	238.67
6466	CD2	LEU	E	45	20.552	64.584	-16.486	1.00	238.67
6467	C	LEU	E	45	17.030	64.445	-19.194	1.00	238.67
6468	O	LEU	E	45	17.195	64.244	-20.401	1.00	247.61
6469	N	SER	E	46	16.630	65.616	-18.700	1.00	247.61
6470	CA	SER	E	46	16.339	66.768	-19.550	1.00	233.41
6471	CB	SER	E	46	15.009	67.411	-19.131	1.00	233.41
6472	OG	SER	E	46	14.644	68.461	-20.012	1.00	241.98
6473	C	SER	E	46	17.450	67.806	-19.498	1.00	241.98
6474	O	SER	E	46	18.358	67.721	-18.670	1.00	233.41
6475	N	GLU	E	47	17.353	68.798	-20.378	1.00	233.41
6476	CA	GLU	E	47	18.353	69.858	-20.479	1.00	249.69
6477	CB	GLU	E	47	18.508	70.268	-21.943	1.00	249.69
6478	CG	GLU	E	47	18.990	69.136	-22.837	1.00	249.69
6479	CD	GLU	E	47	19.114	69.555	-24.287	1.00	249.69
6480	OE1	GLU	E	47	18.075	69.901	-24.896	1.00	249.69
6481	OE2	GLU	E	47	20.247	69.540	-24.819	1.00	249.69
6482	C	GLU	E	47	18.118	71.111	-19.629	1.00	249.69
6483	O	GLU	E	17	19.014	71.949	-19.500	1.00	249.69
6484	N	GLU	E	48	16.825	71.256	-19.062	1.00	197.12
6485	CA	GLU	E	48	16.652	72.417	-18.231	1.00	197.12
6486	CB	GLU	E	48	15.153	72.734	-18.213	1.00	231.64
6487	CG	GLU	E	48	14.768	73.878	-17.276	1.00	231.64
6488	CD	GLU	E	48	15.355	75.216	-17.688	1.00	231.64
6489	OE1	GLU	E	48	14.884	75.786	-18.695	1.00	231.64
6490	OE2	GLU	E	48	16.286	75.698	-17.004	1.00	231.64
6491	C	GLU	E	48	17.147	72.146	-16.813	1.00	197.12
6492	O	GLU	E	48	17.288	70.990	-16.397	1.00	197.12
6493	N	THR	E	49	17.420	73.221	-16.080	1.00	219.19
6494	CA	THR	E	49	17.801	73.124	-14.707	1.00	219.19
6495	CB	THR	E	49	19.370	73.557	-14.610	1.00	249.63
6496	OG1	THR	E	49	19.517	74.871	-15.170	1.00	249.63
6497	CG2	THR	E	49	20.263	72.574	-15.363	1.00	249.63
6498	C	THR	E	49	17.060	74.007	-13.794	1.00	219.19
6499	O	THR	E	49	16.949	73.749	-12.597	1.00	219.19
6500	N	ASN	E	50	16.475	75.055	-14.364	1.00	248.24
6501	CA	ASN	E	50	15.625	75.963	-13.603	1.00	248.24
6502	CB	ASN	E	50	15.070	77.051	-14.530	1.00	249.69
6503	CG	ASN	E	50	14.389	78.172	-13.770	1.00	249.69
6504	OD1	ASN	E	50	14.025	78.004	-12.606	1.00	249.69
6505	ND2	ASN	E	50	14.201	79.314	-14.428	1.00	249.69

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	6506	C	ASN	E	50	14.479	75.129	-13.024	1.00	248.24
	6507	O	ASN	E	50	14.117	74.104	-13.598	1.00	248.24
	6508	N	SER	E	51	13.906	75.553	-11.900	1.00	208.41
5	6509	CA	SER	E	51	12.811	74.797	-11.296	1.00	208.41
	6510	CB	SER	E	51	12.509	75.325	-9.894	1.00	181.70
	6511	OG	SER	E	51	11.848	76.577	-9.948	1.00	181.70
	6512	C	SER	E	51	11.524	74.814	-12.142	1.00	208.41
	6513	O	SER	E	51	10.625	73.998	-11.929	1.00	208.41
	6514	N	SER	E	52	11.434	75.735	-13.100	1.00	201.05
10	6515	CA	SER	E	52	10.254	75.830	-13.962	1.00	201.05
	6516	CB	SER	E	52	9.717	77.259	-13.995	1.00	181.26
	6517	OG	SER	E	52	9.309	77.679	-12.707	1.00	181.26
	6518	C	SER	E	52	10.551	75.390	-15.385	1.00	201.05
	6519	O	SER	E	52	11.180	76.117	-16.157	1.00	201.05
15	6520	N	LEU	E	53	10.088	74.194	-15.724	1.00	168.60
	6521	CA	LEU	E	53	10.287	73.643	-17.058	1.00	168.60
	6522	CB	LEU	E	53	10.514	72.132	-16.970	1.00	122.87
	6523	CG	LEU	E	53	10.304	71.282	-18.231	1.00	122.87
	6524	CD1	LEU	E	53	10.969	71.906	-19.463	1.00	122.87
20	6525	CD2	LEU	E	53	10.854	69.900	-17.957	1.00	122.87
	6526	C	LEU	E	53	9.077	73.940	-17.340	1.00	168.60
	6527	O	LEU	E	53	8.020	73.327	-17.805	1.00	168.60
	6528	N	ASN	E	54	9.235	74.892	-18.848	1.00	150.56
	6529	CA	ASN	E	54	8.149	75.251	-19.729	1.00	150.56
25	6530	CB	ASN	E	54	8.319	76.683	-20.233	1.00	229.83
	6531	CG	ASN	E	54	8.080	77.699	-19.151	1.00	229.83
	6532	OD1	ASN	E	54	7.052	77.669	-18.479	1.00	229.83
	6533	ND2	ASN	E	54	9.029	78.606	-18.972	1.00	229.83
	6534	C	ASN	E	54	8.032	74.311	-20.905	1.00	150.56
30	6535	O	ASN	E	54	8.977	73.598	-21.260	1.00	150.56
	6536	N	ILE	E	55	6.840	74.322	-21.495	1.00	211.09
	6537	CA	ILE	E	55	6.499	73.504	-22.654	1.00	211.09
	6538	CB	ILE	E	55	5.596	72.306	-22.246	1.00	170.97
	6539	CG2	ILE	E	55	4.804	71.809	-23.445	1.00	170.97
35	6540	CG1	ILE	E	55	6.460	71.189	-21.638	1.00	170.97
	6541	CD1	ILE	E	55	5.686	69.960	-21.201	1.00	170.97
	6542	C	ILE	E	55	5.745	74.400	-23.628	1.00	211.09
	6543	O	ILE	E	55	4.659	74.893	-23.314	1.00	211.09
	6544	N	VAL	E	56	6.329	74.624	-24.799	1.00	155.17
40	6545	CA	VAL	E	56	5.684	75.466	-25.778	1.00	155.17
	6546	CB	VAL	E	56	6.705	76.318	-26.516	1.00	247.89
	6547	CG1	VAL	E	56	6.008	77.514	-27.154	1.00	247.89
	6548	CG2	VAL	E	56	7.780	76.778	-25.550	1.00	247.89
	6549	C	VAL	E	56	4.917	74.606	-26.770	1.00	155.17
45	6550	O	VAL	E	56	4.585	73.468	-26.458	1.00	155.17
	6551	N	ASN	E	57	4.639	75.144	-27.959	1.00	169.22
	6552	CA	ASN	E	57	3.886	74.432	-28.996	1.00	169.22
	6553	CB	ASN	E	57	4.365	74.837	-30.389	1.00	237.27
	6554	CG	ASN	E	57	3.979	76.263	-30.731	1.00	237.27
50	6555	OD1	ASN	E	57	2.817	76.650	-30.605	1.00	237.27
	6556	ND2	ASN	E	57	4.853	77.055	-31.165	1.00	237.27
	6557	C	ASN	E	57	3.941	72.925	-28.825	1.00	169.22
	6558	O	ASN	E	57	4.860	72.255	-29.300	1.00	169.22
	6559	N	ALA	E	58	2.923	72.424	-28.128	1.00	152.74
55	6560	CA	ALA	E	58	2.746	71.015	-27.787	1.00	152.74
	6561	CB	ALA	E	58	1.438	70.847	-27.040	1.00	133.90
	6562	C	ALA	E	58	2.812	70.012	-28.932	1.00	152.74
	6563	O	ALA	E	58	1.888	69.915	-29.751	1.00	152.74
	6564	N	LYS	E	59	3.909	69.258	-28.966	1.00	179.74
60	6565	CA	LYS	E	59	4.128	68.226	-29.976	1.00	179.74
	6566	CB	LYS	E	59	5.572	68.264	-30.469	1.00	249.69
	6567	CG	LYS	E	59	5.967	69.596	-31.093	1.00	249.69
	6568	CD	LYS	E	59	7.446	69.638	-31.470	1.00	249.69
	6569	CE	LYS	E	59	7.825	71.010	-32.032	1.00	249.69
65	6570	NZ	LYS	E	59	9.265	71.091	-32.425	1.00	249.69
	6571	C	LYS	E	59	3.853	66.896	-29.300	1.00	179.74
	6572	O	LYS	E	59	4.242	66.677	-28.156	1.00	179.74
	6573	N	PHE	E	60	3.175	66.009	-30.009	1.00	187.69
	6574	CA	PHE	E	60	2.825	64.706	-29.466	1.00	187.69
70	6575	CB	PHE	E	60	2.441	63.771	-30.613	1.00	249.39

	6576	CG	PHE	E	60	1.209	64.201	-31.352	1.00	249.39
	6577	CD1	PHE	E	60	1.035	63.865	-32.689	1.00	249.39
	6578	CD2	PHE	E	60	0.214	64.830	-30.707	1.00	249.39
	6579	CE1	PHE	E	60	-0.111	64.248	-33.377	1.00	249.39
5	6580	CE2	PHE	E	60	-0.939	65.319	-31.386	1.00	249.39
	6581	CZ	PHE	E	60	-1.101	64.976	-32.724	1.00	249.39
	6582	C	PHE	E	60	3.927	64.073	-28.626	1.00	187.69
	6583	O	PHE	E	60	3.642	63.338	-27.683	1.00	187.69
	6584	N	GLU	E	61	5.181	64.364	-28.965	1.00	196.09
10	6585	CA	GLU	E	61	6.335	63.808	-28.255	1.00	196.09
	6586	CB	GLU	E	61	7.623	64.147	-29.010	1.00	249.51
	6587	CG	GLU	E	61	7.682	63.618	-30.447	1.00	249.51
	6588	CD	GLU	E	61	6.550	64.132	-31.336	1.00	249.51
	6589	OE1	GLU	E	61	6.341	65.363	-31.403	1.00	249.51
15	6590	OE2	GLU	E	61	5.872	63.302	-31.976	1.00	249.51
	6591	C	GLU	E	61	6.433	64.313	-26.820	1.00	196.09
	6592	O	GLU	E	61	7.042	63.668	-25.965	1.00	196.09
	6593	N	ASP	E	62	5.831	65.470	-26.566	1.00	216.24
	6594	:A	ASP	E	62	5.842	66.063	-25.235	1.00	216.24
20	6595	CB	ASP	E	62	5.333	67.500	-25.285	1.00	214.73
	6596	CG	ASP	E	62	6.047	68.327	-26.319	1.00	214.73
	6597	OD1	ASP	E	62	7.249	68.076	-26.535	1.00	214.73
	6598	OD2	ASP	E	62	5.416	69.232	-26.906	1.00	214.73
	6599	C	ASP	E	62	4.971	65.264	-24.279	1.00	216.24
25	6600	O	ASP	E	62	5.152	65.325	-23.063	1.00	216.24
	6601	N	SER	E	63	4.009	64.532	-24.831	1.00	123.78
	6602	CA	SER	E	63	3.127	63.707	-24.015	1.00	123.78
	6603	CB	SER	E	63	2.085	62.988	-24.899	1.00	115.99
	6604	OG	SER	E	63	1.319	63.897	-25.674	1.00	115.99
30	6605	C	SER	E	63	4.011	62.669	-23.301	1.00	123.78
	6606	O	SER	E	63	4.783	61.957	-23.934	1.00	123.78
	6607	N	GLY	E	64	3.908	62.584	-21.986	1.00	143.97
	6608	CA	GLY	E	64	4.723	61.615	-21.294	1.00	143.97
	6609	C	GLY	E	64	4.739	61.721	-19.786	1.00	143.97
35	6610	O	GLY	E	64	3.910	62.406	-19.184	1.00	143.97
	6611	N	GLU	E	65	5.707	61.027	-19.190	1.00	147.25
	6612	CA	GLU	E	65	5.904	60.964	-17.743	1.00	147.25
	6613	CB	GLU	E	65	6.138	59.507	-17.358	1.00	197.50
	6614	CG	GLU	E	65	6.548	59.268	-15.932	1.00	197.50
40	6615	CD	GLU	E	65	7.152	57.894	-15.759	1.00	197.50
	6616	OE1	GLU	E	65	8.198	57.630	-16.379	1.00	197.50
	6617	OE2	GLU	E	65	6.587	57.076	-15.015	1.00	197.50
	6618	C	GLU	E	65	7.097	61.824	-17.309	1.00	147.25
	6619	O	GLU	E	65	8.215	61.604	-17.766	1.00	147.25
45	6620	N	TYR	E	66	6.859	62.792	-16.423	1.00	205.23
	6621	CA	TYR	E	66	7.924	63.682	-15.948	1.00	205.23
	6622	CB	TYR	E	66	7.595	65.141	-16.266	1.00	153.79
	6623	CG	TYR	E	66	7.502	65.522	-17.726	1.00	153.79
	6624	CD1	TYR	E	66	6.391	65.194	-18.490	1.00	153.79
50	6625	CE1	TYR	E	66	6.265	65.628	-19.806	1.00	153.79
	6626	CD2	TYR	E	66	8.491	66.286	-18.316	1.00	153.79
	6627	CE2	TYR	E	66	8.377	66.729	-19.628	1.00	153.79
	6628	CZ	TYR	E	66	7.265	66.403	-20.368	1.00	153.79
	6629	OH	TYR	E	66	7.159	66.870	-21.653	1.00	153.79
55	6630	C	TYR	F	66	8.179	63.597	-14.442	1.00	205.23
	6631	O	TYR	E	66	7.402	62.979	-13.710	1.00	205.23
	6632	N	LYS	E	67	9.261	64.248	-13.997	1.00	187.13
	6633	CA	LYS	E	67	9.646	64.287	-12.580	1.00	187.13
	6634	CB	LYS	E	67	9.961	62.882	-12.071	1.00	169.14
60	6635	CG	LYS	E	67	10.969	62.131	-12.908	1.00	169.14
	6636	CD	LYS	E	67	11.160	60.730	-12.365	1.00	169.14
	6637	CE	LYS	E	67	11.800	59.810	-13.402	1.00	169.14
	6638	NZ	LYS	E	67	12.045	58.414	-12.897	1.00	169.14
	6639	C	LYS	E	67	10.842	65.185	-12.276	1.00	187.13
65	6640	O	LYS	E	67	11.685	65.433	-13.141	1.00	187.13
	6641	N	CYS	E	68	10.902	65.666	-11.032	1.00	161.02
	6642	CA	CYS	E	68	12.004	66.515	-10.582	1.00	161.02
	6643	C	CYS	E	68	12.590	66.008	-9.267	1.00	161.02
	6644	O	CYS	E	68	11.900	65.396	-8.456	1.00	161.02
70	6645	CB	CYS	E	68	11.567	67.993	-10.447	1.00	132.43

	6646	SG	CYS	E	68	10.402	68.415	-9.105	1.00	132.43
	6647	N	GLN	E	69	13.880	66.274	-9.084	1.00	233.39
	6648	CA	GLN	E	69	14.623	65.865	-7.903	1.00	233.39
5	6649	CB	GLN	E	69	15.252	64.494	-8.156	1.00	249.52
	6650	CG	GLN	E	69	16.420	64.156	-7.253	1.00	249.52
	6651	CD	GLN	E	69	17.095	62.850	-7.643	1.00	249.52
	6652	OE1	GLN	E	69	17.462	62.650	-8.803	1.00	249.52
	6653	NE2	GLN	E	69	17.266	61.957	-6.673	1.00	249.52
	6654	C	GLN	E	69	15.709	66.900	-7.632	1.00	233.39
10	6655	O	GLN	E	69	16.242	67.505	-8.563	1.00	233.39
	6656	N	HIS	E	70	16.037	67.108	-6.363	1.00	249.69
	6657	CA	HIS	E	70	17.076	68.070	-6.015	1.00	249.69
	6658	CB	HIS	E	70	16.657	68.885	-4.790	1.00	243.01
	6659	CG	HIS	E	70	15.547	69.852	-5.068	1.00	243.01
15	6660	CD2	HIS	E	70	14.356	70.039	-4.454	1.00	243.01
	6661	ND1	HIS	E	70	15.605	70.774	-6.089	1.00	243.01
	6662	CE1	HIS	E	70	14.495	71.493	-6.096	1.00	243.01
	6663	NE2	HIS	E	70	13.721	71.068	-5.114	1.00	243.01
	6664	C	HIS	E	70	18.414	67.388	-5.761	1.00	249.69
20	6665	O	HIS	E	70	18.575	66.198	-6.034	1.00	249.69
	6666	N	GLN	E	71	19.370	68.148	-5.238	1.00	231.62
	6667	CA	GLN	E	71	20.708	67.634	-4.952	1.00	231.62
	6668	CB	GLN	E	71	21.554	68.756	-4.329	1.00	249.69
	6669	CG	GLN	E	71	23.080	68.559	-4.380	1.00	249.69
25	6670	CD	GLN	E	71	23.634	68.488	-5.803	1.00	249.69
	6671	OE1	GLN	E	71	23.304	69.316	-6.663	1.00	249.69
	6672	NE2	GLN	E	71	24.495	67.503	-6.049	1.00	249.69
	6673	C	GLN	E	71	20.677	66.413	-4.022	1.00	231.62
	6674	O	GLN	E	71	21.311	65.389	-4.298	1.00	231.62
30	6675	N	GLN	E	72	19.928	66.528	-2.928	1.00	249.69
	6676	CA	GLN	E	72	19.819	65.448	-1.951	1.00	249.69
	6677	CB	GLN	E	72	20.601	65.834	-0.689	1.00	249.69
	6678	CG	GLN	E	72	20.626	64.791	0.419	1.00	249.69
	6679	CD	GLN	E	72	21.284	65.315	1.687	1.00	249.69
35	6680	OE1	GLN	E	72	22.439	65.746	1.664	1.00	249.69
	6681	NE2	GLN	E	72	20.549	65.281	2.799	1.00	249.69
	6682	C	GLN	E	72	18.349	65.170	-1.607	1.00	249.69
	6683	O	GLN	E	72	17.948	65.208	-0.444	1.00	249.69
40	6684	N	VAL	E	73	17.544	64.899	-2.627	1.00	249.30
	6685	CA	VAL	E	73	16.128	64.614	-2.427	1.00	249.30
	6686	CB	VAL	E	73	15.243	65.860	-2.707	1.00	249.69
	6687	CG1	VAL	E	73	13.838	65.614	-2.192	1.00	249.69
	6688	CG2	VAL	E	73	15.843	67.101	-2.058	1.00	249.69
	6689	C	VAL	E	73	15.709	63.512	-3.386	1.00	249.30
45	6690	O	VAL	E	73	16.183	63.451	-4.516	1.00	249.30
	6691	N	ASN	E	74	14.817	62.642	-2.937	1.00	249.46
	6692	CA	ASN	E	74	14.345	61.555	-3.783	1.00	249.46
	6693	CB	ASN	E	74	13.714	60.460	-2.912	1.00	249.69
	6694	CG	ASN	E	74	14.665	59.960	-1.825	1.00	249.69
50	6695	OD1	ASN	E	74	15.859	59.769	-2.080	1.00	249.69
	6696	ND2	ASN	E	74	14.139	59.737	-0.621	1.00	249.69
	6697	C	ASN	E	74	13.346	62.081	-4.826	1.00	249.46
	6698	O	ASN	E	74	12.387	62.774	-4.485	1.00	249.46
	6699	N	GLU	E	75	13.587	61.755	-6.094	1.00	249.69
55	6700	CA	GLU	E	75	12.740	62.194	-7.209	1.00	249.69
	6701	CB	GLU	E	75	13.082	61.386	-8.468	1.00	249.69
	6702	CG	GLU	E	75	13.431	59.924	-8.199	1.00	249.69
	6703	CD	GLU	E	75	14.002	59.221	-9.425	1.00	249.69
	6704	OE1	GLU	E	75	14.946	59.768	-10.042	1.00	249.69
60	6705	OE2	GLU	E	75	13.515	58.118	-9.768	1.00	249.69
	6706	C	GLU	E	75	11.233	62.147	-6.941	1.00	249.69
	6707	O	GLU	E	75	10.724	61.213	-6.320	1.00	249.69
	6708	N	SER	E	76	10.531	63.168	-7.428	1.00	190.25
	6709	CA	SER	E	76	9.083	63.302	-7.244	1.00	190.25
65	6710	CB	SER	E	76	8.613	64.671	-7.743	1.00	199.25
	6711	OG	SER	E	76	8.614	64.717	-9.163	1.00	199.25
	6712	C	SER	E	76	8.265	62.236	-7.954	1.00	190.25
	6713	O	SER	E	76	8.728	61.612	-8.907	1.00	190.25
	6714	N	GLU	E	77	7.038	62.044	-7.481	1.00	235.50
70	6715	CA	GLU	E	77	6.135	61.072	-8.079	1.00	235.50

	6716	CB	GLU	E	77	4.839	60.973	-7.269	1.00	249.14
	6717	CG	GLU	E	77	5.029	60.405	-5.870	1.00	249.14
	6718	CD	GLU	E	77	5.532	58.966	-5.879	1.00	249.14
	6719	OE1	GLU	E	77	5.869	58.450	-6.966	1.00	249.14
5	6720	OE2	GLU	E	77	5.594	58.349	-4.795	1.00	249.14
	6721	C	GLU	E	77	5.826	61.543	-9.488	1.00	235.50
	6722	O	GLU	E	77	5.181	62.569	-9.672	1.00	235.50
	6723	N	PRO	E	78	6.280	60.791	-10.505	1.00	173.10
	6724	CD	PRO	E	78	6.805	59.420	-10.383	1.00	109.00
10	6725	CA	PRO	E	78	6.055	61.144	-11.915	1.00	173.10
	6726	CB	PRO	E	78	6.320	59.831	-12.652	1.00	109.00
	6727	CG	PRO	E	78	7.324	59.145	-11.779	1.00	109.00
	6728	C	PRO	E	78	4.648	61.657	-12.182	1.00	173.10
	6729	O	PRO	E	78	3.721	61.375	-11.410	1.00	173.10
15	6730	N	VAL	E	79	4.490	62.430	-13.253	1.00	170.14
	6731	CA	VAL	E	79	3.168	62.929	-13.628	1.00	170.14
	6732	CB	VAL	E	79	2.986	64.448	-13.378	1.00	117.67
	6733	CG1	VAL	E	79	1.708	64.936	-14.057	1.00	117.67
	6734	CG2	VAL	E	79	2.879	64.719	-11.889	1.00	117.67
20	6735	C	VAL	E	79	3.081	62.669	-15.111	1.00	170.14
	6736	O	VAL	E	79	4.093	62.798	-15.803	1.00	170.14
	6737	N	TYR	E	80	1.903	62.292	-15.605	1.00	121.68
	6738	CA	TYR	E	80	1.782	62.023	-17.028	1.00	121.68
	6739	CB	TYR	E	80	1.072	60.700	-17.272	1.00	162.42
25	6740	CG	TYR	E	80	1.291	60.179	-18.675	1.00	162.42
	6741	CD1	TYR	E	80	2.439	59.447	-18.995	1.00	162.42
	6742	CE1	TYR	E	80	2.661	58.981	-20.301	1.00	162.42
	6743	CD2	TYR	E	80	0.370	60.437	-19.696	1.00	162.42
	6744	CE2	TYR	E	80	0.588	59.980	-21.002	1.00	162.42
30	6745	CZ	TYR	E	80	1.732	59.256	-21.290	1.00	162.42
	6746	OH	TYR	E	80	1.960	58.803	-22.557	1.00	162.42
	6747	C	TYR	E	80	1.040	63.132	-17.752	1.00	121.68
	6748	O	TYR	E	80	0.022	63.642	-17.277	1.00	121.68
	6749	N	LEU	E	81	1.562	63.511	-18.906	1.00	108.83
35	6750	CA	LEU	E	81	0.943	64.545	-19.706	1.00	108.83
	6751	CB	LEU	E	81	1.930	65.677	-19.978	1.00	110.26
	6752	CG	LEU	E	81	1.380	66.724	-20.946	1.00	110.26
	6753	CD1	LEU	E	81	0.173	67.390	-20.296	1.00	110.26
	6754	CD2	LEU	E	81	2.432	67.748	-21.292	1.00	110.26
40	6755	C	LEU	E	81	0.514	63.944	-21.028	1.00	108.83
	6756	O	LEU	E	81	1.308	63.312	-21.701	1.00	108.83
	6757	N	GLU	E	82	-0.740	64.132	-21.407	1.00	99.21
	6758	CA	GLU	E	82	-1.194	63.601	-22.679	1.00	99.21
	6759	CB	GLU	E	82	-2.359	62.625	-22.473	1.00	224.57
45	6760	CG	GLU	E	82	-2.479	61.592	-23.590	1.00	224.57
	6761	CD	GLU	E	82	-3.618	60.615	-23.373	1.00	224.57
	6762	OE1	GLU	E	82	-3.903	60.282	-22.198	1.00	224.57
	6763	OE2	GLU	E	82	-4.216	60.166	-24.380	1.00	224.57
	6764	C	GLU	E	82	-1.623	64.749	-23.596	1.00	99.21
50	6765	O	GLU	E	82	-2.287	65.700	-23.142	1.00	99.21
	6766	N	VAL	E	83	-1.231	64.670	-24.876	1.00	128.82
	6767	CA	VAL	E	83	-1.599	65.690	-25.871	1.00	128.82
	6768	CB	VAL	E	83	-0.388	66.250	-26.586	1.00	97.06
	6769	CG1	VAL	E	83	-0.835	67.323	-27.572	1.00	97.06
55	6770	CG2	VAL	E	83	0.585	66.824	-25.562	1.00	97.06
	6771	C	VAL	E	83	-2.564	65.129	-26.915	1.00	128.82
	6772	O	VAL	E	83	-2.424	63.998	-27.378	1.00	128.82
	6773	N	PHE	E	84	-3.528	65.951	-27.302	1.00	126.16
	6774	CA	PHE	E	84	-4.572	65.524	-28.218	1.00	126.16
60	6775	CB	PHE	E	84	-5.893	65.416	-27.473	1.00	129.94
	6776	CG	PHE	E	84	-5.885	64.434	-26.357	1.00	129.94
	6777	CD1	PHE	E	84	-5.361	64.755	-25.107	1.00	129.94
	6778	CD2	PHE	E	84	-6.432	63.191	-26.547	1.00	129.94
	6779	CE1	PHE	E	84	-5.372	63.832	-24.070	1.00	129.94
65	6780	CE2	PHE	E	84	-6.449	62.262	-25.522	1.00	129.94
	6781	CZ	PHE	E	84	-5.924	62.585	-24.278	1.00	129.94
	6782	C	PHE	E	84	-4.872	66.377	-29.422	1.00	126.16
	6783	O	PHE	E	84	-4.588	67.571	-29.466	1.00	126.16
	6784	N	SER	E	85	-5.510	65.732	-30.385	1.00	167.68
70	6785	CA	SER	E	85	-5.960	66.381	-31.604	1.00	167.68

	6786	CB	SER	E	85	-5.136	65.957	-32.815	1.00	221.67
	6787	OG	SER	E	85	-5.627	66.593	-33.981	1.00	221.67
	6788	C	SER	E	85	-7.390	65.909	-31.783	1.00	167.68
	6789	O	SER	E	85	-7.620	64.718	-32.008	1.00	167.68
5	6790	N	ASP	E	86	-8.342	66.840	-31.661	1.00	124.68
	6791	CA	ASP	E	86	-9.766	66.530	-31.793	1.00	124.68
	6792	CB	ASP	E	86	-10.199	65.550	-30.697	1.00	146.90
	6793	CG	ASP	E	86	-11.214	64.542	-31.189	1.00	146.90
	6794	OD1	ASP	E	86	-12.235	64.955	-31.792	1.00	146.90
10	6795	OD2	ASP	E	86	-10.979	63.329	-30.978	1.00	146.90
	6796	C	ASP	E	86	-10.583	67.792	-31.658	1.00	124.68
	6797	O	ASP	E	86	-10.064	68.815	-31.244	1.00	124.68
	6798	N	TRP	E	87	-11.864	67.722	-31.995	1.00	145.58
	6799	CA	TRP	E	87	-12.717	68.901	-31.880	1.00	145.58
15	6800	CB	TRP	E	87	-14.072	68.644	-32.537	1.00	249.10
	6801	CG	TRP	E	87	-14.077	69.003	-33.989	1.00	249.10
	6802	CD2	TRP	E	87	-13.811	68.127	-35.085	1.00	249.10
	6803	CE2	TRP	E	87	-13.877	68.898	-36.268	1.00	249.10
	6804	CE3	TRP	E	87	-13.517	66.759	-35.187	1.00	249.10
20	6805	CD1	TRP	E	87	-14.291	70.241	-34.532	1.00	249.10
	6806	NE1	TRP	E	87	-14.173	70.189	-35.899	1.00	249.10
	6807	CZ2	TRP	E	87	-13.663	68.354	-37.538	1.00	249.10
	6808	CZ3	TRP	E	87	-13.302	66.212	-36.451	1.00	249.10
	6809	CH2	TRP	E	87	-13.379	67.011	-37.610	1.00	249.10
25	6810	C	TRP	E	87	-12.890	69.314	-30.433	1.00	145.58
	6811	O	TRP	E	87	-12.607	70.467	-30.077	1.00	145.58
	6812	N	LEU	E	88	-13.345	68.377	-29.605	1.00	109.18
	6813	CA	LEU	E	88	-13.521	68.658	-28.190	1.00	109.18
	6814	CB	LEU	E	88	-15.001	68.601	-27.819	1.00	123.07
30	6815	CG	LEU	E	88	-15.885	69.659	-28.476	1.00	123.07
	6816	CD1	LEU	E	88	-17.294	69.581	-27.913	1.00	123.07
	6817	CD2	LEU	E	88	-15.326	71.049	-28.223	1.00	123.07
	6818	C	LEU	E	88	-12.715	67.699	-27.298	1.00	109.18
	6819	O	LEU	E	88	-12.590	66.501	-27.598	1.00	109.18
35	6820	N	LEU	E	89	-12.147	68.231	-26.214	1.00	123.09
	6821	CA	LEU	E	89	-11.380	67.420	-25.270	1.00	123.09
	6822	CB	LEU	E	89	-9.891	67.745	-25.358	1.00	138.74
	6823	CG	LEU	E	89	-9.031	66.974	-24.347	1.00	138.74
	6824	CD1	LEU	E	89	-9.313	65.467	-24.460	1.00	138.74
40	6825	CD2	LEU	E	89	-7.565	67.265	-24.589	1.00	138.74
	6826	C	LEU	E	89	-11.865	67.724	-23.864	1.00	123.09
	6827	O	LEU	E	89	-11.959	68.879	-23.478	1.00	123.09
	6828	N	LEU	E	90	-12.184	66.695	-23.097	1.00	99.50
	6829	CA	LEU	E	90	-12.659	66.912	-21.737	1.00	99.50
45	6830	CB	LEU	E	90	-13.556	65.759	-21.305	1.00	113.63
	6831	CG	LEU	E	90	-13.932	65.784	-19.817	1.00	113.63
	6832	CD1	LEU	E	90	-14.685	67.054	-19.527	1.00	113.63
	8833	CD2	LEU	E	90	-14.770	64.565	-19.457	1.00	113.63
	6834	C	LEU	E	90	-11.502	67.023	-20.773	1.00	99.50
50	6835	O	LEU	E	90	-10.779	66.046	-20.570	1.00	99.50
	6836	N	GLN	E	91	-11.316	68.194	-20.170	1.00	92.89
	6837	CA	GLN	E	91	-10.202	68.367	-19.228	1.00	92.89
	6838	CB	GLN	E	91	-9.505	69.690	-19.467	1.00	161.25
	6839	CG	GLN	E	91	-8.933	69.836	-20.848	1.00	161.25
55	6840	CD	GLN	E	91	-8.254	71.177	-21.039	1.00	161.25
	6841	OE1	GLN	E	91	-8.877	72.232	-20.866	1.00	161.25
	6842	NE2	GLN	E	91	-6.968	71.149	-21.398	1.00	161.25
	6843	C	GLN	E	91	-10.632	68.289	-17.770	1.00	92.89
	6844	O	GLN	E	91	-11.680	68.833	-17.391	1.00	92.89
60	6845	N	ALA	E	92	-9.814	67.612	-16.961	1.00	113.22
	6846	CA	ALA	E	92	-10.114	67.458	-15.544	1.00	113.22
	6847	CB	ALA	E	92	-10.393	65.997	-15.212	1.00	187.04
	6848	C	ALA	E	92	-8.942	67.975	-14.720	1.00	113.22
	6849	O	ALA	E	92	-7.777	67.802	-15.105	1.00	113.22
65	6850	N	SER	E	93	-9.271	68.623	-13.596	1.00	114.34
	6851	CA	SER	E	93	-8.279	69.178	-12.676	1.00	114.34
	6852	CB	SER	E	93	-8.973	69.762	-11.425	1.00	137.73
	6853	OG	SER	E	93	-9.879	68.858	-10.813	1.00	137.73
	6854	C	SER	E	93	-7.326	68.043	-12.300	1.00	114.34
70	6855	O	SER	E	93	-6.140	68.078	-12.593	1.00	114.34

	6856	N	ALA	E	94	-7.869	67.028	-11.653	1.00	121.13
	6857	CA	ALA	E	94	-7.113	65.858	-11.255	1.00	121.13
	6858	CB	ALA	E	94	-6.898	65.855	-9.748	1.00	206.55
	6859	C	ALA	E	94	-8.008	64.684	-11.671	1.00	121.13
5	6860	O	ALA	E	94	-9.235	64.832	-11.768	1.00	121.13
	6861	N	GLU	E	95	-7.424	63.520	-11.937	1.00	135.32
	6862	CA	GLU	E	95	-8.238	62.378	-12.347	1.00	135.32
	6863	CB	GLU	E	95	-7.496	61.564	-13.390	1.00	189.07
	6864	CG	GLU	E	95	-7.262	62.342	-14.660	1.00	189.07
10	6865	CD	GLU	E	95	-6.736	61.482	-15.780	1.00	189.07
	6866	OE1	GLU	E	95	-6.466	62.025	-16.876	1.00	189.07
	6867	OE2	GLU	E	95	-6.596	60.259	-15.563	1.00	189.07
	6868	C	GLU	E	95	-8.632	61.500	-11.171	1.00	135.32
	6869	O	GLU	E	95	-9.632	60.772	-11.247	1.00	135.32
15	6870	N	VAL	E	96	-7.854	61.581	-10.085	1.00	121.52
	6871	CA	VAL	E	96	-8.118	60.807	-8.865	1.00	121.52
	6872	CB	VAL	E	96	-6.994	59.808	-8.591	1.00	138.26
	6873	CG1	VAL	E	96	-7.480	58.754	-7.615	1.00	138.26
	6874	CG2	VAL	E	96	-6.534	59.178	-9.895	1.00	138.26
20	6875	C	VAL	E	96	-8.237	61.741	-7.664	1.00	121.52
	6876	O	VAL	E	96	-7.376	62.598	-7.462	1.00	121.52
	6877	N	VAL	E	97	-9.278	61.566	-6.854	1.00	165.05
	6878	CA	VAL	E	97	-9.458	62.462	-5.725	1.00	165.05
	6879	CB	VAL	E	97	-10.499	63.511	-6.048	1.00	119.89
25	6880	CG1	VAL	E	97	-10.338	64.666	-5.113	1.00	119.89
	6881	CG2	VAL	E	97	-10.373	63.961	-7.482	1.00	119.89
	6882	C	VAL	E	97	-9.856	61.866	-4.380	1.00	165.05
	6883	O	VAL	E	97	-10.545	60.844	-4.325	1.00	165.05
	6884	N	MET	E	98	-9.427	62.544	-3.306	1.00	159.57
30	6885	CA	MET	E	98	-9.713	62.161	-1.914	1.00	159.57
	6886	CB	MET	E	98	-8.657	62.750	-0.973	1.00	249.69
	6887	CG	MET	E	98	-7.247	62.228	-1.152	1.00	249.69
	6888	SD	MET	E	98	-7.038	60.577	-0.463	1.00	249.69
	6889	CE	MET	E	98	-6.946	60.948	1.288	1.00	249.69
35	6890	C	MET	E	98	-11.071	62.740	-1.522	1.00	159.57
	6891	O	MET	E	98	-11.268	63.954	-1.606	1.00	159.57
	6892	N	GLU	E	99	-11.993	61.888	-1.075	1.00	145.00
	6893	CA	GLU	E	99	-13.327	62.349	-0.683	1.00	145.00
	6894	CB	GLU	E	99	-13.989	61.342	0.261	1.00	208.72
40	6895	CG	GLU	E	99	-15.505	61.399	0.247	1.00	208.72
	6896	CD	GLU	E	99	-16.126	60.618	1.385	1.00	208.72
	6897	OE1	GLU	E	99	-15.593	59.542	1.731	1.00	208.72
	6898	OE2	GLU	E	99	-17.154	61.079	1.923	1.00	208.72
	6899	C	GLU	E	99	-13.241	63.699	0.022	1.00	145.00
45	6900	O	GLU	E	99	-12.518	63.854	0.993	1.00	145.00
	6901	N	GLY	E	100	-13.970	64.686	-0.473	1.00	140.46
	6902	CA	GLY	E	100	-13.941	65.989	0.164	1.00	140.46
	6903	C	GLY	E	100	-13.192	67.070	-0.585	1.00	140.46
	6904	O	GLY	E	100	-13.449	68.256	-0.353	1.00	140.46
50	6905	N	GLN	E	101	-12.279	66.679	-1.475	1.00	158.90
	6906	CA	GLN	E	101	-11.483	67.641	-2.259	1.00	158.90
	6907	CB	GLN	E	101	-10.255	66.969	-2.835	1.00	248.74
	6908	CG	GLN	E	101	-9.216	66.625	-1.810	1.00	248.74
	6909	CD	GLN	E	101	-9.002	67.764	-0.831	1.00	248.74
55	6910	OE1	GLN	E	101	-9.873	68.070	-0.017	1.00	248.74
	6911	NE2	GLN	E	101	-7.848	68.409	-0.919	1.00	248.74
	6912	C	GLN	E	101	-12.290	68.324	-3.371	1.00	158.90
	6913	O	GLN	E	101	-13.445	67.987	-3.628	1.00	158.90
	6914	N	PRO	E	102	-11.657	69.302	-4.050	1.00	164.28
60	6915	CD	PRO	E	102	-10.406	69.971	-3.720	1.00	154.28
	6916	CA	PRO	E	102	-12.358	69.987	-5.140	1.00	164.28
	6917	CB	PRO	E	102	-11.739	71.379	-5.074	1.00	154.28
	6918	CG	PRO	E	102	-10.312	71.040	-4.796	1.00	154.28
	6919	C	PRO	E	102	-12.161	69.327	-6.496	1.00	164.28
65	6920	O	PRO	E	102	-11.119	68.720	-6.771	1.00	164.28
	6921	N	LEU	E	103	-13.169	69.467	-7.358	1.00	176.34
	6922	CA	LEU	E	103	-13.127	68.873	-8.679	1.00	176.34
	6923	CB	LEU	E	103	-13.983	67.617	-8.690	1.00	122.49
	6924	CG	LEU	E	103	-13.722	66.849	-9.971	1.00	122.49
70	6925	CD1	LEU	E	103	-12.310	66.308	-9.883	1.00	122.49

	6926	CD2	LEU	E	103	-14.724	65.736	-10.156	1.00	122.49
	6927	C	LEU	E	103	-13.618	69.805	-9.776	1.00	176.34
	6928	O	LEU	E	103	-14.736	70.305	-9.696	1.00	176.34
	6929	N	PHE	E	104	-12.805	70.027	-10.806	1.00	126.68
5	6930	CA	PHE	E	104	-13.233	70.890	-11.903	1.00	126.68
	6931	CB	PHE	E	104	-12.412	72.174	-11.954	1.00	239.90
	6932	CG	PHE	E	104	-12.405	72.934	-10.681	1.00	239.90
	6933	CD1	PHE	E	104	-11.612	72.520	-9.623	1.00	239.90
	6934	CD2	PHE	E	104	-13.201	74.060	-10.528	1.00	239.90
10	6935	CE1	PHE	E	104	-11.608	73.221	-8.416	1.00	239.90
	6936	CE2	PHE	E	104	-13.211	74.770	-9.331	1.00	239.90
	6937	CZ	PHE	E	104	-12.410	74.349	-8.269	1.00	239.90
	6938	C	PHE	E	104	-13.110	70.197	-13.250	1.00	126.68
	6939	O	PHE	E	104	-12.033	69.723	-13.600	1.00	126.68
15	6940	N	LEU	E	105	-14.208	70.136	-14.003	1.00	132.08
	6941	CA	LEU	E	105	-14.176	69.524	-15.327	1.00	132.08
	6942	CB	LEU	E	105	-15.249	68.452	-15.456	1.00	106.14
	6943	CG	LEU	E	105	-15.131	67.347	-14.414	1.00	106.14
	6944	CD1	LEU	E	105	-16.174	66.283	-14.719	1.00	106.14
20	6945	CD2	LEU	E	105	-13.704	66.777	-14.429	1.00	106.14
	6946	C	LEU	E	105	-14.413	70.618	-16.344	1.00	132.08
	6947	O	LEU	E	105	-15.119	71.592	-16.064	1.00	132.08
	6948	N	ARG	E	106	-13.848	70.456	-17.532	1.00	113.14
	6949	CA	ARG	E	106	-13.996	71.486	-18.543	1.00	113.14
25	6950	CB	ARG	E	106	-12.753	72.363	-18.492	1.00	157.66
	6951	CG	ARG	E	106	-12.740	73.498	-19.454	1.00	157.66
	6952	CD	ARG	E	106	-11.397	74.197	-19.428	1.00	157.66
	6953	NE	ARG	E	106	-11.356	75.192	-20.478	1.00	157.66
	6954	CZ	ARG	E	106	-10.256	75.566	-21.103	1.00	157.66
30	6955	NH1	ARG	E	106	-9.094	75.020	-20.774	1.00	157.66
	6956	NH2	ARG	E	106	-10.331	76.473	-22.071	1.00	157.66
	6957	C	ARG	E	106	-14.172	70.905	-19.932	1.00	113.14
	6958	O	ARG	E	106	-13.363	70.068	-20.365	1.00	113.14
	6959	N	CYS	E	107	-15.235	71.312	-20.620	1.00	132.92
35	6960	CA	CYS	E	107	-15.456	70.829	-21.979	1.00	132.92
	6961	C	CYS	E	107	-14.646	71.786	-22.808	1.00	132.92
	6962	O	CYS	E	107	-15.068	72.922	-22.996	1.00	132.92
	6963	CB	CYS	E	107	-16.923	70.942	-22.370	1.00	146.71
	6964	SG	CYS	E	107	-17.372	70.056	-23.927	1.00	146.71
40	6965	N	HIS	E	108	-13.483	71.339	-23.282	1.00	154.76
	6966	CA	HIS	E	108	-12.576	72.195	-24.052	1.00	154.76
	6967	CB	HIS	E	108	-11.130	71.911	-23.639	1.00	172.76
	6968	CG	HIS	E	108	-10.136	72.910	-24.161	1.00	172.76
	6969	CD2	HIS	E	108	-8.957	72.738	-24.810	1.00	172.76
45	6970	ND1	HIS	E	108	-10.277	74.262	-23.967	1.00	172.76
	6971	CE1	HIS	E	108	-9.221	74.888	-24.473	1.00	172.76
	6972	NE2	HIS	E	108	-8.409	73.987	-24.986	1.00	172.76
	6973	C	HIS	E	108	-12.688	72.087	-25.560	1.00	154.76
	6974	O	HIS	E	108	-12.576	70.997	-26.129	1.00	154.76
50	6975	N	GLY	E	109	-12.892	73.240	-26.194	1.00	128.76
	6976	CA	GLY	E	109	-13.007	73.287	-27.637	1.00	128.76
	6977	C	GLY	E	109	-11.632	73.334	-28.260	1.00	128.76
	6978	O	GLY	E	109	-10.666	73.574	-27.552	1.00	128.76
	6979	N	TRP	E	110	-11.539	73.092	-29.566	1.00	154.27
55	6980	CA	TRP	E	110	-10.260	73.136	-30.251	1.00	154.27
	6981	CB	TRP	E	110	-10.312	72.268	-31.503	1.00	170.55
	6982	CG	TRP	E	110	-9.107	72.411	-32.397	1.00	170.55
	6983	CD2	TRP	E	110	-7.963	71.539	-32.468	1.00	170.55
	6984	CE2	TRP	E	110	-7.073	72.098	-33.406	1.00	170.55
60	6985	CE3	TRP	E	110	-7.606	70.345	-31.825	1.00	170.55
	6986	CD1	TRP	E	110	-8.863	73.422	-33.270	1.00	170.55
	6987	NE1	TRP	E	110	-7.645	73.242	-33.877	1.00	170.55
	6988	CZ2	TRP	E	110	-5.840	71.501	-33.719	1.00	170.55
	6989	CZ3	TRP	E	110	-6.375	69.755	-32.137	1.00	170.55
65	6990	CH2	TRP	E	110	-5.509	70.339	-33.077	1.00	170.55
	6991	C	TRP	E	110	-9.897	74.586	-30.600	1.00	154.27
	6992	O	TRP	E	110	-10.786	75.431	-30.767	1.00	154.27
	6993	N	ARG	E	111	-8.596	74.878	-30.693	1.00	180.74
	6994	CA	ARG	E	111	-8.116	76.229	-30.994	1.00	180.74
70	6995	CB	ARG	E	111	-8.361	76.580	-32.460	1.00	249.46

	6996	CG	ARG	E	111	-7.220	76.198	-33.381	1.00	249.46
	6997	CD	ARG	E	111	-7.366	76.870	-34.738	1.00	249.46
	6998	NE	ARG	E	111	-6.076	77.324	-35.248	1.00	249.46
	6999	CZ	ARG	E	111	-5.295	78.200	-34.623	1.00	249.46
5	7000	NH1	ARG	E	111	-5.672	78.720	-33.463	1.00	249.46
	7001	NH2	ARG	E	111	-4.136	78.557	-35.155	1.00	249.46
	7002	C	ARG	E	111	-8.804	77.263	-30.104	1.00	180.74
	7003	O	ARG	E	111	-9.013	78.408	-30.490	1.00	180.74
	7004	N	ASN	E	112	-9.156	76.839	-28.903	1.00	179.60
10	7005	CA	ASN	E	112	-9.815	77.702	-27.949	1.00	179.60
	7006	CB	ASN	E	112	-8.820	78.719	-27.388	1.00	235.58
	7007	CG	ASN	E	112	-9.314	79.373	-26.110	1.00	235.58
	7008	OD1	ASN	E	112	-10.493	79.276	-25.757	1.00	235.58
	7009	ND2	ASN	E	112	-8.413	80.052	-25.412	1.00	235.58
15	7010	C	ASN	E	112	-11.002	78.426	-28.579	1.00	179.60
	7011	O	ASN	E	112	-11.299	79.551	-28.193	1.00	179.60
	7012	N	TRP	E	113	-11.671	77.798	-29.550	1.00	181.35
	7013	CA	TRP	E	113	-12.841	78.420	-30.174	1.00	181.35
	7014	CB	TRP	E	113	-13.343	77.633	-31.368	1.00	198.74
20	7015	CG	TRP	E	113	-12.618	77.902	-32.604	1.00	198.74
	7016	CD2	TRP	E	113	-12.345	76.965	-33.651	1.00	198.74
	7017	CE2	TRP	E	113	-11.666	77.674	-34.676	1.00	198.74
	7018	CE3	TRP	E	113	-12.603	75.599	-33.823	1.00	198.74
	7019	CD1	TRP	E	113	-12.114	79.099	-33.018	1.00	198.74
25	7020	NE1	TRP	E	113	-11.527	78.973	-34.267	1.00	198.74
	7021	CZ2	TRP	E	113	-11.246	77.052	-35.861	1.00	198.74
	7022	CZ3	TRP	E	113	-12.185	74.983	-34.994	1.00	198.74
	7023	CH2	TRP	E	113	-11.515	75.711	-36.001	1.00	198.74
	7024	C	TRP	E	113	-13.968	78.478	-29.164	1.00	181.35
30	7025	O	TRP	E	113	-13.763	78.229	-27.974	1.00	181.35
	7026	N	ASP	E	114	-15.168	78.806	-29.629	1.00	198.96
	7027	CA	ASP	E	114	-16.312	78.881	-28.724	1.00	198.96
	7028	CB	ASP	E	114	-17.015	80.250	-28.852	1.00	241.05
	7029	CG	ASP	E	114	-16.337	81.350	-28.026	1.00	241.05
35	7030	OD1	ASP	E	114	-16.217	81.193	-26.790	1.00	241.05
	7031	OD2	ASP	E	114	-15.928	82.374	-28.614	1.00	241.05
	7032	C	ASP	E	114	-17.299	77.746	-28.994	1.00	198.96
	7033	O	ASP	E	114	-17.646	77.470	-30.151	1.00	198.96
	7034	N	VAL	E	115	-17.732	77.083	-27.922	1.00	162.46
40	7035	CA	VAL	E	115	-18.686	75.985	-28.039	1.00	162.46
	7036	CB	VAL	E	115	-18.191	74.726	-27.316	1.00	122.72
	7037	CG1	VAL	E	115	-19.018	73.528	-27.751	1.00	122.72
	7038	CG2	VAL	E	115	-16.727	74.493	-27.603	1.00	122.72
	7039	C	VAL	E	115	-20.033	76.382	-27.434	1.00	162.46
45	7040	O	VAL	E	115	-20.084	77.042	-26.385	1.00	162.46
	7041	N	TYR	E	116	-21.114	75.972	-28.096	1.00	116.01
	7042	CA	TYR	E	116	-22.468	76.285	-27.648	1.00	116.01
	7043	CB	TYR	E	116	-23.177	77.143	-28.693	1.00	231.08
	7044	CG	TYR	E	116	-22.540	78.498	-28.877	1.00	231.08
50	7045	CD1	TYR	E	116	-21.643	78.743	-29.918	1.00	231.08
	7046	CE1	TYR	E	116	-21.024	79.992	-30.062	1.00	231.08
	7047	CD2	TYR	E	116	-22.805	79.531	-27.984	1.00	231.08
	7048	CE2	TYR	E	116	-22.194	80.780	-28.114	1.00	231.08
	7049	CZ	TYR	E	116	-21.306	81.006	-29.154	1.00	231.08
55	7050	OH	TYR	E	116	-20.705	82.241	-29.278	1.00	231.08
	7051	C	TYR	E	116	-23.279	75.007	-27.387	1.00	116.01
	7052	O	TYR	E	116	-22.829	73.909	-27.722	1.00	116.01
	7053	N	LYS	E	117	-24.472	75.163	-26.792	1.00	118.22
	7054	CA	LYS	E	117	-25.359	74.042	-26.454	1.00	118.22
60	7055	CB	LYS	E	117	-26.062	73.531	-27.701	1.00	223.92
	7056	CG	LYS	E	117	-27.319	74.305	-28.079	1.00	223.92
	7057	CD	LYS	E	117	-28.221	73.481	-29.013	1.00	223.92
	7058	CE	LYS	E	117	-28.639	72.150	-28.354	1.00	223.92
	7059	NZ	LYS	E	117	-29.508	71.267	-29.203	1.00	223.92
65	7060	C	LYS	E	117	-24.619	72.877	-25.764	1.00	118.22
	7061	O	LYS	E	117	-24.736	71.712	-26.150	1.00	118.22
	7062	N	VAL	E	118	-23.883	73.200	-24.714	1.00	129.60
	7063	CA	VAL	E	118	-23.120	72.205	-23.991	1.00	129.60
	7064	CB	VAL	E	118	-21.888	72.855	-23.349	1.00	89.69
70	7065	CG1	VAL	E	118	-21.403	72.044	-22.155	1.00	89.69

	7066	CG2	VAL	E	118	-20.796	72.955	-24.377	1.00	89.69
	7067	C	VAL	E	118	-23.869	71.403	-22.939	1.00	129.60
	7068	O	VAL	E	118	-24.702	71.913	-22.190	1.00	129.60
5	7069	N	ILE	E	119	-23.522	70.124	-22.896	1.00	95.90
	7070	CA	ILE	E	119	-24.087	69.164	-21.965	1.00	95.90
	7071	CB	ILE	E	119	-25.146	68.311	-22.666	1.00	119.63
	7072	CG2	ILE	E	119	-25.826	67.375	-21.651	1.00	119.63
	7073	CG1	ILE	E	119	-26.147	69.225	-23.373	1.00	119.63
	7074	CD1	ILE	E	119	-26.848	68.560	-24.500	1.00	119.63
10	7075	C	ILE	E	119	-22.989	68.219	-21.503	1.00	95.90
	7076	O	ILE	E	119	-22.248	67.666	-22.322	1.00	95.90
	7077	N	TYR	E	120	-22.869	68.034	-20.202	1.00	107.56
	7078	CA	TYR	E	120	-21.875	67.106	-19.719	1.00	107.56
	7079	CB	TYR	E	120	-21.255	67.604	-18.439	1.00	104.01
15	7080	CG	TYR	E	120	-20.386	68.807	-18.628	1.00	104.01
	7081	CD1	TYR	E	120	-20.926	70.082	-18.631	1.00	104.01
	7082	CE1	TYR	E	120	-20.114	71.219	-18.804	1.00	104.01
	7083	CD2	TYR	E	120	-19.015	68.678	-18.804	1.00	104.01
	7084	CE2	TYR	E	120	-18.202	69.795	-18.983	1.00	104.01
20	7085	CZ	TYR	E	120	-18.752	71.061	-18.983	1.00	104.01
	7086	OH	TYR	E	120	-17.933	72.151	-19.184	1.00	104.01
	7087	C	TYR	E	120	-22.604	65.814	-19.436	1.00	107.56
	7088	O	TYR	E	120	-23.806	65.843	-19.141	1.00	107.56
	7089	N	TYR	E	121	-21.908	64.685	-19.536	1.00	107.48
25	7090	CA	TYR	E	121	-22.543	63.401	-19.260	1.00	107.48
	7091	CB	TYR	E	121	-22.756	62.594	-20.561	1.00	135.25
	7092	CG	TYR	E	121	-23.773	63.118	-21.547	1.00	135.25
	7093	CD1	TYR	E	121	-23.626	64.371	-22.119	1.00	135.25
	7094	CE1	TYR	E	121	-24.513	64.825	-23.097	1.00	135.25
30	7095	CD2	TYR	E	121	-24.837	62.324	-21.967	1.00	135.25
	7096	CE2	TYR	E	121	-25.730	62.763	-22.942	1.00	135.25
	7097	CZ	TYR	E	121	-25.567	64.011	-23.507	1.00	135.25
	7098	OH	TYR	E	121	-26.438	64.440	-24.498	1.00	135.25
	7099	C	TYR	E	121	-21.706	62.546	-18.293	1.00	107.48
35	7100	O	TYR	E	121	-20.476	62.430	-18.440	1.00	107.48
	7101	N	LYS	E	122	-22.376	61.938	-17.315	1.00	117.16
	7102	CA	LYS	E	122	-21.694	61.059	-16.384	1.00	117.16
	7103	CB	LYS	E	122	-21.760	61.615	-14.969	1.00	184.34
	7104	CG	LYS	E	122	-21.046	60.734	-13.965	1.00	184.34
40	7105	CD	LYS	E	122	-21.385	61.133	-12.559	1.00	184.34
	7106	CE	LYS	E	122	-20.792	60.167	-11.568	1.00	184.34
	7107	NZ	LYS	E	122	-21.266	60.513	-10.209	1.00	184.34
	7108	C	LYS	E	122	-22.391	59.709	-16.426	1.00	117.16
	7109	O	LYS	E	122	-23.564	59.597	-16.064	1.00	117.16
45	7110	N	ASP	E	123	-21.669	58.684	-16.864	1.00	145.37
	7111	CA	ASP	E	123	-22.228	57.333	-16.960	1.00	145.37
	7112	CB	ASP	E	123	-22.532	56.766	-15.574	1.00	150.82
	7113	CG	ASP	E	123	-21.271	56.378	-14.821	1.00	150.82
	7114	OD1	ASP	E	123	-20.424	55.649	-15.391	1.00	150.82
50	7115	OD2	ASP	E	123	-21.128	56.795	-13.657	1.00	150.82
	7116	C	ASP	E	123	-23.483	57.247	-17.825	1.00	145.37
	7117	O	ASP	E	123	-24.508	56.696	-17.395	1.00	145.37
	7118	N	GLY	E	124	-23.389	57.796	-19.040	1.00	162.19
	7119	CA	GLY	E	124	-24.497	57.764	-19.983	1.00	162.19
55	7120	C	GLY	E	124	-25.683	58.666	-19.698	1.00	162.19
	7121	O	GLY	E	124	-26.586	58.768	-20.526	1.00	162.19
	7122	N	GLU	E	125	-25.683	59.324	-18.541	1.00	143.04
	7123	CA	GLU	E	125	-26.776	60.216	-18.134	1.00	143.04
	7124	CB	GLU	E	125	-27.041	60.063	-16.627	1.00	249.69
60	7125	CG	GLU	E	125	-27.627	58.724	-16.208	1.00	249.69
	7126	CD	GLU	E	125	-29.094	58.592	-16.573	1.00	249.69
	7127	OE1	GLU	E	125	-29.901	59.390	-16.051	1.00	249.69
	7128	OE2	GLU	E	125	-29.440	57.696	-17.379	1.00	249.69
	7129	C	GLU	E	125	-26.510	61.692	-18.437	1.00	143.04
65	7130	O	GLU	E	125	-25.384	62.166	-18.309	1.00	143.04
	7131	N	ALA	E	126	-27.550	62.414	-18.843	1.00	144.33
	7132	CA	ALA	E	126	-27.416	63.838	-19.120	1.00	144.33
	7133	CB	ALA	E	126	-28.693	64.365	-19.726	1.00	160.82
	7134	C	ALA	E	126	-27.187	64.451	-17.754	1.00	144.33
70	7135	O	ALA	E	126	-27.835	64.054	-16.791	1.00	144.33

	7136	N	LEU	E	127	-26.285	65.419	-17.645	1.00	143.63
	7137	CA	LEU	E	127	-26.002	65.998	-16.319	1.00	143.63
	7138	CB	LEU	E	127	-24.565	65.687	-15.904	1.00	101.20
	7139	CG	LEU	E	127	-24.442	65.621	-14.395	1.00	101.20
5	7140	CD1	LEU	E	127	-25.446	64.623	-13.859	1.00	101.20
	7141	CD2	LEU	E	127	-23.029	65.214	-14.036	1.00	101.20
	7142	C	LEU	E	127	-26.247	ͺ7.484	-16.121	1.00	143.63
	7143	O	LEU	E	127	-27.036	67.875	-15.264	1.00	143.63
	7144	N	LYS	E	128	-25.532	68.305	-16.880	1.00	117.01
10	7145	CA	LYS	E	128	-25.707	69.747	-16.812	1.00	117.01
	7146	CB	LYS	E	128	-24.508	70.394	-16.141	1.00	217.61
	7147	CG	LYS	E	128	-24.263	69.930	-14.718	1.00	217.61
	7148	CD	LYS	E	128	-25.300	70.474	-13.748	1.00	217.61
	7149	CE	LYS	E	128	-24.958	70.073	-12.316	1.00	217.61
15	7150	NZ	LYS	E	128	-25.780	70.793	-11.306	1.00	217.61
	7151	C	LYS	E	128	-25.842	70.272	-18.245	1.00	117.01
	7152	O	LYS	E	128	-25.417	69.599	-19.194	1.00	117.01
	7153	N	TYR	E	129	-26.424	71.461	-18.406	1.00	145.51
20	7154	CA	TYR	E	129	-26.601	ͺ2.029	-19.736	1.00	145.51
	7155	CB	TYR	E	129	-27.928	71.565	-20.322	1.00	135.80
	7156	CG	TYR	E	129	-28.368	72.425	-21.479	1.00	135.80
	7157	CD1	TYR	E	129	-27.913	72.180	-22.768	1.00	135.80
	7158	CE1	TYR	E	129	-28.292	73.003	-23.829	1.00	135.80
25	7159	CD2	TYR	E	129	-29.214	73.521	-21.273	1.00	135.80
	7160	CE2	TYR	E	129	-29.599	74.344	-22.318	1.00	135.80
	7161	CZ	TYR	E	129	-29.135	74.078	-23.595	1.00	135.80
	7162	OH	TYR	E	129	-29.523	74.878	-24.643	1.00	135.80
	7163	C	TYR	E	129	-26.557	73.557	-19.774	1.00	145.51
30	7164	O	TYR	E	129	-27.124	74.221	-18.907	1.00	145.51
	7165	N	TRP	E	130	-25.900	74.105	-20.800	1.00	157.70
	7166	CA	TRP	E	130	-25.786	75.554	-20.976	1.00	157.70
	7167	CB	TRP	E	130	-24.539	76.108	-20.279	1.00	223.39
	7168	CG	TRP	E	130	-24.287	75.631	-18.878	1.00	223.39
35	7169	CD2	TRP	E	130	-24.485	76.370	-17.677	1.00	223.39
	7170	CE2	TRP	E	130	-24.066	75.557	-16.598	1.00	223.39
	7171	CE3	TRP	E	130	-24.971	77.660	-17.393	1.00	223.39
	7172	CD1	TRP	E	130	-23.782	74.419	-18.498	1.00	223.39
	7173	NE1	TRP	E	130	-23.638	74.364	-17.134	1.00	223.39
	7174	CZ2	TRP	E	130	-24.117	75.974	-15.268	1.00	223.39
40	7175	CZ3	TRP	E	130	-25.023	78.083	-16.063	1.00	223.39
	7176	CH2	TRP	E	130	-24.605	77.238	-15.018	1.00	223.39
	7177	C	TRP	E	130	-25.699	75.944	-22.451	1.00	157.70
	7178	O	TRP	E	130	-25.526	75.103	-23.321	1.00	157.70
	7179	N	TYR	E	131	-25.812	77.239	-22.718	1.00	154.17
45	7180	CA	TYR	E	131	-25.721	77.775	-24.074	1.00	154.17
	7181	CB	TYR	E	131	-26.551	79.040	-24.193	1.00	200.28
	7182	CG	TYR	E	131	-26.730	79.484	-25.605	1.00	200.28
	7183	CD1	TYR	E	131	-27.576	78.794	-26.465	1.00	200.28
	7184	CE1	TYR	E	131	-27.722	79.186	-27.789	1.00	200.28
50	7185	CD2	TYR	E	131	-26.028	80.579	-26.100	1.00	200.28
	7186	CE2	TYR	E	131	-26.166	80.979	-27.426	1.00	200.28
	7187	CZ	TYR	E	131	-27.012	80.277	-28.267	1.00	200.28
	7188	OH	TYR	E	131	-27.129	80.671	-29.584	1.00	200.28
	7189	C	TYR	E	131	-24.238	78.105	-24.250	1.00	154.17
55	7190	O	TYR	E	131	-23.462	77.259	-24.690	1.00	154.17
	7191	N	GLU	E	132	-23.848	79.340	-23.930	1.00	210.53
	7192	CA	GLU	E	132	-22.436	79.713	-23.979	1.00	210.53
	7193	CB	GLU	E	132	-22.234	81.158	-23.507	1.00	249.69
	7194	CG	GLU	E	132	-22.565	82.244	-24.531	1.00	249.69
60	7195	CD	GLU	E	132	-21.342	83.062	-24.912	1.00	249.69
	7196	OE1	GLU	E	132	-20.307	82.939	-24.219	1.00	249.69
	7197	OE2	GLU	E	132	-21.411	83.832	-25.895	1.00	249.69
	7198	C	GLU	E	132	-21.980	78.737	-22.905	1.00	210.53
	7199	O	GLU	E	132	-22.554	78.723	-21.809	1.00	210.53
65	7200	N	ASN	E	133	-20.962	77.929	-23.182	1.00	143.28
	7201	CA	ASN	E	133	-20.610	76.931	-22.193	1.00	143.28
	7202	CB	ASN	E	133	-19.691	75.833	-22.820	1.00	158.57
	7203	CG	ASN	E	133	-18.215	76.179	-22.850	1.00	158.57
	7204	OD1	ASN	E	133	-17.820	77.296	-23.201	1.00	158.57
70	7205	ND2	ASN	E	133	-17.378	75.183	-22.520	1.00	158.57

	7206	C	ASN	E	133	-20.152	77.365	-20.796	1.00	143.28
	7207	O	ASN	E	133	-20.202	78.541	-20.431	1.00	143.28
	7208	N	HIS	E	134	-19.772	76.381	-19.995	1.00	154.96
	7209	CA	HIS	E	134	-19.363	76.622	-18.635	1.00	154.96
5	7210	CB	HIS	E	134	-20.574	76.432	-17.724	1.00	249.69
	7211	CG	HIS	E	134	-20.319	76.834	-16.296	1.00	249.69
	7212	CD2	HIS	E	134	-20.339	76.096	-15.160	1.00	249.69
	7213	ND1	HIS	E	134	-19.981	78.107	-15.945	1.00	249.69
	7214	CE1	HIS	E	134	-19.792	78.160	-14.625	1.00	249.69
10	7215	NE2	HIS	E	134	-20.003	76.958	-14.134	1.00	249.69
	7216	C	HIS	E	134	-18.282	75.617	-18.297	1.00	154.96
	7217	O	HIS	E	134	-17.703	74.988	-19.184	1.00	154.96
	7218	N	ASN	E	135	-18.018	75.457	-17.009	1.00	128.43
	7219	CA	ASN	E	135	-17.003	74.531	-16.537	1.00	128.43
15	7220	CB	ASN	E	135	-15.677	75.279	-16.366	1.00	226.02
	7221	CG	ASN	E	135	-15.086	75.721	-17.696	1.00	226.02
	7222	OD1	ASN	E	135	-15.047	74.928	-18.643	1.00	226.02
	7223	ND2	ASN	E	135	-14.602	76.963	-17.776	1.00	226.02
	7224	C	ASN	E	135	-17.436	73.896	-15.226	1.00	128.43
20	7225	O	ASN	E	135	-17.046	74.363	-14.166	1.00	128.43
	7226	N	ILE	E	136	-18.253	72.842	-15.318	1.00	149.25
	7227	CA	ILE	E	136	-18.788	72.102	-14.159	1.00	149.25
	7228	CB	ILE	E	136	-19.268	70.698	-14.588	1.00	170.48
	7229	CG2	ILE	E	136	-18.140	69.955	-15.266	1.00	170.48
25	7230	CG1	ILE	E	136	-19.748	69.897	-13.378	1.00	170.48
	7231	CD1	ILE	E	136	-20.169	68.485	-13.726	1.00	170.48
	7232	C	ILE	E	136	-17.824	71.949	-12.975	1.00	149.25
	7233	O	ILE	E	136	-16.894	71.133	-13.008	1.00	149.25
	7234	N	SER	E	137	-18.096	72.718	-11.918	1.00	150.66
30	7235	CA	SER	E	137	-17.258	72.738	-10.724	1.00	150.66
	7236	CB	SER	E	137	-16.914	74.185	-10.367	1.00	213.03
	7237	OG	SER	E	137	-16.282	74.247	-9.104	1.00	213.03
	7238	C	SER	E	137	-17.783	72.047	-9.478	1.00	150.66
	7239	O	SER	E	137	-18.969	72.041	-9.203	1.00	150.66
35	7240	N	ILE	E	138	-16.853	71.504	-8.709	1.00	157.82
	7241	CA	ILE	E	138	-17.154	70.795	-7.483	1.00	157.82
	7242	CB	ILE	E	138	-17.060	69.286	-7.712	1.00	122.12
	7243	CG2	ILE	E	138	-17.033	68.548	-6.388	1.00	122.12
	7244	CG1	ILE	E	138	-18.240	68.834	-8.550	1.00	122.12
40	7245	CD1	ILE	E	138	-18.110	67.429	-9.027	1.00	122.12
	7246	C	ILE	E	138	-16.219	71.180	-6.339	1.00	157.82
	7247	O	ILE	E	138	-15.000	71.039	-6.435	1.00	157.82
	7248	N	THR	E	139	-16.813	71.655	-5.251	1.00	216.52
	7249	CA	THR	E	139	-16.073	72.066	-4.067	1.00	216.52
45	7250	CB	THR	E	139	-16.922	73.033	-3.250	1.00	203.55
	7251	OG1	THR	E	139	-18.202	72.437	-2.992	1.00	203.55
	7252	CG2	THR	E	139	-17.135	74.324	-4.026	1.00	203.55
	7253	C	THR	E	139	-15.745	70.839	-3.224	1.00	216.52
	7254	O	THR	E	139	-14.637	70.307	-3.273	1.00	216.52
50	7255	N	ASN	E	140	-16.726	70.402	-2.446	1.00	176.56
	7256	CA	ASN	E	140	-16.589	69.224	-1.603	1.00	176.56
	7257	CB	ASN	E	140	-17.543	69.336	-0.405	1.00	249.69
	7258	CG	ASN	E	140	-17.486	68.128	0.504	1.00	249.69
	7259	OD1	ASN	E	140	-17.585	66.992	0.040	1.00	249.69
55	7260	ND2	ASN	E	140	-17.347	68.365	1.805	1.00	249.69
	7261	C	ASN	E	140	-16.974	68.036	-2.490	1.00	176.56
	7262	O	ASN	E	140	-18.084	67.989	-3.026	1.00	176.56
	7263	N	ALA	E	141	-16.060	67.084	-2.648	1.00	151.69
	7264	CA	ALA	E	141	-16.311	65.924	-3.498	1.00	151.69
60	7265	CB	ALA	E	141	-15.045	65.594	-4.302	1.00	113.23
	7266	C	ALA	E	141	-16.816	64.665	-2.788	1.00	151.69
	7267	O	ALA	E	141	-16.218	64.183	-1.826	1.00	151.69
	7268	N	THR	E	142	-17.925	64.133	-3.292	1.00	151.96
	7269	CA	THR	E	142	-18.534	62.921	-2.754	1.00	151.96
65	7270	CB	THR	E	142	-20.050	62.908	-2.974	1.00	230.06
	7271	OG1	THR	E	142	-20.612	64.142	-2.510	1.00	230.06
	7272	CG2	THR	E	142	-20.678	61.760	-2.218	1.00	230.06
	7273	C	THR	E	142	-17.947	61.753	-3.520	1.00	151.96
	7274	O	THR	E	142	-17.415	61.923	-4.625	1.00	151.96
70	7275	N	VAL	E	143	-18.040	60.560	-2.949	1.00	131.28

	7276	CA	VAL	E	143	-17.493	59.381	-3.631	1.00	131.28
	7277	CB	VAL	E	143	-17.368	58.167	-2.692	1.00	141.04
	7278	CG1	VAL	E	143	-18.738	57.589	-2.393	1.00	141.04
5	7279	CG2	VAL	E	143	-16.485	57.127	-3.322	1.00	141.04
	7280	C	VAL	E	143	-18.402	58.987	-4.781	1.00	131.28
	7281	O	VAL	E	143	-17.971	58.336	-5.719	1.00	131.28
	7282	N	GLU	E	144	-19.667	59.388	-4.697	1.00	177.47
	7283	CA	GLU	E	144	-20.614	59.063	-5.746	1.00	177.47
	7284	CB	GLU	E	144	-22.048	59.323	-5.298	1.00	249.69
10	7285	CG	GLU	E	144	-22.470	58.500	-4.105	1.00	249.69
	7286	CD	GLU	E	144	-22.694	59.353	-2.886	1.00	249.69
	7287	OE1	GLU	E	144	-23.589	60.221	-2.939	1.00	249.69
	7288	OE2	GLU	E	144	-21.977	59.167	-1.880	1.00	249.69
	7289	C	GLU	E	144	-20.316	59.875	-6.986	1.00	177.47
15	7290	O	GLU	E	144	-20.847	59.583	-8.050	1.00	177.47
	7291	N	ASP	E	145	-19.467	60.895	-6.851	1.00	122.39
	7292	CA	ASP	E	145	-19.091	61.723	-7.994	1.00	122.39
	7293	CB	ASP	E	145	-18.410	62.997	-7.532	1.00	174.03
20	7294	CG	ASP	E	145	-19.396	64.013	-7.012	1.00	174.03
	7295	OD1	ASP	E	145	-20.326	64.372	-7.768	1.00	174.03
	7296	OD2	ASP	E	145	-19.244	64.459	-5.854	1.00	174.03
	7297	C	ASP	E	145	-18.165	60.969	-8.943	1.00	122.39
	7298	O	ASP	E	145	-17.996	61.363	-10.098	1.00	122.39
25	7299	N	SER	E	146	-17.580	59.870	-8.458	1.00	134.53
	7300	CA	SER	E	146	-16.672	59.031	-9.263	1.00	134.53
	7301	CB	SER	E	146	-16.037	57.940	-8.393	1.00	131.44
	7302	OG	SER	E	146	-15.340	58.481	-7.281	1.00	131.44
	7303	C	SER	E	146	-17.412	58.362	-10.418	1.00	134.53
30	7304	O	SER	E	146	-18.431	57.729	-10.211	1.00	134.53
	7305	N	GLY	E	147	-16.892	58.500	-11.628	1.00	156.93
	7306	CA	GLY	E	147	-17.542	57.888	-12.769	1.00	156.93
	7307	C	GLY	E	147	-16.839	58.176	-14.083	1.00	156.93
	7308	O	GLY	E	147	-15.656	58.545	-14.095	1.00	156.93
35	7309	N	THR	E	148	-17.559	58.006	-15.194	1.00	115.73
	7310	CA	THR	E	148	-16.993	58.263	-16.530	1.00	115.73
	7311	CB	THR	E	148	-16.985	56.964	-17.380	1.00	136.83
	7312	OG1	THR	E	148	-18.127	56.934	-18.238	1.00	136.83
	7313	CG2	THR	E	148	-17.031	55.746	-16.476	1.00	136.83
40	7314	C	THR	E	148	-17.755	59.409	-17.266	1.00	115.73
	7315	O	THR	E	148	-18.927	59.283	-17.642	1.00	115.73
	7316	N	TYR	E	149	-17.068	60.533	-17.457	1.00	98.03
	7317	CA	TYR	E	149	-17.660	61.699	-18.084	1.00	98.03
	7318	CB	TYR	E	149	-17.292	62.968	-17.301	1.00	106.49
	7319	CG	TYR	E	149	-17.670	62.986	-15.828	1.00	106.49
45	7320	CD1	TYR	E	149	-16.951	62.244	-14.885	1.00	106.49
	7321	CE1	TYR	E	149	-17.293	62.279	-13.545	1.00	106.49
	7322	CD2	TYR	E	149	-18.740	63.766	-15.378	1.00	106.49
	7323	CE2	TYR	E	149	-19.081	63.812	-14.046	1.00	106.49
50	7324	CZ	TYR	E	149	-18.358	63.065	-13.137	1.00	106.49
	7325	OH	TYR	E	149	-18.715	63.098	-11.815	1.00	106.49
	7326	C	TYR	E	149	-17.229	61.914	-19.518	1.00	98.03
	7327	O	TYR	E	149	-16.224	61.346	-19.972	1.00	98.03
	7328	N	TYR	E	150	-18.002	62.767	-20.200	1.00	87.55
55	7329	CA	TYR	E	150	-17.780	63.194	-21.595	1.00	87.55
	7330	CB	TYR	E	150	-18.019	62.028	-22.591	1.00	125.81
	7331	CG	TYR	E	150	-19.456	61.684	-22.936	1.00	125.81
	7332	CD1	TYR	E	150	-20.224	62.527	-23.739	1.00	125.81
	7333	CE1	TYR	E	150	-21.551	62.200	-24.087	1.00	125.81
60	7334	CD2	TYR	E	150	-20.041	60.496	-22.482	1.00	125.81
	7335	CE2	TYR	E	150	-21.371	60.157	-22.828	1.00	125.81
	7336	CZ	TYR	E	150	-22.116	61.018	-23.631	1.00	125.81
	7337	OH	TYR	E	150	-23.405	60.699	-23.991	1.00	125.81
	7338	C	TYR	E	150	-18.765	64.338	-21.835	1.00	87.55
65	7339	O	TYR	E	150	-19.801	64.418	-21.160	1.00	87.55
	7340	N	CYS	E	151	-18.456	65.235	-22.763	1.00	108.53
	7341	CA	CYS	E	151	-19.370	66.343	-23.043	1.00	108.53
	7342	C	CYS	E	151	-19.724	66.457	-24.522	1.00	108.53
	7343	O	CYS	E	151	-19.030	65.919	-25.385	1.00	108.53
70	7344	CB	CYS	E	151	-18.749	67.647	-22.588	1.00	127.42
	7345	SG	CYS	E	151	-17.166	68.090	-23.414	1.00	127.42

	7346	N	THR	E	152	-20.816	67.151	-24.810	1.00	109.73
	7347	CA	THR	E	152	-21.249	67.343	-26.184	1.00	109.73
	7348	CB	THR	E	152	-22.546	66.577	-26.478	1.00	160.87
	7349	OG1	THR	E	152	-23.649	67.242	-25.840	1.00	160.87
5	7350	CG2	THR	E	152	-22.443	65.158	-25.963	1.00	160.87
	7351	C	THR	E	152	-21.530	68.832	-26.420	1.00	109.73
	7352	O	THR	E	152	-21.983	69.541	-25.509	1.00	109.73
	7353	N	GLY	E	153	-21.284	69.305	-27.640	1.00	146.21
	7354	CA	GLY	E	153	-21.530	70.706	-27.927	1.00	146.21
10	7355	C	GLY	E	153	-21.486	71.046	-29.398	1.00	146.21
	7356	O	GLY	E	153	-21.040	70.244	-30.204	1.00	146.21
	7357	N	LYS	E	154	-21.947	72.247	-29.739	1.00	118.16
	7358	CA	LYS	E	154	-21.973	72.704	-31.114	1.00	118.16
	7359	CB	LYS	E	154	-23.332	73.316	-31.423	1.00	235.84
15	7360	CG	LYS	E	154	-23.517	73.732	-32.861	1.00	235.84
	7361	CD	LYS	E	154	-24.925	74.260	-33.087	1.00	235.84
	7362	CE	LYS	E	154	-25.120	74.744	-34.517	1.00	235.84
	7363	NZ	LYS	E	154	-26.493	75.280	-34.746	1.00	235.84
	7364	C	LYS	E	154	-20.864	73.716	-31.376	1.00	118.16
20	7365	O	LYS	E	154	-20.821	74.780	-30.758	1.00	118.16
	7366	N	VAL	E	155	-19.957	73.364	-32.288	1.00	164.34
	7367	CA	VAL	E	155	-18.825	74.214	-32.686	1.00	164.34
	7368	CB	VAL	E	155	-17.520	73.384	-32.768	1.00	138.01
	7369	CG1	VAL	E	155	-16.369	74.233	-33.254	1.00	138.01
25	7370	CG2	VAL	E	155	-17.198	72.808	-31.398	1.00	138.01
	7371	C	VAL	E	155	-19.166	74.746	-34.073	1.00	164.34
	7372	O	VAL	E	155	-19.503	73.962	-34.965	1.00	164.34
	7373	N	TRP	E	156	-19.058	76.060	-34.268	1.00	249.37
	7374	CA	TRP	E	156	-19.413	76.665	-35.557	1.00	249.37
30	7375	CB	TRP	E	156	-18.639	76.057	-36.746	1.00	249.69
	7376	CG	TRP	E	156	-17.160	76.335	-36.808	1.00	249.69
	7377	CD2	TRP	E	156	-16.521	77.599	-37.045	1.00	249.69
	7378	CE2	TRP	E	156	-15.126	77.369	-37.030	1.00	249.69
	7379	CE3	TRP	E	156	-16.992	78.898	-37.283	1.00	249.69
35	7380	CD1	TRP	E	156	-16.152	75.425	-36.653	1.00	249.69
	7381	NE1	TRP	E	156	-14.929	76.035	-36.786	1.00	249.69
	7382	CZ2	TRP	E	156	-14.197	78.389	-37.233	1.00	249.69
	7383	CZ3	TRP	E	156	-16.067	79.915	-37.486	1.00	249.69
	7384	CH2	TRP	E	156	-14.684	79.652	-37.459	1.00	249.69
40	7385	C	TRP	E	156	-20.881	76.332	-35.750	1.00	249.37
	7386	O	TRP	E	156	-21.762	77.001	-35.194	1.00	249.37
	7387	N	GLN	E	157	-21.128	75.279	-36.536	1.00	132.72
	7388	CA	GLN	E	157	-22.489	74.837	-36.802	1.00	132.72
	7389	CB	GLN	E	157	-23.006	75.460	-38.103	1.00	249.69
45	7390	CG	GLN	E	157	-23.387	76.941	-37.974	1.00	249.69
	7391	CD	GLN	E	157	-24.572	77.181	-37.037	1.00	249.69
	7392	OE1	GLN	E	157	-25.685	76.713	-37.291	1.00	249.69
	7393	NE2	GLN	E	157	-24.334	77.914	-35.949	1.00	249.69
	7394	C	GLN	E	157	-22.668	73.317	-36.834	1.00	132.72
50	7395	O	GLN	E	157	-23.628	72.812	-37.423	1.00	132.72
	7396	N	LEU	E	158	-21.756	72.587	-36.195	1.00	229.55
	7397	CA	LEU	E	158	-21.863	71.130	-36.137	1.00	229.55
	7398	CB	LEU	E	158	-20.818	70.467	-37.038	1.00	228.12
	7399	CG	LEU	E	158	-21.063	70.461	-38.553	1.00	228.12
55	7400	CD1	LEU	E	158	-20.552	69.140	-39.108	1.00	228.12
	7401	CD2	LEU	E	158	-22.544	70.590	-38.874	1.00	228.12
	7402	C	LEU	E	158	-21.716	70.605	-34.713	1.00	229.55
	7403	O	LEU	E	158	-21.041	71.216	-33.885	1.00	229.55
	7404	N	ASP	E	159	-22.357	69.472	-34.438	1.00	199.14
60	7405	CA	ASP	E	159	-22.299	68.862	-33.114	1.00	199.14
	7406	CB	ASP	E	159	-23.567	68.050	-32.848	1.00	198.75
	7407	CG	ASP	E	159	-24.829	68.854	-33.075	1.00	198.75
	7408	OD1	ASP	E	159	-25.033	69.866	-32.365	1.00	198.75
	7409	OD2	ASP	E	159	-25.613	68.475	-33.970	1.00	198.75
65	7410	C	ASP	E	159	-21.082	67.948	-32.988	1.00	199.14
	7411	O	ASP	E	159	-20.656	67.333	-33.963	1.00	199.14
	7412	N	TYR	E	160	-20.522	67.887	-31.784	1.00	164.98
	7413	CA	TYR	E	160	-19.368	67.017	-31.543	1.00	164.98
70	7414	CB	TYR	E	160	-18.071	67.782	-31.730	1.00	170.02
	7415	CG	TYR	E	160	-17.959	68.445	-33.079	1.00	170.02

	7416	CD1	TYR E	160	-18.428	69.746	-33.285	1.00	170.02
	7417	CE1	TYR E	160	-18.291	70.376	-34.516	1.00	170.02
	7418	CD2	TYR E	160	-17.362	67.787	-34.147	1.00	170.02
	7419	CE2	TYR E	160	-17.221	68.407	-35.390	1.00	170.02
5	7420	CZ	TYR E	160	-17.685	69.700	-35.562	1.00	170.02
	7421	OH	TYR E	160	-17.517	70.325	-36.771	1.00	170.02
	7422	C	TYR E	160	-19.385	66.416	-30.153	1.00	164.98
	7423	O	TYR E	160	-19.844	67.025	-29.185	1.00	164.98
	7424	N	GLU E	161	-18.861	65.204	-30.073	1.00	121.76
10	7425	CA	GLU E	161	-18.805	64.435	-28.835	1.00	121.76
	7426	CB	GLU E	161	-19.432	63.056	-29.104	1.00	238.30
	7427	CG	GLU E	161	-19.437	62.062	-27.962	1.00	238.30
	7428	CD	GLU E	161	-20.385	60.898	-28.227	1.00	238.30
	7429	OE1	GLU E	161	-20.217	59.834	-27.596	1.00	238.30
15	7430	OE2	GLU E	161	-21.310	61.051	-29.058	1.00	238.30
	7431	C	GLU E	161	-17.340	64.330	-28.425	1.00	121.76
	7432	O	GLU E	161	-16.464	64.228	-29.275	1.00	121.76
	7433	N	SER E	162	-17.079	64.384	-27.125	1.00	141.30
20	7434	CA	SER E	162	-15.712	64.316	-26.603	1.00	141.30
	7435	CB	SER E	162	-15.579	65.188	-25.350	1.00	137.77
	7436	OG	SER E	162	-16.423	64.719	-24.305	1.00	137.77
	7437	C	SER E	162	-15.318	62.905	-26.240	1.00	141.30
	7438	O	SER E	162	-16.181	62.046	-26.067	1.00	141.30
	7439	N	GLU E	163	-14.015	62.662	-26.132	1.00	137.45
25	7440	CA	GLU E	163	-13.553	61.335	-25.739	1.00	137.45
	7441	CB	GLU E	163	-12.021	61.264	-25.770	1.00	249.69
	7442	CG	GLU E	163	-11.400	61.173	-27.169	1.00	249.69
	7443	CD	GLU E	163	-11.585	59.804	-27.826	1.00	249.69
	7444	OE1	GLU E	163	-11.171	58.791	-27.226	1.00	249.69
30	7445	OE2	GLU E	163	-12.138	59.742	-28.944	1.00	249.69
	7446	C	GLU E	163	-14.057	61.170	-24.309	1.00	137.45
	7447	O	GLU E	163	-14.182	62.171	-23.593	1.00	137.45
	7448	N	PRO E	164	-14.377	59.935	-23.877	1.00	95.03
	7449	CD	PRO E	164	-14.382	58.681	-24.662	1.00	218.77
35	7450	CA	PRO E	164	-14.877	59.684	-22.521	1.00	95.03
	7451	CB	PRO E	164	-15.570	58.345	-22.657	1.00	218.77
	7452	CG	PRO E	164	-14.657	57.637	-23.594	1.00	218.77
	7453	C	PRO E	164	-13.761	59.664	-21.475	1.00	95.03
	7454	O	PRO E	164	-12.660	59.202	-21.764	1.00	95.03
40	7455	N	LEU E	165	-14.046	60.133	-20.267	1.00	132.61
	7456	CA	LEU E	165	-13.021	60.175	-19.240	1.00	132.61
	7457	CB	LEU E	165	-12.581	61.627	-19.014	1.00	87.30
	7458	CG	LEU E	165	-11.475	61.851	-17.979	1.00	87.30
45	7459	CD1	LEU E	165	-10.446	60.707	-18.043	1.00	87.30
	7460	CD2	LEU E	165	-10.812	63.181	-18.220	1.00	87.30
	7461	C	LEU E	165	-13.411	59.560	-17.905	1.00	132.61
	7462	O	LEU E	165	-14.470	59.883	-17.367	1.00	132.61
	7463	N	ASN E	166	-12.545	58.690	-17.364	1.00	112.66
50	7464	CA	ASN E	166	-12.794	58.050	-16.068	1.00	112.66
	7465	CB	ASN E	166	-12.116	56.693	-16.002	1.00	172.55
	7466	CG	ASN E	166	-13.038	55.560	-16.402	1.00	172.55
	7467	OD1	ASN E	166	-14.264	55.679	-16.328	1.00	172.55
	7468	ND2	ASN E	166	-12.445	54.443	-16.804	1.00	172.55
55	7469	C	ASN E	166	-12.294	58.889	-14.909	1.00	112.66
	7470	O	ASN E	166	-11.246	59.511	-14.999	1.00	112.66
	7471	N	ILE E	167	-13.032	58.887	-13.807	1.00	147.51
	7472	CA	ILE E	167	-12.643	59.658	-12.628	1.00	147.51
	7473	CB	ILE E	167	-13.409	60.966	-12.546	1.00	109.60
	7474	CG2	ILE E	167	-13.051	61.688	-11.260	1.00	109.60
60	7475	CG1	ILE E	167	-13.086	61.820	-13.760	1.00	109.60
	7476	CD1	ILE E	167	-13.847	63.089	-13.806	1.00	109.60
	7477	C	ILE E	167	-12.904	58.901	-11.343	1.00	147.51
	7478	O	ILE E	167	-14.007	58.401	-11.115	1.00	147.51
	7479	N	THR E	168	-11.903	58.840	-10.481	1.00	104.75
65	7480	CA	THR E	168	-12.093	58.106	-9.251	1.00	104.75
	7481	CB	THR E	168	-11.250	56.819	-9.263	1.00	148.63
	7482	OG1	THR E	168	-11.607	56.040	-10.408	1.00	148.63
	7483	CG2	THR E	168	-11.516	55.997	-8.014	1.00	148.63
	7484	C	THR E	168	-11.831	58.886	-7.956	1.00	104.75
70	7485	O	THR E	168	-10.763	59.432	-7.718	1.00	104.75

	7486	N	VAL	E	169	-12.849	58.924	-7.117	1.00	128.03
	7487	CA	VAL	E	169	-12.771	59.592	-5.835	1.00	128.03
	7488	CB	VAL	E	169	-14.028	60.478	-5.592	1.00	104.73
	7489	CG1	VAL	E	169	-14.231	60.741	-4.125	1.00	104.73
5	7490	CG2	VAL	E	169	-13.853	61.798	-6.296	1.00	104.73
	7491	C	VAL	E	169	-12.683	58.492	-4.783	1.00	128.03
	7492	O	VAL	E	169	-13.645	57.767	-4.542	1.00	128.03
	7493	N	ILE	E	170	-11.510	58.363	-4.171	1.00	164.43
	7494	CA	ILE	E	170	-11.265	57.356	-3.135	1.00	164.43
10	7495	CB	ILE	E	170	-9.826	56.804	-3.258	1.00	148.98
	7496	CG2	ILE	E	170	-9.566	56.357	-4.685	1.00	148.98
	7497	CG1	ILE	E	170	-8.816	57.897	-2.906	1.00	148.98
	7498	CD1	ILE	E	170	-7.368	57.440	-2.961	1.00	148.98
	7499	C	ILE	E	170	-11.467	57.968	-1.744	1.00	164.43
15	7500	O	ILE	E	170	-11.524	59.184	-1.610	1.00	164.43
	7501	N	LYS	E	171	-11.560	57.141	-0.709	1.00	181.58
	7502	CA	LYS	E	171	-11.775	57.672	0.633	1.00	181.58
	7503	CB	LYS	E	171	-13.118	57.176	1.157	1.00	249.69
	7504	CG	LYS	E	171	-13.230	55.666	1.123	1.00	249.69
20	7505	CD	LYS	E	171	-14.675	55.211	0.996	1.00	249.69
	7506	CE	LYS	E	171	-15.530	55.712	2.154	1.00	249.69
	7507	NZ	LYS	E	171	-16.931	55.206	2.058	1.00	249.69
	7508	C	LYS	E	171	-10.673	57.327	1.632	1.00	181.58
	7509	O	LYS	E	171	-10.810	57.585	2.833	1.00	181.58
25	7510	C1	NAG	E	221	2.209	79.546	-26.386	1.00	249.69
	7511	C2	NAG	E	221	0.889	80.273	-26.643	1.00	249.69
	7512	N2	NAG	E	221	-0.170	79.298	-26.828	1.00	249.69
	7513	C7	NAG	E	221	-1.431	79.634	-26.596	1.00	249.69
	7514	O7	NAG	E	221	-1.768	80.762	-26.235	1.00	249.69
30	7515	C8	NAG	E	221	-2.476	78.553	-26.806	1.00	249.69
	7516	C3	NAG	E	221	1.001	81.165	-27.881	1.00	249.69
	7517	O3	NAG	E	221	-0.178	81.953	-28.009	1.00	249.69
	7518	C4	NAG	E	221	2.237	82.087	-27.816	1.00	249.69
	7519	O4	NAG	E	221	2.396	82.690	-29.116	1.00	249.69
35	7520	C5	NAG	E	221	3.502	81.275	-27.447	1.00	249.69
	7521	O5	NAG	E	221	3.276	80.502	-26.244	1.00	249.69
	7522	C6	NAG	E	221	4.726	82.136	-27.185	1.00	249.69
	7523	O6	NAG	E	221	4.477	83.098	-26.171	1.00	249.69
	7524	C1	NAG	E	222	3.181	83.831	-29.256	1.00	249.69
40	7525	C2	NAG	E	222	2.456	84.839	-30.180	1.00	249.69
	7526	N2	NAG	E	222	1.186	85.239	-29.587	1.00	249.69
	7527	C7	NAG	E	222	0.936	86.518	-29.301	1.00	249.69
	7528	O7	NAG	E	222	1.741	87.429	-29.516	1.00	249.69
	7529	C8	NAG	E	222	-0.420	86.835	-28.681	1.00	249.69
45	7530	C3	NAG	E	222	2.220	84.191	-31.568	1.00	249.69
	7531	O3	NAG	E	222	1.662	85.147	-32.469	1.00	249.69
	7532	C4	NAG	E	222	3.543	83.638	-32.143	1.00	249.69
	7533	O4	NAG	E	222	3.281	82.909	-33.338	1.00	248.69
	7534	C5	NAG	E	222	4.233	82.718	-31.115	1.00	249.69
50	7535	O5	NAG	E	222	4.427	83.426	-29.859	1.00	249.69
	7536	C6	NAG	E	222	5.592	82.211	-31.572	1.00	249.69
	7537	O6	NAG	E	222	5.701	80.806	-31.409	1.00	249.69
	7538	C1	NAG	E	242	7.147	59.017	-23.850	1.00	193.96
	7539	C2	NAG	E	242	7.463	59.646	-25.212	1.00	193.96
55	7540	N2	NAG	E	242	8.286	60.830	-25.064	1.00	193.96
	7541	C7	NAG	E	242	9.478	60.868	-25.645	1.00	193.96
	7542	O7	NAG	E	242	9.927	59.930	-26.305	1.00	193.96
	7543	C8	NAG	E	242	10.299	62.130	-25.465	1.00	193.96
	7544	C3	NAG	E	242	6.151	59.995	-25.913	1.00	193.96
60	7545	O3	NAG	E	242	6.418	60.545	-27.194	1.00	193.96
	7546	C4	NAG	E	242	5.284	58.740	-26.060	1.00	193.96
	7547	O4	NAG	E	242	3.983	59.116	-26.566	1.00	193.96
	7548	C5	NAG	E	242	5.124	58.005	-24.698	1.00	193.96
	7549	O5	NAG	E	242	6.411	57.799	-24.050	1.00	193.96
65	7550	C6	NAG	E	242	4.509	56.624	-24.872	1.00	193.96
	7551	O6	NAG	E	242	3.211	56.550	-24.304	1.00	193.96
	7552	C1	NAG	E	243	3.598	58.568	-27.770	1.00	215.12
	7553	C2	NAG	E	243	2.085	58.638	-27.907	1.00	215.12
	7554	N2	NAG	E	243	1.433	57.909	-26.843	1.00	215.12
70	7555	C7	NAG	E	243	0.428	58.482	-26.182	1.00	215.12

	7556	O7	NAG E	243	0.027	59.633	-26.423	1.00	215.12
	7557	C8	NAG E	243	-0.230	57.665	-25.075	1.00	215.12
	7558	C3	NAG E	243	1.685	58.056	-29.247	1.00	215.12
	7559	O3	NAG E	243	0.272	58.105	-29.401	1.00	215.12
5	7560	C4	NAG E	243	2.344	58.866	-30.339	1.00	215.12
	7561	O4	NAG E	243	1.898	58.318	-31.574	1.00	215.12
	7562	C5	NAG E	243	3.883	58.823	-30.140	1.00	215.12
	7563	O5	NAG E	243	4.208	59.328	-28.814	1.00	215.12
	7564	C6	NAG E	243	4.624	59.699	-31.116	1.00	215.12
10	7565	O6	NAG E	243	4.268	61.057	-30.933	1.00	215.12
	7566	C1	MAN E	244	1.748	59.080	-32.701	1.00	219.74
	7567	C2	MAN E	244	2.233	58.170	-33.738	1.00	219.74
	7568	O2	MAN E	244	1.708	56.848	-33.490	1.00	219.74
	7569	C3	MAN E	244	1.963	58.748	-35.107	1.00	219.74
15	7570	O3	MAN E	244	2.548	57.949	-36.119	1.00	219.74
	7571	C4	MAN E	244	0.488	58.983	-35.314	1.00	219.74
	7572	O4	MAN E	244	0.264	59.475	-36.620	1.00	219.74
	7573	C5	MAN E	244	0.038	59.992	-34.253	1.00	219.74
	7574	O5	MAN E	244	0.282	59.4 . .	-32.908	1.00	219.74
20	7575	C6	MAN E	244	-1.419	60.489	-34.434	1.00	219.74
	7576	O6	MAN E	244	-2.389	59.610	-33.877	1.00	219.74
	7577	C1	NAG E	250	12.894	79.616	-14.981	1.00	249.69
	7578	C2	NAG E	250	12.331	80.923	-14.392	1.00	249.69
	7579	N2	NAG E	250	12.256	80.832	-12.946	1.00	249.69
25	7580	C7	NAG E	250	13.100	81.532	-12.196	1.00	249.69
	7581	O7	NAG E	250	13.967	82.276	-12.673	1.00	249.69
	7582	C8	NAG E	250	12.966	81.387	-10.683	1.00	249.69
	7583	C3	NAG E	250	10.934	81.188	-14.970	1.00	249.69
	7584	O3	NAG E	250	10.442	82.440	-14.506	1.00	249.69
30	7585	C4	NAG E	250	10.987	81.183	-16.508	1.00	249.69
	7586	O4	NAG E	250	9.667	81.305	-17.032	1.00	249.69
	7587	C5	NAG E	250	11.643	79.872	-17.010	1.00	249.69
	7588	O5	NAG E	250	12.954	79.705	-16.412	1.00	249.69
	7589	C6	NAG E	250	11.833	79.816	-18.522	1.00	249.69
35	7590	O6	NAG E	250	12.752	78.791	-18.892	1.00	249.69
	7591	C1	NAG E	274	14.635	58.650	0.211	1.00	249.69
	7592	C2	NAG E	274	13.525	58.145	1.158	1.00	249.69
	7593	N2	NAG E	274	13.058	59.230	2.009	1.00	249.69
	7594	C7	NAG E	274	11.826	59.208	2.513	1.00	249.69
40	7595	O7	NAG E	274	11.030	58.289	2.302	1.00	249.69
	7596	C8	NAG E	274	11.415	60.380	3.387	1.00	249.69
	7597	C3	NAG E	274	14.058	56.984	2.020	1.00	249.69
	7598	O3	NAG E	274	12.997	56.422	2.785	1.00	249.69
	7599	C4	NAG E	274	14.687	55.894	1.134	1.00	249.69
45	7600	O4	NAG E	274	15.298	54.900	1.951	1.00	249.69
	7601	C5	NAG E	274	15.736	56.513	0.196	1.00	249.69
	7602	O5	NAG E	274	15.136	57.567	-0.595	1.00	249.69
	7603	C6	NAG E	274	16.324	55.500	-0.775	1.00	249.69
	7604	O6	NAG E	274	17.151	56.129	-1.748	1.00	249.69
50	7605	C1	NAG E	335	-13.218	77.155	-18.184	1.00	248.99
	7606	C2	NAG E	335	-12.377	77.952	-17.147	1.00	248.99
	7607	N2	NAG E	335	-13.025	77.859	-15.850	1.00	248.99
	7608	C7	NAG E	335	-12.415	77.253	-14.835	1.00	248.99
	7609	O7	NAG E	335	-11.291	76.751	-14.921	1.00	248.99
55	7610	C8	NAG E	335	-13.169	77.199	-13.517	1.00	248.99
	7611	C3	NAG E	335	-12.169	79.444	-17.498	1.00	248.99
	7612	O3	NAG E	335	-11.051	79.949	-16.774	1.00	248.99
	7613	C4	NAG E	335	-11.918	79.636	-18.990	1.00	248.99
	7614	O4	NAG E	335	-11.812	81.021	-19.294	1.00	248.99
60	7615	C5	NAG E	335	-13.079	79.014	-19.748	1.00	248.99
	7616	O5	NAG E	335	-13.060	77.584	-19.562	1.00	248.99
	7617	C6	NAG E	335	-12.991	79.270	-21.238	1.00	248.99
	7618	O6	NAG E	335	-14.176	79.882	-21.722	1.00	248.99
	7619	C1	NAG E	340	-18.408	67.970	2.712	1.00	249.69
65	7620	C2	NAG E	340	-17.972	66.798	3.606	1.00	249.69
	7621	N2	NAG E	340	-17.526	65.688	2.783	1.00	249.69
	7622	C7	NAG E	340	-16.380	65.065	3.055	1.00	249.69
	7623	O7	NAG E	340	-15.644	65.372	4.003	1.00	249.69
	7624	C8	NAG E	340	-15.987	63.917	2.140	1.00	249.69
70	7625	C3	NAG E	340	-19.162	66.374	4.487	1.00	249.69

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	7626	O3	NAG	E	340	-18.769	65.355	5.395	1.00	249.69
	7627	C4	NAG	E	340	-19.704	67.580	5.273	1.00	249.69
	7628	O4	NAG	E	340	-20.884	67.199	5.975	1.00	249.69
5	7629	C5	NAG	E	340	-20.011	68.748	4.305	1.00	249.69
	7630	O5	NAG	E	340	-18.836	69.073	3.520	1.00	249.69
	7631	C6	NAG	E	340	-20.450	70.028	5.000	1.00	249.69
	7632	O6	NAG	E	340	-20.520	71.112	4.081	1.00	249.69
	7633	C1	NAG	E	366	-13.236	53.354	-17.338	1.00	200.99
	7634	C2	NAG	E	366	-12.501	52.697	-18.503	1.00	200.99
10	7635	N2	NAG	E	366	-12.267	53.689	-19.539	1.00	200.99
	7636	C7	NAG	E	366	-11.142	54.405	-19.544	1.00	200.99
	7637	O7	NAG	E	366	-10.251	54.258	-18.697	1.00	200.99
	7638	C8	NAG	E	366	-10.974	55.435	-20.659	1.00	200.99
	7639	C3	NAG	E	366	-13.344	51.559	-19.064	1.00	200.99
15	7640	O3	NAG	E	366	-12.589	50.845	-20.024	1.00	200.99
	7641	C4	NAG	E	366	-13.814	50.601	-17.968	1.00	200.99
	7642	O4	NAG	E	366	-14.809	49.714	-18.523	1.00	200.99
	7643	C5	NAG	E	366	-14.427	51.387	-16.796	1.00	200.99
	7644	O5	NAG	E	366	-13.511	52.389	-16.333	1.00	200.99
20	7645	C6	NAG	E	366	-14.780	50.532	-15.594	1.00	200.99
	7646	O6	NAG	E	366	-15.500	51.287	-14.628	1.00	200.99
	7647	C1	NAG	E	367	-14.595	48.351	-18.366	1.00	248.88
	7648	C2	NAG	E	367	-15.915	47.598	-18.528	1.00	248.88
	7649	N2	NAG	E	367	-16.897	48.084	-17.575	1.00	248.88
25	7650	C7	NAG	E	367	-17.964	48.748	-18.004	1.00	248.88
	7651	O7	NAG	E	367	-18.175	48.977	-19.195	1.00	248.88
	7652	C8	NAG	E	367	-18.948	49.229	-16.950	1.00	248.88
	7653	C3	NAG	E	367	-15.646	46.102	-18.325	1.00	248.88
	7654	O3	NAG	E	367	-16.851	45.362	-18.485	1.00	248.88
30	7655	C4	NAG	E	367	-14.602	45.631	-19.346	1.00	248.88
	7656	O4	NAG	E	367	-14.273	44.271	-19.099	1.00	248.88
	7657	C5	NAG	E	367	-13.334	46.502	-19.256	1.00	248.88
	7658	O5	NAG	E	367	-13.668	47.911	-19.373	1.00	248.88
	7659	C6	NAG	E	367	-12.347	46.188	-20.363	1.00	248.88
35	7660	O6	NAG	E	367	-12.226	47.271	-21.276	1.00	248.88

Table 7. Atomic coordinates of PhFcεRIα$_{1-176}$, Form M2

ATOM NUMBER	ATOM TYPE	RESIDUE	#	X	Y	Z	OCC	B
1	CB	VAL A	1	54.132	-20.714	8.499	1.00	178.10
2	CG1	VAL A	1	52.843	-21.062	7.774	1.00	175.86
3	CG2	VAL A	1	54.598	-21.899	9.342	1.00	170.07
4	C	VAL A	1	55.044	-18.854	6.922	1.00	182.13
5	O	VAL A	1	54.219	-18.626	6.045	1.00	181.45
6	N	VAL A	1	56.560	-20.445	8.067	1.00	185.40
7	CA	VAL A	1	55.237	-20.291	7.470	1.00	181.27
8	N	PRO A	2	55.807	-17.881	7.435	1.00	180.05
9	CD	PRO A	2	55.929	-17.840	8.889	1.00	177.25
10	CA	PRO A	2	55.680	-16.493	6.950	1.00	173.64
11	CB	PRO A	2	56.618	-15.752	7.867	1.00	173.09
12	CG	PRO A	2	56.407	-16.439	9.184	1.00	173.72
13	C	PRO A	2	55.836	-16.175	5.460	1.00	167.05
14	O	PRO A	2	55.605	-15.044	5.015	1.00	168.35
15	N	GLN A	3	56.252	-17.165	4.696	1.00	154.29
16	CA	GLN A	3	56.695	-17.039	3.302	1.00	144.07
17	CB	GLN A	3	56.716	-18.462	2.775	1.00	152.72
18	CG	GLN A	3	57.593	-19.352	3.656	1.00	159.56
19	CD	GLN A	3	58.812	-18.642	4.253	1.00	162.34
20	OE1	GLN A	3	59.151	-17.549	3.808	1.00	167.23
21	NE2	GLN A	3	59.600	-19.090	5.219	1.00	166.20
22	C	GLN A	3	56.117	-15.992	2.286	1.00	134.57
23	O	GLN A	3	56.663	-15.988	1.196	1.00	145.79
24	N	LYS A	4	55.146	-15.111	2.520	1.00	114.68
25	CA	LYS A	4	54.768	-14.237	1.357	1.00	91.89
26	CB	LYS A	4	53.529	-14.805	0.655	1.00	93.44
27	CG	LYS A	4	52.415	-15.272	1.595	1.00	116.31
28	CD	LYS A	4	51.061	-15.271	0.914	1.00	123.93
29	CE	LYS A	4	50.072	-16.156	1.643	1.00	131.64
30	NZ	LYS A	4	49.049	-16.742	0.732	1.00	135.93
31	C	LYS A	4	54.546	-12.760	1.718	1.00	72.33
32	O	LYS A	4	54.002	-12.486	2.790	1.00	69.94
33	N	PRO A	5	54.961	-11.818	0.861	1.00	46.80
34	CD	PRO A	5	55.670	-12.005	-0.413	1.00	34.03
35	CA	PRO A	5	54.807	-10.400	1.180	1.00	35.08
36	CB	PRO A	5	55.351	-9.708	-0.066	1.00	27.27
37	CG	PRO A	5	56.350	-10.674	-0.591	1.00	18.92
38	C	PRO A	5	53.320	-10.124	1.371	1.00	41.36
39	O	PRO A	5	52.473	-10.945	1.030	1.00	59.20
40	N	LYS A	6	52.988	-8.970	1.915	1.00	45.12
41	CA	LYS A	6	51.591	-8.644	2.112	1.00	58.01
42	CB	LYS A	6	51.207	-8.907	3.570	1.00	31.24
43	CG	LYS A	6	49.726	-8.775	3.844	1.00	63.36
44	CD	LYS A	6	49.203	-10.005	4.566	1.00	81.81
45	CE	LYS A	6	47.699	-9.917	4.797	1.00	83.24
46	NZ	LYS A	6	47.156	-11.172	5.406	1.00	80.30
47	C	LYS A	6	51.392	-7.177	1.734	1.00	61.99
48	O	LYS A	6	51.822	-6.280	2.460	1.00	80.08
49	N	VAl A	7	50.773	-6.936	0.583	1.00	46.06
50	CA	VAL A	7	50.542	-5.574	0.153	1.00	39.39
51	CB	VAL A	7	49.937	-5.529	-1.254	1.00	45.45
52	CG1	VAL A	7	49.551	-4.097	-1.603	1.00	49.77
53	CG2	VAL A	7	50.947	-6.057	-2.270	1.00	22.27
54	C	VAL A	7	49.594	-4.890	1.125	1.00	44.09
55	O	VAL A	7	48.558	-5.446	1.493	1.00	37.53
56	N	SER A	8	49.970	-3.686	1.546	1.00	52.74
57	CA	SER A	8	49.162	-2.909	2.474	1.00	53.44
58	CB	SER A	8	49.936	-2.627	3.752	1.00	61.38
59	OG	SER A	8	50.799	-1.517	3.558	1.00	88.92
60	C	SER A	8	48.886	-1.598	1.772	1.00	51.41
61	O	SER A	8	49.698	-1.134	0.963	1.00	45.35
62	N	LEU A	9	47.753	-0.988	2.080	1.00	44.36
63	CA	LEU A	9	47.422	0.260	1.422	1.00	49.82
64	CB	LEU A	9	46.027	0.193	0.778	1.00	64.30

	65	CG	LEU	A	9	45.511	-1.067	0.080	1.00	48.97
	66	CD1	LEU	A	9	44.236	-0.713	-0.646	1.00	42.71
	67	CD2	LEU	A	9	46.536	-1.600	-0.898	1.00	20.50
5	68	C	LEU	A	9	47.429	1.408	2.405	1.00	39.97
	69	O	LEU	A	9	47.003	1.263	3.551	1.00	31.04
	70	N	ASN	A	10	47.892	2.557	1.937	1.00	39.17
	71	CA	ASN	A	10	47.888	3.747	2.758	1.00	38.83
	72	CB	ASN	A	10	49.249	3.992	3.387	1.00	56.48
	73	CG	ASN	A	10	49.281	5.278	4.188	1.00	70.12
10	74	OD1	ASN	A	10	48.500	5.445	5.135	1.00	58.68
	75	ND2	ASN	A	10	50.169	6.205	3.807	1.00	68.79
	76	C	ASN	A	10	47.518	4.957	1.909	1.00	31.34
	77	O	ASN	A	10	48.302	5.400	1.040	1.00	26.78
	78	N	PRO	A	11	46.305	5.494	2.124	1.00	9.37
15	79	CD	PRO	A	11	45.988	6.856	1.655	1.00	13.93
	80	CA	PRO	A	11	45.313	5.030	3.102	1.00	18.39
	81	CB	PRO	A	11	44.263	6.137	3.082	1.00	26.39
	82	CG	PRO	A	11	45.107	7.388	2.763	1.00	26.16
	83	C	PRO	A	11	44.718	3.662	2.745	1.00	29.16
20	84	O	PRO	A	11	44.619	3.300	1.579	1.00	42.47
	85	N	PRO	A	12	44.277	2.911	3.759	1.00	29.44
	86	CD	PRO	A	12	44.139	3.482	5.107	1.00	42.51
	87	CA	PRO	A	12	43.673	1.578	3.725	1.00	43.05
	88	CB	PRO	A	12	43.049	1.454	5.115	1.00	41.74
25	89	CG	PRO	A	12	43.957	2.251	5.951	1.00	59.93
	90	C	PRO	A	12	42.625	1.358	2.645	1.00	51.72
	91	O	PRO	A	12	42.384	0.223	2.220	1.00	61.36
	92	N	TRP	A	13	41.985	2.444	2.231	1.00	52.05
	93	CA	TRP	A	13	40.926	2.405	1.232	1.00	45.67
30	94	CB	TRP	A	13	40.423	3.818	1.033	1.00	48.38
	95	CG	TRP	A	13	40.354	4.497	2.343	1.00	49.00
	96	CD2	TRP	A	13	39.731	3.991	3.519	1.00	33.76
	97	CE2	TRP	A	13	39.943	4.934	4.542	1.00	31.11
	98	CE3	TRP	A	13	39.013	2.827	3.809	1.00	30.50
35	99	CD1	TRP	A	13	40.908	5.693	2.685	1.00	46.06
	100	NE1	TRP	A	13	40.667	5.962	4.005	1.00	48.28
	101	CZ2	TRP	A	13	39.463	4.755	5.837	1.00	28.30
	102	CZ3	TRP	A	13	38.536	2.646	5.102	1.00	40.23
	103	CH2	TRP	A	13	38.764	3.610	6.100	1.00	32.97
40	104	C	TRP	A	13	41.348	1.802	-0.087	1.00	47.41
	105	O	TRP	A	13	42.162	2.382	-0.809	1.00	45.41
	106	N	ASN	A	14	40.796	0.627	-0.386	1.00	52.08
	107	CA	ASN	A	14	41.102	-0.084	-1.622	1.00	50.75
45	108	CB	ASN	A	14	40.891	-1.578	-1.434	1.00	45.92
	109	CG	ASN	A	14	39.442	-1.920	-1.257	1.00	58.48
	110	OD1	ASN	A	14	38.790	-1.435	-0.331	1.00	59.48
	111	ND2	ASN	A	14	38.916	-2.747	-2.153	1.00	60.88
	112	C	ASN	A	14	40.171	0.433	-2.716	1.00	49.24
50	113	O	ASN	A	14	40.280	0.060	-3.881	1.00	55.28
	114	N	ARG	A	15	39.238	1.284	-2.317	1.00	40.77
	115	CA	ARG	A	15	38.310	1.895	-3.250	1.00	33.20
	116	CB	ARG	A	15	36.875	1.556	-2.879	1.00	21.25
	117	CG	ARG	A	15	36.724	0.305	-2.085	1.00	42.18
55	118	CD	ARG	A	15	35.250	0.125	-1.761	1.00	35.91
	119	NE	ARG	A	15	34.488	-0.087	-2.981	1.00	10.90
	120	CZ	ARG	A	15	33.194	0.157	-3.092	1.00	35.38
	121	NH1	ARG	A	15	32.538	0.624	-2.051	1.00	33.36
	122	NH2	ARG	A	15	32.563	-0.078	-4.231	1.00	59.41
60	123	C	ARG	A	15	38.518	3.406	-3.108	1.00	32.71
	124	O	ARG	A	15	38.262	3.995	-2.058	1.00	18.86
	125	N	ILE	A	16	38.965	4.051	-4.168	1.00	25.83
	126	CA	ILE	A	16	39.191	5.470	-4.083	1.00	22.32
	127	CB	ILE	A	16	40.666	5.698	-4.000	1.00	4.67
65	128	CG2	ILE	A	16	41.229	4.810	-2.957	1.00	24.87
	129	CG1	ILE	A	16	41.319	5.326	-5.326	1.00	5.49
	130	CD1	ILE	A	16	42.840	5.449	-5.311	1.00	5.72
	131	C	ILE	A	16	38.620	6.262	-5.253	1.00	27.38
	132	O	ILE	A	16	38.407	5.729	-6.332	1.00	50.75
	133	N	PHE	A	17	38.380	7.545	-5.024	1.00	29.15
70	134	CA	PHE	A	17	37.877	8.447	-6.047	1.00	14.06

	135	CB	PHE	A	17	37.408	9.741	-5.400	1.00	10.31
	136	CG	PHE	A	17	36.041	9.655	-4.819	1.00	5.03
	137	CD1	PHE	A	17	35.697	10.396	-3.697	1.00	17.85
	138	CD2	PHE	A	17	35.071	8.885	-5.431	1.00	6.30
5	139	CE1	PHE	A	17	34.385	10.376	-3.190	1.00	28.74
	140	CE2	PHE	A	17	33.743	8.853	-4.934	1.00	28.88
	141	CZ	PHE	A	17	33.399	9.598	-3.817	1.00	19.77
	142	C	PHE	A	17	38.975	8.769	-7.051	1.00	25.28
	143	O	PHE	A	17	40.159	8.770	-6.717	1.00	27.78
10	144	N	LYS	A	18	38.567	9.041	-8.283	1.00	38.02
	145	CA	LYS	A	18	39.502	9.379	-9.346	1.00	41.11
	146	CB	LYS	A	18	38.736	9.665	-10.645	1.00	37.45
	147	CG	LYS	A	18	39.565	10.297	-11.754	1.00	38.42
	148	CD	LYS	A	18	38.672	10.698	-12.919	1.00	71.68
15	149	CE	LYS	A	18	39.477	11.290	-14.078	1.00	82.18
	150	NZ	LYS	A	18	40.148	12.572	-13.720	1.00	90.91
	151	C	LYS	A	18	40.280	10.612	-8.932	1.00	42.58
	152	O	LYS	A	18	39.707	11.549	-8.376	1.00	50.79
	153	N	GLY	A	19	41.582	10.607	-9.193	1.00	38.08
20	154	CA	GLY	A	19	42.389	11.763	-8.843	1.00	50.88
	155	C	GLY	A	19	42.987	11.754	-7.445	1.00	51.07
	156	O	GLY	A	19	43.838	12.600	-7.117	1.00	53.98
	157	N	GLU	A	20	42.537	10.820	-6.609	1.00	35.00
	158	CA	GLU	A	20	43.081	10.712	-5.266	1.00	30.62
25	159	CB	GLU	A	20	42.113	9.993	-4.338	1.00	17.69
	160	CG	GLU	A	20	40.753	10.651	-4.261	1.00	52.43
	161	CD	GLU	A	20	39.951	10.197	-3.050	1.00	59.33
	162	OE1	GLU	A	20	39.832	8.970	-2.842	1.00	67.80
	163	OE2	GLU	A	20	39.437	11.064	-2.306	1.00	52.52
30	164	C	GLU	A	20	44.402	9.953	-5.301	1.00	40.13
	165	O	GLU	A	20	44.789	9.367	-6.321	1.00	29.35
	166	N	ASN	A	21	45.089	9.958	-4.171	1.00	39.02
	167	CA	ASN	A	21	46.375	9.303	-4.083	1.00	35.97
	168	CB	ASN	A	21	47.390	10.310	-3.549	1.00	52.23
35	169	CG	ASN	A	21	47.721	11.379	-4.569	1.00	60.60
	170	OD1	ASN	A	21	48.190	11.032	-5.657	1.00	71.53
	171	ND2	ASN	A	21	47.493	12.658	-4.253	1.00	51.64
	172	C	ASN	A	21	46.307	8.066	-3.204	1.00	39.75
	173	O	ASN	A	21	45.377	7.916	-2.390	1.00	35.49
40	174	N	VAL	A	22	47.263	7.160	-3.393	1.00	30.65
	175	CA	VAL	A	22	47.311	5.934	-2.597	1.00	25.06
	176	CB	VAL	A	22	46.241	4.918	-3.040	1.00	31.80
	177	CG1	VAL	A	22	46.606	4.337	-4.418	1.00	36.39
	178	CG2	VAL	A	22	46.083	3.825	-1.985	1.00	5.71
45	179	C	VAL	A	22	48.678	5.312	-2.761	1.00	33.39
	180	O	VAL	A	22	49.291	5.422	-3.833	1.00	34.28
	181	N	THR	A	23	49.168	4.669	-1.704	1.00	44.00
	182	CA	THR	A	23	50.499	4.073	-1.755	1.00	47.12
	183	CB	THR	A	23	51.497	4.815	-0.829	1.00	48.39
50	184	OG1	THR	A	23	51.516	6.216	-1.138	1.00	51.20
	185	CG2	THR	A	23	52.903	4.243	-1.015	1.00	33.54
	186	C	THR	A	23	50.508	2.610	-1.356	1.00	39.06
	187	O	THR	A	23	50.146	2.261	-0.228	1.00	40.82
	188	N	LEU	A	24	50.920	1.758	-2.286	1.00	36.12
55	189	CA	LEU	A	24	50.982	0.337	-2.012	1.00	42.23
	190	CB	LEU	A	24	50.773	-0.471	-3.294	1.00	36.69
	191	CG	LEU	A	24	49.429	-0.222	-3.968	1.00	33.10
	192	CD1	LEU	A	24	49.240	-1.186	-5.117	1.00	50.66
	193	CD2	LEU	A	24	48.321	-0.391	-2.938	1.00	31.21
60	194	C	LEU	A	24	52.352	0.044	-1.444	1.00	42.69
	195	O	LEU	A	24	53.364	0.492	-1.991	1.00	30.60
	196	N	THR	A	25	52.392	-0.704	-0.346	1.00	52.44
	197	CA	THR	A	25	53.667	-1.046	0.263	1.00	58.07
	198	CB	THR	A	25	53.806	-0.422	1.652	1.00	62.06
65	199	OG1	THR	A	25	53.423	0.958	1.601	1.00	59.04
	200	CG2	THR	A	25	55.252	-0.519	2.115	1.00	57.89
	201	C	THR	A	25	53.820	-2.557	0.373	1.00	58.45
	202	O	THR	A	25	52.874	-3.261	0.754	1.00	57.55
	203	N	CYS	A	26	55.015	-3.039	0.035	1.00	48.91
70	204	CA	CYS	A	26	55.334	-4.465	0.061	1.00	53.25

205	C	CYS	A	26	56.187	-4.793	1.272	1.00	65.21
206	O	CYS	A	26	57.370	-4.444	1.305	1.00	62.05
207	CB	CYS	A	26	56.103	-4.833	-1.201	1.00	58.57
208	SG	CYS	A	26	56.163	-6.602	-1.640	1.00	76.24
209	N	ASN	A	27	55.594	-5.489	2.266	1.00	76.22
210	CA	ASN	A	27	56.319	-5.806	3.490	1.00	94.33
211	CB	ASN	A	27	55.742	-5.025	4.670	1.00	99.45
212	CG	ASN	A	27	54.369	-5.518	5.080	1.00	114.67
213	OD1	ASN	A	27	53.835	-6.457	4.490	1.00	126.31
214	ND2	ASN	A	27	53.792	-4.886	6.095	1.00	113.87
215	C	ASN	A	27	56.288	-7.302	3.775	1.00	96.08
216	O	ASN	A	27	55.477	-8.061	3.274	1.00	101.25
217	N	GLY	A	28	57.227	-7.729	4.653	1.00	92.99
218	CA	GLY	A	28	57.316	-9.125	5.042	1.00	93.67
219	C	GLY	A	28	58.420	-9.329	6.058	1.00	97.85
220	O	GLY	A	28	59.153	-8.393	6.368	1.00	107.57
221	N	ASN	A	29	58.544	-10.542	6.583	1.00	96.86
222	CA	ASN	A	29	59.581	-10.846	7.561	1.00	94.84
223	CB	ASN	A	29	59.517	-12.310	7.954	1.00	99.10
224	CG	ASN	A	29	58.106	-12.811	8.040	1.00	116.98
225	OD1	ASN	A	29	57.352	-12.453	8.948	1.00	116.13
226	ND2	ASN	A	29	57.726	-13.631	7.077	1.00	132.36
227	C	ASN	A	29	60.941	-10.562	6.954	1.00	97.30
228	O	ASN	A	29	61.245	-11.011	5.846	1.00	100.89
229	N	ASN	A	30	61.761	-9.821	7.683	1.00	95.34
230	CA	ASN	A	30	63.090	-9.479	7.209	1.00	100.29
231	CB	ASN	A	30	63.751	-8.483	8.165	1.00	108.20
232	CG	ASN	A	30	62.971	-7.188	8.288	1.00	117.57
233	OD1	ASN	A	30	62.798	-6.453	7.314	1.00	118.50
234	ND2	ASN	A	30	62.494	-6.900	9.498	1.00	125.45
235	C	ASN	A	30	63.979	-10.709	7.086	1.00	99.61
236	O	ASN	A	30	65.174	-10.573	6.812	1.00	111.39
237	N	PHE	A	31	63.407	-11.903	7.278	1.00	87.84
238	CA	PHE	A	31	64.181	-13.146	7.201	1.00	71.61
239	CB	PHE	A	31	63.288	-14.344	6.949	1.00	63.53
240	CG	PHE	A	31	63.993	-15.645	7.148	1.00	71.95
241	CD1	PHE	A	31	64.017	-16.257	8.395	1.00	79.52
242	CD2	PHE	A	31	64.687	-16.234	6.099	1.00	82.44
243	CE1	PHE	A	31	64.724	-17.444	8.595	1.00	77.29
244	CE2	PHE	A	31	65.400	-17.420	6.284	1.00	89.06
245	CZ	PHE	A	31	65.420	-18.025	7.538	1.00	83.28
246	C	PHE	A	31	65.252	-13.102	6.111	1.00	69.17
247	O	PHE	A	31	66.452	-13.207	6.393	1.00	84.06
248	N	PHE	A	32	64.809	-12.971	4.865	1.00	59.43
249	CA	PHE	A	32	65.736	-12.851	3.750	1.00	52.65
250	CB	PHE	A	32	65.255	-13.673	2.565	1.00	41.66
251	CG	PHE	A	32	65.585	-15.134	2.659	1.00	47.56
252	CD1	PHE	A	32	64.584	-16.073	2.907	1.00	44.68
253	CD2	PHE	A	32	66.897	-15.575	2.492	1.00	51.53
254	CE1	PHE	A	32	64.883	-17.433	2.989	1.00	43.51
255	CE2	PHE	A	32	67.208	-16.938	2.580	1.00	51.46
256	CZ	PHE	A	32	66.196	-17.866	2.824	1.00	52.70
257	C	PHE	A	32	65.794	-11.375	3.345	1.00	58.83
258	O	PHE	A	32	64.773	-10.698	3.278	1.00	56.92
259	N	GLU	A	33	66.990	-10.875	3.080	1.00	62.55
260	CA	GLU	A	33	67.152	-9.482	2.695	1.00	69.28
261	CB	GLU	A	33	68.640	-9.164	2.586	1.00	88.52
262	CG	GLU	A	33	69.291	-8.758	3.901	1.00	69.46
263	CD	GLU	A	33	70.782	-8.585	3.753	1.00	84.74
264	OE1	GLU	A	33	71.225	-8.087	2.697	1.00	88.47
265	OE2	GLU	A	33	71.516	-8.945	4.693	1.00	105.94
266	C	GLU	A	33	66.436	-9.106	1.391	1.00	64.49
267	O	GLU	A	33	66.268	-9.936	0.490	1.00	58.36
268	N	VAL	A	34	66.045	-7.837	1.292	1.00	53.30
269	CA	VAL	A	34	65.345	-7.329	0.123	1.00	45.11
270	CB	VAL	A	34	63.852	-7.116	0.440	1.00	48.71
271	CG1	VAL	A	34	63.143	-6.517	-0.760	1.00	64.13
272	CG2	VAL	A	34	63.207	-8.418	0.846	1.00	12.46
273	C	VAL	A	34	65.902	-5.992	-0.379	1.00	53.63
274	O	VAL	A	34	65.671	-4.944	0.233	1.00	61.37

	275	N	SER	A	35	66.614	-6.020	-1.499	1.00	49.22
	276	CA	SER	A	35	67.155	-4.790	-2.063	1.00	59.53
	277	CB	SER	A	35	68.650	-4.931	-2.345	1.00	70.72
	278	OG	SER	A	35	68.886	-5.671	-3.532	1.00	78.30
5	279	C	SER	A	35	66.438	-4.442	-3.362	1.00	65.71
	280	O	SER	A	35	66.894	-3.576	-4.106	1.00	79.59
	281	N	SER	A	36	65.325	-5.122	-3.631	1.00	71.64
	282	CA	SER	A	36	64.546	-4.889	-4.849	1.00	68.57
	283	CB	SER	A	36	65.307	-5.378	-6.084	1.00	72.44
10	284	OG	SER	A	36	65.260	-6.790	-6.186	1.00	79.50
	285	C	SER	A	36	63.197	-5.593	-4.805	1.00	63.12
	286	O	SER	A	36	63.070	-6.691	-4.265	1.00	64.24
	287	N	THR	A	37	62.189	-4.961	-5.391	1.00	60.88
	288	CA	THR	A	37	60.850	-5.529	-5.417	1.00	47.23
15	289	CB	THR	A	37	59.864	-4.621	-4.687	1.00	45.28
	290	OG1	THR	A	37	60.421	-4.251	-3.420	1.00	61.45
	291	CG2	THR	A	37	58.521	-5.336	-4.477	1.00	29.55
	292	C	THR	A	37	60.363	-5.712	-6.854	1.00	48.75
	293	O	THR	A	37	60.992	-5.240	-7.809	1.00	46.94
20	294	N	LYS	A	38	59.244	-6.406	-7.002	1.00	44.37
	295	CA	LYS	A	38	58.658	-6.655	-8.308	1.00	27.76
	296	CB	LYS	A	38	58.820	-8.117	-8.693	1.00	41.96
	297	CG	LYS	A	38	59.620	-8.368	-9.929	1.00	34.76
	298	CD	LYS	A	38	61.033	-7.877	-9.768	1.00	57.35
25	299	CE	LYS	A	38	61.944	-8.534	-10.793	1.00	65.86
	300	NZ	LYS	A	38	61.835	-10.029	-10.698	1.00	34.19
	301	C	LYS	A	38	57.184	-6.351	-8.160	1.00	39.95
	302	O	LYS	A	38	56.489	-6.975	-7.341	1.00	37.00
	303	N	TRP	A	39	56.705	-5.384	-8.934	1.00	51.66
30	304	CA	TRP	A	39	55.292	-5.012	-8.878	1.00	46.32
	305	CB	TRP	A	39	55.130	-3.498	-8.736	1.00	37.04
	306	CG	TRP	A	39	55.477	-3.023	-7.372	1.00	41.46
	307	CD2	TRP	A	39	54.615	-3.022	-6.233	1.00	14.22
	308	CE2	TRP	A	39	55.360	-2.534	-5.141	1.00	5.00
35	309	CE3	TRP	A	39	53.284	-3.389	-6.025	1.00	27.18
	310	CD1	TRP	A	39	56.685	-2.548	-6.940	1.00	38.68
	311	NE1	TRP	A	39	56.622	-2.252	-5.597	1.00	29.64
	312	CZ2	TRP	A	39	54.819	-2.396	-3.864	1.00	25.70
	313	CZ3	TRP	A	39	52.745	-3.253	-4.742	1.00	38.07
40	314	CH2	TRP	A	39	53.514	-2.761	-3.683	1.00	26.72
	315	C	TRP	A	39	54.531	-5.501	-10.102	1.00	35.61
	316	O	TRP	A	39	55.080	-5.587	-11.209	1.00	19.21
	317	N	PHE	A	40	53.266	-5.833	-9.898	1.00	11.64
	318	CA	PHE	A	40	52.480	-6.327	-10.994	1.00	6.70
45	319	CB	PHE	A	40	52.340	-7.853	-10.899	1.00	19.61
	320	CG	PHE	A	40	53.644	-8.595	-11.029	1.00	22.54
	321	CD1	PHE	A	40	54.445	-8.807	-9.935	1.00	38.72
	322	CD2	PHE	A	40	54.100	-9.019	-12.262	1.00	33.22
	323	CE1	PHE	A	40	55.673	-9.409	-10.067	1.00	29.68
50	324	CE2	PHE	A	40	55.334	-9.625	-12.395	1.00	36.71
	325	CZ	PHE	A	40	56.117	-9.818	-11.296	1.00	35.88
	326	C	PHE	A	40	51.108	-5.687	-11.031	1.00	37.09
	327	O	PHE	A	40	50.263	-5.931	-10.145	1.00	42.94
	328	N	HIS	A	41	50.902	-4.846	-12.040	1.00	41.78
55	329	CA	HIS	A	41	49.604	-4.207	-12.245	1.00	41.13
	330	CB	HIS	A	41	49.734	-2.831	-12.878	1.00	45.29
	331	CG	HIS	A	41	48.457	-2.055	-12.857	1.00	22.20
	332	CD2	HIS	A	41	48.178	-0.784	-13.225	1.00	33.03
	333	ND1	HIS	A	41	47.288	-2.576	-12.347	1.00	36.74
60	334	CE1	HIS	A	41	46.341	-1.656	-12.396	1.00	31.11
	335	NE2	HIS	A	41	46.856	-0.558	-12.924	1.00	55.47
	336	C	HIS	A	41	48.903	-5.131	-13.215	1.00	29.92
	337	O	HIS	A	41	49.468	-5.495	-14.246	1.00	19.98
	338	N	ASN	A	42	47.688	-5.532	-12.876	1.00	26.06
65	339	CA	ASN	A	42	46.968	-6.458	-13.730	1.00	33.33
	340	CB	ASN	A	42	46.265	-5.680	-14.834	1.00	17.02
	341	CG	ASN	A	42	45.045	-4.956	-14.334	1.00	32.02
	342	OD1	ASN	A	42	44.490	-5.335	-13.274	1.00	29.56
	343	ND2	ASN	A	42	44.618	-3.945	-15.101	1.00	13.43
70	344	C	ASN	A	42	47.924	-7.520	-14.333	1.00	38.30

	345	O	ASN A	42	47.954	-7.738	-15.548	1.00	35.70
	346	N	GLY A	43	48.723	-8.150	-13.476	1.00	39.92
	347	CA	GLY A	43	49.640	-9.182	-13.926	1.00	32.70
	348	C	GLY A	43	50.880	-8.741	-14.686	1.00	36.33
5	349	O	GLY A	43	51.786	-9.544	-14.891	1.00	40.53
	350	N	SER A	44	50.946	-7.489	-15.117	1.00	34.42
	351	CA	SER A	44	52.124	-7.048	-15.862	1.00	44.42
	352	CB	SER A	44	51.738	-6.055	-16.957	1.00	57.35
	353	OG	SER A	44	50.928	-6.677	-17.942	1.00	77.66
10	354	C	SER A	44	53.128	-6.402	-14.947	1.00	42.83
	355	O	SER A	44	52.755	-5.629	-14.072	1.00	48.20
	356	N	LEU A	45	54.404	-6.713	-15.153	1.00	46.97
	357	CA	LEU A	45	55.472	-6.160	-14.322	1.00	46.50
	358	CB	LEU A	45	56.819	-6.805	-14.665	1.00	33.26
15	359	CG	LEU A	45	58.045	-6.173	-13.999	1.00	34.18
	360	CD1	LEU A	45	57.912	-6.233	-12.476	1.00	58.24
	361	CD2	LEU A	45	59.287	-6.896	-14.445	1.00	39.00
	362	C	LEU A	45	55.581	-4.658	-14.501	1.00	46.94
	363	O	LEU A	45	55.627	-4.180	-15.611	1.00	34.79
20	364	N	SER A	46	55.612	-3.922	-13.400	1.00	60.24
	365	CA	SER A	46	55.721	-2.478	-13.456	1.00	54.99
	366	CB	SER A	46	55.040	-1.857	-12.240	1.00	58.08
	367	OG	SER A	46	55.175	-0.446	-12.254	1.00	81.72
	368	C	SER A	46	57.191	-2.132	-13.442	1.00	58.15
25	369	O	SER A	46	58.023	-2.965	-13.100	1.00	70.14
	370	N	GLU A	47	57.513	-0.902	-13.819	1.00	57.45
	371	CA	GLU A	47	58.900	-0.462	-13.822	1.00	65.18
	372	CB	GLU A	47	59.070	0.748	-14.735	1.00	75.20
	373	CG	GLU A	47	58.981	0.417	-16.207	1.00	98.71
30	374	CD	GLU A	47	59.119	1.648	-17.075	1.00	118.62
	375	OE1	GLU A	47	58.207	2.505	-17.038	1.00	131.08
	376	OE2	GLU A	47	60.140	1.761	-17.788	1.00	126.76
	377	C	GLU A	47	59.352	-0.109	-12.408	1.00	63.59
	378	O	GLU A	47	60.551	-0.117	-12.108	1.00	67.24
35	379	N	GLU A	48	58.382	0.193	-11.546	1.00	53.32
	380	CA	GLU A	48	58.653	0.539	-10.156	1.00	55.75
	381	CB	GLU A	48	57.343	0.802	-9.422	1.00	58.11
	382	CG	GLU A	48	57.530	1.166	-7.964	1.00	86.91
	383	CD	GLU A	48	58.235	2.501	-7.781	1.00	104.21
40	384	OE1	GLU A	48	57.545	3.548	-7.752	1.00	116.45
	385	OE2	GLU A	48	59.483	2.499	-7.681	1.00	107.36
	386	C	GLU A	48	59.403	-0.581	-9.442	1.00	57.10
	387	O	GLU A	48	59.016	-1.744	-9.518	1.00	64.00
	388	N	THR A	49	60.471	-0.230	-8.735	1.00	54.72
45	389	CA	THR A	49	61.253	-1.238	-8.024	1.00	63.14
	390	CB	THR A	49	62.646	-1.380	-8.647	1.00	63.41
	391	OG1	THR A	49	62.980	-0.174	-9.345	1.00	62.51
	392	CG2	THR A	49	62.677	-2.552	-9.603	1.00	64.13
	393	C	THR A	49	61.415	-1.015	-6.521	1.00	62.86
50	394	O	THR A	49	62.066	-1.806	-5.839	1.00	69.10
	395	N	ASN A	50	60.821	0.052	-6.003	1.00	54.53
	396	CA	ASN A	50	60.918	0.341	-4.580	1.00	61.75
	397	CB	ASN A	50	60.864	1.860	-4.331	1.00	76.64
	398	CG	ASN A	50	61.974	2.623	-5.065	1.00	80.85
55	399	OD1	ASN A	50	63.136	2.211	-5.063	1.00	73.80
	400	ND2	ASN A	50	61.615	3.745	-5.686	1.00	83.17
	401	C	ASN A	50	59.795	-0.365	-3.827	1.00	60.45
	402	O	ASN A	50	58.718	-0.579	-4.361	1.00	64.31
	403	N	SER A	51	60.053	-0.723	-2.579	1.00	64.42
60	404	CA	SER A	51	59.067	-1.417	-1.767	1.00	69.19
	405	CB	SER A	51	59.649	-1.690	-0.383	1.00	83.18
	406	OG	SER A	51	60.136	-0.498	0.207	1.00	98.67
	407	C	SER A	51	57.757	-0.651	-1.633	1.00	72.43
	408	O	SER A	51	56.779	-1.160	-1.076	1.00	75.57
65	409	N	SER A	52	57.738	0.577	-2.138	1.00	72.75
	410	CA	SER A	52	56.535	1.391	-2.069	1.00	72.90
	411	CB	SER A	52	56.766	2.600	-1.165	1.00	77.27
	412	OG	SER A	52	57.143	2.182	0.137	1.00	104.21
	413	C	SER A	52	56.106	1.858	-3.449	1.00	69.39
70	414	O	SER A	52	56.806	2.617	-4.114	1.00	66.69

415	N	LEU	A	53	54.950	1.376	-3.883	1.00	70.92
416	CA	LEU	A	53	54.405	1.754	-5.176	1.00	66.04
417	CB	LEU	A	53	53.747	0.542	-5.841	1.00	64.62
418	CG	LEU	A	53	52.954	0.809	-7.120	1.00	57.82
419	CD1	LEU	A	53	53.761	1.661	-8.068	1.00	53.42
420	CD2	LEU	A	53	52.593	-0.504	-7.758	1.00	52.64
421	C	LEU	A	53	53.383	2.879	-4.975	1.00	58.35
422	O	LEU	A	53	52.319	2.688	-4.348	1.00	38.80
423	N	ASN	A	54	53.708	4.055	-5.500	1.00	47.61
424	CA	ASN	A	54	52.820	5.195	-5.344	1.00	60.77
425	CB	ASN	A	54	53.638	6.453	-5.089	1.00	62.70
426	CG	ASN	A	54	54.433	6.376	-3.804	1.00	72.45
427	OD1	ASN	A	54	53.865	6.317	-2.708	1.00	70.70
428	ND2	ASN	A	54	55.761	6.373	-3.927	1.00	70.84
429	C	ASN	A	54	51.905	5.420	-6.534	1.00	55.42
430	O	ASN	A	54	52.308	5.246	-7.678	1.00	52.22
431	N	ILE	A	55	50.669	5.807	-6.241	1.00	47.52
432	CA	ILE	A	55	49.681	6.089	-7.267	1.00	48.77
433	CB	ILE	A	55	48.459	5.177	-7.138	1.00	48.20
434	CG2	ILE	A	55	47.338	5.670	-8.055	1.00	64.85
435	CG1	ILE	A	55	48.848	3.746	-7.493	1.00	17.58
436	CD1	ILE	A	55	47.667	2.811	-7.511	1.00	22.96
437	C	ILE	A	55	49.242	7.528	-7.070	1.00	53.16
438	O	ILE	A	55	48.602	7.862	-6.062	1.00	50.16
439	N	VAL	A	56	49.576	8.374	-8.041	1.00	53.12
440	CA	VAL	A	56	49.298	9.784	-7.939	1.00	55.98
441	CB	VAL	A	56	50.475	10.660	-8.216	1.00	53.06
442	CG1	VAL	A	56	50.160	12.096	-7.893	1.00	67.53
443	CG2	VAL	A	56	51.656	10.181	-7.396	1.00	38.93
444	C	VAL	A	56	48.109	10.214	-8.867	1.00	54.49
445	O	VAL	A	56	48.152	9.979	-10.075	1.00	42.98
446	N	ASN	A	57	47.094	10.850	-8.287	1.00	63.99
447	CA	ASN	A	57	45.941	11.323	-9.041	1.00	72.29
448	CB	ASN	A	57	46.339	12.495	-9.945	1.00	88.41
449	CG	ASN	A	57	46.916	13.667	-9.157	1.00	95.72
450	OD1	ASN	A	57	46.274	14.182	-8.236	1.00	90.65
451	ND2	ASN	A	57	48.133	14.089	-9.512	1.00	90.43
452	C	ASN	A	57	45.413	10.169	-9.866	1.00	67.43
453	O	ASN	A	57	45.349	10.232	-11.089	1.00	76.76
454	N	ALA	A	58	45.046	9.107	-9.161	1.00	65.44
455	CA	ALA	A	58	44.526	7.893	-9.764	1.00	59.50
456	CB	ALA	A	58	43.813	7.065	-8.715	1.00	51.61
457	C	ALA	A	58	43.591	8.128	-10.925	1.00	56.95
458	O	ALA	A	58	42.696	8.976	-10.860	1.00	59.56
459	N	LYS	A	59	43.815	7.356	-11.984	1.00	54.03
460	CA	LYS	A	59	42.999	7.392	-13.188	1.00	56.80
461	CB	LYS	A	59	43.897	7.371	-14.432	1.00	52.13
462	CG	LYS	A	59	44.932	8.485	-14.454	1.00	75.19
463	CD	LYS	A	59	46.010	8.238	-15.500	1.00	87.07
464	CE	LYS	A	59	47.122	9.272	-15.379	1.00	101.21
465	NZ	LYS	A	59	48.271	8.958	-16.271	1.00	106.25
466	C	LYS	A	59	42.171	6.106	-13.095	1.00	51.59
467	O	LYS	A	59	42.354	5.318	-12.167	1.00	37.92
468	N	PHE	A	60	41.241	5.888	-14.015	1.00	54.25
469	CA	PHE	A	60	40.470	4.657	-13.946	1.00	48.76
470	CB	PHE	A	60	39.250	4.729	-14.854	1.00	54.70
471	CG	PHE	A	60	38.304	5.832	-14.506	1.00	37.20
472	CD1	PHE	A	60	38.495	7.117	-15.002	1.00	29.43
473	CD2	PHE	A	60	37.215	5.583	-13.684	1.00	37.72
474	CE1	PHE	A	60	37.606	8.134	-14.687	1.00	40.04
475	CE2	PHE	A	60	36.315	6.597	-13.358	1.00	23.38
476	CZ	PHE	A	60	36.510	7.875	-13.860	1.00	30.49
477	C	PHE	A	60	41.388	3.529	-14.397	1.00	45.95
478	O	PHE	A	60	41.263	2.389	-13.957	1.00	37.39
479	N	GLU	A	61	42.326	3.865	-15.276	1.00	48.08
480	CA	GLU	A	61	43.279	2.887	-15.782	1.00	61.34
481	CB	GLU	A	61	44.195	3.525	-16.842	1.00	72.31
482	CG	GLU	A	61	43.508	3.900	-18.170	1.00	91.97
483	CD	GLU	A	61	42.606	5.127	-18.061	1.00	102.49
484	OE1	GLU	A	61	43.123	6.227	-17.758	1.00	100.34

	485	OE2	GLU	A	61	41.381	4.993	-18.283	1.00	100.98
	486	C	GLU	A	61	44.116	2.335	-14.625	1.00	57.54
	487	O	GLU	A	61	44.781	1.306	-14.754	1.00	53.72
	488	N	ASP	A	62	44.078	3.027	-13.493	1.00	48.67
5	489	CA	ASP	A	62	44.837	2.597	-12.330	1.00	40.78
	490	CB	ASP	A	62	45.141	3.784	-11.407	1.00	58.38
	491	CG	ASP	A	62	46.284	4.654	-11.920	1.00	55.63
	492	OD1	ASP	A	62	47.343	4.090	-12.281	1.00	50.67
	493	OD2	ASP	A	62	46.122	5.898	-11.947	1.00	65.51
10	494	C	ASP	A	62	44.104	1.519	-11.547	1.00	32.95
	495	O	ASP	A	62	44.699	0.839	-10.711	1.00	33.25
	496	N	SER	A	63	42.808	1.374	-11.800	1.00	27.08
	497	CA	SER	A	63	42.038	0.346	-11.111	1.00	24.76
	498	CB	SER	A	63	40.574	0.381	-11.542	1.00	32.81
15	499	OG	SER	A	63	39.976	1.632	-11.254	1.00	57.02
	500	C	SER	A	63	42.639	-1.002	-11.500	1.00	36.75
	501	O	SER	A	63	43.468	-1.094	-12.419	1.00	31.64
	502	N	GLY	A	64	42.236	-2.057	-10.809	1.00	34.81
	503	CA	GLY	A	64	42.790	-3.348	-11.160	1.00	42.02
20	504	C	GLY	A	64	43.349	-4.182	-10.021	1.00	50.47
	505	O	GLY	A	64	43.011	-4.005	-8.650	1.00	48.47
	506	N	GLU	A	65	44.224	-5.107	-10.387	1.00	51.85
	507	CA	GLU	A	65	44.836	-6.021	-9.436	1.00	43.33
	508	CB	GLU	A	65	44.691	-7.448	-9.953	1.00	52.77
25	509	CG	GLU	A	65	45.405	-8.502	-9.135	1.00	52.38
	510	CD	GLU	A	65	45.636	-9.792	-9.907	1.00	58.39
	511	OE1	GLU	A	65	46.528	-9.798	-10.801	1.00	43.40
	512	OE2	GLU	A	65	44.917	-10.782	-9.610	1.00	51.74
	513	C	GLU	A	65	46.309	-5.711	-9.240	1.00	45.24
30	514	O	GLU	A	65	47.057	-5.550	-10.212	1.00	39.10
	515	N	TYR	A	66	46.726	-5.644	-7.981	1.00	40.60
	516	CA	TYR	A	66	48.119	-5.363	-7.664	1.00	35.48
	517	CB	TYR	A	66	48.259	-4.029	-6.936	1.00	18.93
	518	CG	TYR	A	66	48.056	-2.817	-7.810	1.00	24.42
35	519	CD1	TYR	A	66	46.801	-2.218	-7.927	1.00	27.62
	520	CE1	TYR	A	66	46.618	-1.068	-8.707	1.00	20.61
	521	CD2	TYR	A	66	49.131	-2.240	-8.493	1.00	20.62
	522	CE2	TYR	A	66	48.968	-1.093	-9.268	1.00	19.14
	523	CZ	TYR	A	66	47.708	-0.506	-9.375	1.00	37.26
40	524	OH	TYR	A	66	47.546	0.631	-10.149	1.00	20.86
	525	C	TYR	A	66	48.692	-6.454	-6.789	1.00	35.81
	526	O	TYR	A	66	47.992	-6.973	-5.888	1.00	26.54
	527	N	LYS	A	67	49.950	-6.803	-7.071	1.00	20.27
	528	CA	LYS	A	67	50.672	-7.827	-6.316	1.00	42.77
45	529	CB	LYS	A	67	50.277	-9.255	-6.735	1.00	42.46
	530	CG	LYS	A	67	50.131	-9.502	-8.223	1.00	70.28
	531	CD	LYS	A	67	49.867	-10.987	-8.489	1.00	66.50
	532	CE	LYS	A	67	49.313	-11.233	-9.888	1.00	73.20
50	533	NZ	LYS	A	67	49.387	-12.668	-10.255	1.00	55.01
	534	C	LYS	A	67	52.161	-7.648	-6.480	1.00	49.35
	535	O	LYS	A	67	52.656	-7.502	-7.596	1.00	49.27
	536	N	CYS	A	68	52.872	-7.632	-5.359	1.00	55.09
	537	CA	CYS	A	68	54.314	-7.450	-5.384	1.00	54.74
55	538	C	CYS	A	68	54.966	-8.793	-5.171	1.00	42.46
	539	O	CYS	A	68	54.285	-9.748	-4.779	1.00	18.20
	540	CB	CYS	A	68	54.750	-6.451	-4.309	1.00	64.47
	541	SG	CYS	A	68	54.393	-6.915	-2.586	1.00	100.38
	542	N	GLN	A	69	56.267	-8.876	-5.444	1.00	26.58
60	543	CA	GLN	A	69	56.968	-10.142	-5.299	1.00	26.57
	544	CB	GLN	A	69	56.693	-10.973	-6.556	1.00	15.18
	545	CG	GLN	A	69	57.877	-11.704	-7.156	1.00	38.54
	546	CD	GLN	A	69	57.573	-12.192	-8.567	1.00	36.61
	547	OE1	GLN	A	69	56.511	-12.787	-8.816	1.00	18.42
65	548	NE2	GLN	A	69	58.497	-11.941	-9.498	1.00	36.58
	549	C	GLN	A	69	58.472	-10.000	-5.034	1.00	41.83
	550	O	GLN	A	69	59.174	-9.343	-5.804	1.00	24.51
	551	N	HIS	A	70	58.951	-10.602	-3.938	1.00	59.31
	552	CA	HIS	A	70	60.375	-10.552	-3.568	1.00	54.15
70	553	CB	HIS	A	70	60.550	-10.461	-2.050	1.00	49.67
	554	CG	HIS	A	70	60.025	-9.194	-1.451	1.00	57.18

	555	CD2	HIS	A	70	59.202	-8.984	-0.397	1.00	57.85
	556	ND1	HIS	A	70	60.376	-7.946	-1.918	1.00	60.44
	557	CE1	HIS	A	70	59.796	-7.021	-1.178	1.00	62.11
5	558	NE2	HIS	A	70	59.078	-7.624	-0.246	1.00	69.17
	559	C	HIS	A	70	61.065	-11.814	-4.055	1.00	45.74
	560	O	HIS	A	70	60.390	-12.760	-4.466	1.00	48.46
	561	N	GLN	A	71	62.397	-11.824	-4.020	1.00	34.41
	562	CA	GLN	A	71	63.170	-12.998	-4.434	1.00	34.74
	563	CB	GLN	A	71	64.631	-12.609	-4.631	1.00	28.64
10	564	CG	GLN	A	71	65.521	-13.746	-5.061	1.00	28.58
	565	CD	GLN	A	71	67.021	-13.427	-4.933	1.00	44.36
	566	OE1	GLN	A	71	67.508	-12.432	-5.447	1.00	24.64
	567	NE2	GLN	A	71	67.749	-14.289	-4.246	1.00	82.76
	568	C	GLN	A	71	63.098	-14.123	-3.476	1.00	42.41
15	569	O	GLN	A	71	63.036	-13.876	-2.168	1.00	58.78
	570	N	GLN	A	72	63.116	-15.369	-3.622	1.00	36.65
	571	CA	GLN	A	72	63.062	-16.493	-2.873	1.00	56.26
	572	CB	GLN	A	72	64.225	-16.440	-1.894	1.00	66.55
	573	CG	GLN	A	72	65.522	-16.962	-2.419	1.00	74.96
20	574	CD	GLN	A	72	66.614	-16.771	-1.409	1.00	81.18
	575	OE1	GLN	A	72	66.932	-15.625	-1.027	1.00	46.66
	576	NE2	GLN	A	72	67.196	-17.886	-0.944	1.00	86.79
	577	C	GLN	A	72	61.791	-16.614	-2.044	1.00	47.57
	578	O	GLN	A	72	61.763	-17.206	-1.035	1.00	53.55
25	579	N	VAL	A	73	60.740	-15.937	-2.457	1.00	25.14
	580	CA	VAL	A	73	59.499	-16.027	-1.737	1.00	27.76
	581	CB	VAL	A	73	59.434	-14.865	-0.770	1.00	24.20
	582	CG1	VAL	A	73	58.034	-14.638	-0.284	1.00	61.77
	583	CG2	VAL	A	73	60.349	-15.143	0.383	1.00	48.95
30	584	C	VAL	A	73	58.330	-16.018	-2.730	1.00	38.97
	585	O	VAL	A	73	58.405	-15.385	-3.793	1.00	50.48
	586	N	ASN	A	74	57.261	-16.735	-2.392	1.00	30.12
	587	CA	ASN	A	74	56.080	-16.794	-3.251	1.00	54.75
	588	CB	ASN	A	74	55.023	-17.677	-2.576	1.00	65.77
35	589	CG	ASN	A	74	55.444	-19.138	-2.523	1.00	77.30
	590	OD1	ASN	A	74	55.408	-19.840	-3.538	1.00	66.84
	591	ND2	ASN	A	74	55.871	-19.586	-1.341	1.00	98.68
	592	C	ASN	A	74	55.514	-15.392	-3.593	1.00	61.15
	593	O	ASN	A	74	55.945	-14.384	-3.027	1.00	65.55
40	594	N	GLU	A	75	54.553	-15.322	-4.523	1.00	62.19
	595	CA	GLU	A	75	53.871	-14.057	-4.951	1.00	63.45
	596	CB	GLU	A	75	53.296	-14.213	-6.314	1.00	82.08
	597	CG	GLU	A	75	54.237	-14.649	-7.425	1.00	101.46
	598	CD	GLU	A	75	53.533	-14.804	-8.759	1.00	105.08
45	599	OE1	GLU	A	75	52.308	-14.564	-8.815	1.00	85.23
	600	OE2	GLU	A	75	54.204	-15.167	-9.747	1.00	113.01
	601	C	GLU	A	75	52.979	-13.531	-3.920	1.00	46.81
	602	O	GLU	A	75	52.180	-14.279	-3.376	1.00	63.28
	603	N	SER	A	76	53.008	-12.216	-3.667	1.00	44.23
50	604	CA	SER	A	76	52.104	-11.602	-2.698	1.00	44.01
	605	CB	SER	A	76	52.265	-10.080	-2.698	1.00	52.11
	606	OG	SER	A	76	51.674	-9.502	-3.854	1.00	49.14
	607	C	SER	A	76	50.658	-11.942	-3.036	1.00	40.30
	608	O	SER	A	76	50.351	-12.409	-4.122	1.00	37.45
55	609	N	GLU	A	77	49.787	-11.733	-2.074	1.00	47.16
	610	CA	GLU	A	77	48.373	-11.965	-2.345	1.00	50.65
	611	CB	GLU	A	77	47.596	-12.125	-1.037	1.00	64.23
	612	CG	GLU	A	77	48.051	-13.299	-0.184	1.00	100.08
	613	CD	GLU	A	77	49.143	-12.917	0.795	1.00	121.85
60	614	OE1	GLU	A	77	49.535	-11.731	0.817	1.00	113.34
	615	OE2	GLU	A	77	49.607	-13.804	1.543	1.00	135.86
	616	C	GLU	A	77	47.780	-10.837	-3.181	1.00	57.00
	617	O	GLU	A	77	48.203	-9.696	-2.996	1.00	70.10
	618	N	PRO	A	78	46.905	-11.147	-4.089	1.00	60.36
65	619	CD	PRO	A	78	46.349	-12.453	-4.468	1.00	76.75
	620	CA	PRO	A	78	46.348	-10.084	-4.915	1.00	45.94
	621	CB	PRO	A	78	45.380	-10.826	-5.830	1.00	63.85
	622	CG	PRO	A	78	45.954	-12.210	-5.903	1.00	74.36
	623	C	PRO	A	78	45.640	-9.054	-4.055	1.00	46.99
70	624	O	PRO	A	78	45.047	-9.380	-3.014	1.00	44.78

	625	N	VAL	A	79	45.723	-7.806	-4.493	1.00	38.75
	626	CA	VAL	A	79	45.066	-6.708	-3.808	1.00	46.98
	627	CB	VAL	A	79	46.101	-5.836	-3.067	1.00	48.31
	628	CG1	VAL	A	79	45.700	-4.371	-3.099	1.00	58.66
5	629	CG2	VAL	A	79	46.195	-6.289	-1.639	1.00	43.93
	630	C	VAL	A	79	44.344	-5.925	-4.907	1.00	41.63
	631	O	VAL	A	79	44.974	-5.465	-5.869	1.00	31.43
	632	N	TYR	A	80	43.024	-5.799	-4.786	1.00	36.26
	633	CA	TYR	A	80	42.258	-5.105	-5.807	1.00	43.25
10	634	CB	TYR	A	80	40.986	-5.889	-6.142	1.00	43.58
	635	CG	TYR	A	80	41.315	-7.289	-6.619	1.00	62.18
	636	CD1	TYR	A	80	41.297	-8.370	-5.734	1.00	59.18
	637	CE1	TYR	A	80	41.695	-9.639	-6.138	1.00	63.70
	638	CD2	TYR	A	80	41.738	-7.521	-7.932	1.00	64.60
15	639	CE2	TYR	A	80	42.141	-8.793	-8.341	1.00	72.36
	640	CZ	TYR	A	80	42.116	-9.843	-7.439	1.00	71.99
	641	OH	TYR	A	80	42.511	-11.096	-7.848	1.00	86.14
	642	C	TYR	A	80	41.920	-3.677	-5.468	1.00	39.91
	643	O	TYR	A	80	41.299	-3.392	-4.445	1.00	39.73
20	644	N	LEU	A	81	42.350	-2.791	-6.356	1.00	42.49
	645	CA	LEU	A	81	42.130	-1.367	-6.236	1.00	39.83
	646	CB	LEU	A	81	43.462	-0.645	-6.434	1.00	29.82
	647	CG	LEU	A	81	43.433	0.870	-6.520	1.00	35.37
	648	CD1	LEU	A	81	42.862	1.449	-5.246	1.00	54.76
25	649	CD2	LEU	A	81	44.841	1.363	-6.750	1.00	51.99
	650	C	LEU	A	81	41.113	-0.953	-7.307	1.00	40.44
	651	O	LEU	A	81	41.218	-1.335	-8.479	1.00	44.23
	652	N	GLU	A	82	40.119	-0.175	-6.903	1.00	34.19
	653	CA	GLU	A	82	39.108	0.266	-7.850	1.00	43.16
30	654	CB	GLU	A	82	37.833	-0.540	-7.615	1.00	43.29
	655	CG	GLU	A	82	36.683	-0.166	-8.517	1.00	64.74
	656	CD	GLU	A	82	35.546	-1.157	-8.415	1.00	79.52
	657	OE1	GLU	A	82	35.177	-1.505	-7.272	1.00	89.05
	658	OE2	GLU	A	82	35.023	-1.586	-9.468	1.00	95.85
35	659	C	GLU	A	82	38.802	1.778	-7.803	1.00	36.44
	660	O	GLU	A	82	38.213	2.268	-6.840	1.00	20.88
	661	N	VAL	A	83	39.200	2.505	-8.849	1.00	17.32
	662	CA	VAL	A	83	38.957	3.947	-8.947	1.00	20.25
	663	CB	VAL	A	83	39.842	4.587	-10.012	1.00	16.19
40	664	CG1	VAL	A	83	39.647	6.071	-9.895	1.00	22.13
	665	CG2	VAL	A	83	41.280	4.219	-9.786	1.00	30.28
	666	C	VAL	A	83	37.503	4.274	-9.323	1.00	24.88
	667	O	VAL	A	83	36.946	3.744	-10.285	1.00	47.06
	668	N	PHE	A	84	36.894	5.162	-8.555	1.00	14.13
45	669	CA	PHE	A	84	35.520	5.575	-8.800	1.00	26.86
	670	CB	PHE	A	84	34.646	5.374	-7.564	1.00	13.44
	671	CG	PHE	A	84	34.475	3.964	-7.163	1.00	34.33
	672	CD1	PHE	A	84	35.571	3.183	-6.840	1.00	45.55
	673	CD2	PHE	A	84	33.205	3.420	-7.070	1.00	44.61
50	674	CE1	PHE	A	84	35.405	1.865	-6.433	1.00	65.24
	675	CE2	PHE	A	84	33.022	2.106	-6.667	1.00	42.90
	676	CZ	PHE	A	84	34.122	1.325	-6.343	1.00	65.66
	677	C	PHE	A	84	35.462	7.061	-9.146	1.00	45.25
	678	O	PHE	A	84	36.490	7.760	-9.178	1.00	38.34
55	679	N	SER	A	85	34.234	7.512	-6.399	1.00	46.62
	680	CA	SER	A	85	33.919	8.899	-9.712	1.00	37.65
	681	CB	SER	A	85	34.232	9.236	-11.159	1.00	40.40
	682	OG	SER	A	85	34.067	10.629	-11.358	1.00	35.89
	683	C	SER	A	85	32.438	9.035	-9.467	1.00	22.78
60	684	O	SER	A	85	31.630	8.613	-10.264	1.00	37.65
	685	N	ASP	A	86	32.098	9.604	-8.326	1.00	14.50
	686	CA	ASP	A	86	30.713	9.771	-7.919	1.00	9.43
	687	CB	ASP	A	86	30.133	8.405	-7.554	1.00	12.45
	688	CG	ASP	A	86	28.611	8.418	-7.427	1.00	51.60
65	689	OD1	ASP	A	86	28.054	9.224	-6.645	1.00	55.89
	690	OD2	ASP	A	86	27.960	7.606	-8.115	1.00	79.60
	691	C	ASP	A	86	30.746	10.707	-6.680	1.00	28.99
	692	O	ASP	A	86	31.827	11.076	-6.199	1.00	31.21
	693	N	TRP	A	87	29.583	11.104	-6.171	1.00	14.11
70	694	CA	TRP	A	87	29.543	11.991	-5.024	1.00	41.60

	695	CB	TRP	A	87	28.161	12.643	-4.893	1.00	67.93
	696	CG	TRP	A	87	27.790	13.509	-6.057	1.00	79.67
	697	CD2	TRP	A	87	28.221	14.858	-6.312	1.00	97.15
	698	CE2	TRP	A	87	27.641	15.256	-7.532	1.00	98.87
5	699	CE3	TRP	A	87	29.040	15.762	-5.626	1.00	106.42
	700	CD1	TRP	A	87	26.995	13.162	-7.102	1.00	73.69
	701	NE1	TRP	A	87	26.898	14.205	-7.994	1.00	66.94
	702	CZ2	TRP	A	87	27.851	16.513	-8.083	1.00	111.64
	703	CZ3	TRP	A	87	29.246	17.010	-6.174	1.00	116.11
10	704	CH2	TRP	A	87	28.654	17.375	-7.392	1.00	119.60
	705	C	TRP	A	87	29.900	11.273	-3.735	1.00	44.35
	706	O	TRP	A	87	30.629	11.811	-2.915	1.00	41.60
	707	N	LEU	A	88	29.368	10.071	-3.546	1.00	50.46
	708	CA	LEU	A	88	29.659	9.311	-2.340	1.00	36.94
15	709	CB	LEU	A	88	28.394	9.038	-1.530	1.00	4.59
	710	CG	LEU	A	88	27.705	10.219	-0.861	1.00	21.69
	711	CD1	LEU	A	88	26.690	9.649	0.161	1.00	11.07
	712	CD2	LEU	A	88	28.720	11.117	-0.155	1.00	21.48
	713	C	LEU	A	88	30.289	7.981	-2.655	1.00	28.38
20	714	O	LEU	A	88	29.805	7.248	-3.508	1.00	29.21
	715	N	LEU	A	89	31.370	7.676	-1.948	1.00	45.92
	716	CA	LEU	A	89	32.077	6.409	-2.092	1.00	35.41
	717	CB	LEU	A	89	33.474	6.637	-2.623	1.00	12.22
	718	CG	LEU	A	89	34.333	5.406	-2.839	1.00	32.05
25	719	CD1	LEU	A	89	33.477	4.296	-3.405	1.00	25.06
	720	CD2	LEU	A	89	35.530	5.774	-3.801	1.00	25.39
	721	C	LEU	A	89	32.153	5.786	-0.721	1.00	21.36
	722	O	LEU	A	89	32.513	6.454	0.234	1.00	48.70
	723	N	LEU	A	90	31.757	4.528	-0.602	1.00	31.16
30	724	CA	LEU	A	90	31.798	3.848	0.690	1.00	20.27
	725	CB	LEU	A	90	30.677	2.856	0.796	1.00	4.59
	726	CG	LEU	A	90	30.650	2.184	2.145	1.00	5.03
	727	CD1	LEU	A	90	30.229	3.221	3.170	1.00	5.42
	728	CD2	LEU	A	90	29.601	1.067	2.147	1.00	18.53
35	729	C	LEU	A	90	33.099	3.096	0.757	1.00	29.48
	730	O	LEU	A	90	33.291	2.129	0.017	1.00	49.50
	731	N	GLN	A	91	34.004	3.557	1.612	1.00	33.11
	732	CA	GLN	A	91	35.308	2.930	1.724	1.00	34.25
	733	CB	GLN	A	91	36.389	4.007	1.872	1.00	29.25
40	734	CG	GLN	A	91	36.487	4.900	0.664	1.00	4.72
	735	CD	GLN	A	91	37.564	5.950	0.795	1.00	24.07
	736	OE1	GLN	A	91	37.492	6.821	1.657	1.00	33.85
	737	NE2	GLN	A	91	38.566	5.885	-0.075	1.00	25.90
	738	C	GLN	A	91	35.339	1.961	2.892	1.00	39.46
45	739	O	GLN	A	91	34.607	2.134	3.875	1.00	41.60
	740	N	ALA	A	92	36.162	0.922	2.774	1.00	33.12
	741	CA	ALA	A	92	36.256	-0.064	3.844	1.00	44.90
	742	CB	ALA	A	92	35.425	-1.288	3.498	1.00	44.46
	743	C	ALA	A	92	37.696	-0.476	4.151	1.00	45.76
50	744	O	ALA	A	92	38.544	-0.586	3.253	1.00	51.50
	745	N	SER	A	93	37.962	-0.702	5.432	1.00	48.03
	746	CA	SER	A	93	39.286	-1.103	5.881	1.00	52.40
	747	CB	SER	A	93	39.265	-1.381	7.380	1.00	48.05
	748	OG	SER	A	93	38.305	-2.377	7.689	1.00	47.42
55	749	C	SER	A	93	39.671	-2.364	5.142	1.00	49.91
	750	O	SER	A	93	40.837	-2.593	4.836	1.00	54.70
	751	N	ALA	A	94	38.659	-3.170	4.856	1.00	47.64
	752	CA	ALA	A	94	38.830	-4.430	4.161	1.00	40.55
	753	CB	ALA	A	94	39.567	-5.404	5.048	1.00	44.76
60	754	C	ALA	A	94	37.441	-4.968	3.823	1.00	53.40
	755	O	ALA	A	94	36.554	-5.033	4.688	1.00	40.13
	756	N	GLU	A	95	37.249	-5.347	2.565	1.00	63.75
	757	CA	GLU	A	95	35.964	-5.865	2.125	1.00	61.37
	758	CB	GLU	A	95	35.952	-5.940	0.603	1.00	77.66
65	759	CG	GLU	A	95	36.118	-4.576	-0.059	1.00	76.66
	760	CD	GLU	A	95	36.098	-4.640	-1.582	1.00	96.68
	761	OE1	GLU	A	95	36.111	-3.565	-2.217	1.00	107.34
	762	OE2	GLU	A	95	36.073	-5.754	-2.151	1.00	100.79
	763	C	GLU	A	95	35.680	-7.231	2.750	1.00	54.28
70	764	O	GLU	A	95	34.527	-7.667	2.838	1.00	42.98

	765	N	VAL	A	96	36.739	-7.903	3.193	1.00	61.87
	766	CA	VAL	A	96	36.604	-9.205	3.851	1.00	61.01
	767	CB	VAL	A	96	36.933	-10.354	2.897	1.00	56.77
5	768	CG1	VAL	A	96	36.541	-11.670	3.536	1.00	39.60
	769	CG2	VAL	A	96	36.215	-10.149	1.576	1.00	53.03
	770	C	VAL	A	96	37.520	-9.306	5.084	1.00	56.97
	771	O	VAL	A	96	38.751	-9.202	4.985	1.00	45.37
	772	N	VAL	A	97	36.900	-9.512	6.241	1.00	53.01
	773	CA	VAL	A	97	37.614	-9.606	7.499	1.00	56.01
10	774	CB	VAL	A	97	37.188	-8.448	8.435	1.00	57.61
	775	CG1	VAL	A	97	37.790	-8.628	9.802	1.00	87.18
	776	CG2	VAL	A	97	37.637	-7.122	7.858	1.00	68.07
	777	C	VAL	A	97	37.372	-10.944	8.209	1.00	61.52
	778	O	VAL	A	97	36.278	-11.542	8.158	1.00	38.67
15	779	N	MET	A	98	38.412	-11.411	8.879	1.00	64.69
	780	CA	MET	A	98	38.335	-12.644	9.633	1.00	62.72
	781	CB	MET	A	98	39.745	-13.081	10.013	1.00	71.28
	782	CG	MET	A	98	39.901	-14.561	10.252	1.00	94.38
	783	SD	MET	A	98	39.346	-15.500	8.803	1.00	75.29
20	784	CE	MET	A	98	37.821	-16.041	9.448	1.00	93.84
	785	C	MET	A	98	37.520	-12.336	10.894	1.00	58.92
	786	O	MET	A	98	37.748	-11.318	11.552	1.00	61.33
	787	N	GLU	A	99	36.573	-13.201	11.241	1.00	61.37
	788	CA	GLU	A	99	35.762	-12.971	12.436	1.00	59.89
25	789	CB	GLU	A	99	34.950	-14.211	12.797	1.00	52.02
	790	CG	GLU	A	99	34.153	-14.039	14.072	1.00	64.75
	791	CD	GLU	A	99	33.366	-15.285	14.456	1.00	90.18
	792	OE1	GLU	A	99	33.983	-16.375	14.536	1.00	106.04
	793	OE2	GLU	A	99	32.137	-15.170	14.685	1.00	84.66
30	794	C	GLU	A	99	36.621	-12.587	13.633	1.00	66.15
	795	O	GLU	A	99	37.583	-13.284	13.972	1.00	81.55
	796	N	GLY	A	100	36.265	-11.478	14.271	1.00	58.33
	797	CA	GLY	A	100	37.016	-11.021	15.419	1.00	54.87
35	798	C	GLY	A	100	37.943	-9.872	15.088	1.00	54.97
	799	O	GLY	A	100	38.293	-9.087	15.960	1.00	69.91
	800	N	GLN	A	101	38.367	-9.772	13.836	1.00	54.17
	801	CA	GLN	A	101	39.237	-8.671	13.445	1.00	57.48
	802	CB	GLN	A	101	39.942	-8.998	12.125	1.00	60.93
40	803	CG	GLN	A	101	41.016	-10.063	12.237	1.00	76.51
	804	CD	GLN	A	101	42.059	-9.719	13.290	1.00	90.62
	805	OE1	GLN	A	101	41.825	-9.891	14.490	1.00	100.86
	806	NE2	GLN	A	101	43.212	-9.215	12.846	1.00	85.92
	807	C	GLN	A	101	38.445	-7.353	13.311	1.00	56.15
45	808	O	GLN	A	101	37.210	-7.337	13.344	1.00	44.69
	809	N	PRO	A	102	39.151	-6.222	13.180	1.00	56.36
	810	CD	PRO	A	102	40.600	-5.991	13.326	1.00	60.77
	811	CA	PRO	A	102	38.438	-4.954	13.048	1.00	55.67
	812	CB	PRO	A	102	39.483	-3.933	13.458	1.00	47.18
50	813	CG	PRO	A	102	40.742	-4.538	12.918	1.00	47.65
	814	C	PRO	A	102	37.915	-4.716	11.631	1.00	58.48
	815	O	PRO	A	102	38.567	-5.036	10.635	1.00	58.71
	816	N	LEU	A	103	36.719	-4.151	11.569	1.00	61.34
	817	CA	LEU	A	103	36.041	-3.833	10.320	1.00	47.87
55	818	CB	LEU	A	103	34.728	-4.610	10.248	1.00	54.63
	819	CG	LEU	A	103	33.811	-4.304	9.073	1.00	54.99
	820	CD1	LEU	A	103	34.546	-4.596	7.767	1.00	57.13
	821	CD2	LEU	A	103	32.537	-5.130	9.206	1.00	49.78
	822	C	LEU	A	103	35.761	-2.332	10.359	1.00	39.79
60	823	O	LEU	A	103	35.046	-1.847	11.254	1.00	21.76
	824	N	PHE	A	104	36.300	-1.598	9.391	1.00	18.87
	825	CA	PHE	A	104	36.111	-0.157	9.393	1.00	30.54
	826	CB	PHE	A	104	37.466	0.500	9.616	1.00	41.57
	827	CG	PHE	A	104	37.385	1.948	9.969	1.00	54.55
65	828	CD1	PHE	A	104	37.282	2.351	11.301	1.00	72.72
	829	CD2	PHE	A	104	37.441	2.917	8.975	1.00	57.49
	830	CE1	PHE	A	104	37.227	3.706	11.640	1.00	70.88
	831	CE2	PHE	A	104	37.385	4.273	9.297	1.00	60.17
	832	CZ	PHE	A	104	37.285	4.670	10.633	1.00	66.74
	833	C	PHE	A	104	35.466	0.437	8.137	1.00	35.62
70	834	O	PHE	A	104	36.079	0.468	7.066	1.00	37.03

	835	N	LEU	A	105	34.234	0.922	8.269	1.00	36.14
	836	CA	LEU	A	105	33.541	1.550	7.144	1.00	48.60
	837	CB	LEU	A	105	32.073	1.154	7.125	1.00	46.94
	838	CG	LEU	A	105	31.870	-0.297	6.725	1.00	52.90
5	839	CD1	LEU	A	105	30.385	-0.564	6.516	1.00	46.80
	840	CD2	LEU	A	105	32.663	-0.562	5.442	1.00	53.92
	841	C	LEU	A	105	33.658	3.072	7.195	1.00	46.53
	842	O	LEU	A	105	33.938	3.645	8.241	1.00	50.68
	843	N	ARG	A	106	33.406	3.725	6.066	1.00	45.66
10	844	CA	ARG	A	106	33.539	5.172	5.962	1.00	26.49
	845	CB	ARG	A	106	35.021	5.513	5.786	1.00	36.08
	846	CG	ARG	A	106	35.354	6.951	5.450	1.00	14.61
	847	CD	ARG	A	106	36.798	7.050	4.915	1.00	5.55
	848	NE	ARG	A	106	37.271	8.435	4.831	1.00	20.40
15	849	CZ	ARG	A	106	38.344	8.828	4.148	1.00	31.42
	850	NH1	ARG	A	106	39.064	7.946	3.479	1.00	46.98
	851	NH2	ARG	A	106	38.700	10.107	4.129	1.00	48.19
	852	C	ARG	A	106	32.770	5.674	4.756	1.00	33.55
	853	O	ARG	A	106	32.812	5.073	3.681	1.00	52.61
20	854	N	CYS	A	107	32.077	6.789	4.929	1.00	27.72
	855	CA	CYS	A	107	31.320	7.373	3.829	1.00	41.84
	856	C	CYS	A	107	32.088	8.567	3.283	1.00	22.10
	857	O	CYS	A	107	31.791	9.699	3.617	1.00	21.70
	858	CB	CYS	A	107	29.941	7.816	4.309	1.00	53.08
25	859	SG	CYS	A	107	28.736	8.075	2.959	1.00	81.46
	860	N	HIS	A	108	33.097	8.301	2.461	1.00	28.20
	861	CA	HIS	A	108	33.951	9.338	1.869	1.00	34.09
	862	CB	HIS	A	108	35.203	8.680	1.301	1.00	40.04
	863	CG	HIS	A	108	36.204	9.643	0.762	1.00	35.83
30	864	CD2	HIS	A	108	36.947	9.629	-0.371	1.00	36.86
	865	ND1	HIS	A	108	36.593	10.766	1.460	1.00	36.99
	866	CE1	HIS	A	108	37.536	11.397	0.779	1.00	45.07
	867	NE2	HIS	A	108	37.767	10.725	-0.334	1.00	23.01
	868	C	HIS	A	108	33.251	10.165	0.774	1.00	42.71
35	869	O	HIS	A	108	32.719	9.638	-0.199	1.00	37.25
	870	N	GLY	A	109	33.269	11.480	0.946	1.00	49.87
	871	CA	GLY	A	109	32.623	12.365	-0.006	1.00	29.45
	872	C	GLY	A	109	33.537	12.894	-1.088	1.00	26.33
	873	O	GLY	A	109	34.721	13.111	-0.879	1.00	19.36
40	874	N	TRP	A	110	32.939	13.111	-2.263	1.00	35.74
	875	CA	TRP	A	110	33.697	13.598	-3.404	1.00	32.65
	876	CB	TRP	A	110	32.731	13.903	-4.564	1.00	20.29
	877	CG	TRP	A	110	33.447	14.390	-5.792	1.00	22.58
	878	CD2	TRP	A	110	34.199	13.610	-6.731	1.00	26.60
45	879	CE2	TRP	A	110	34.759	14.506	-7.667	1.00	16.42
	880	CE3	TRP	A	110	34.452	12.242	-6.864	1.00	20.97
	881	CD1	TRP	A	110	33.564	15.673	-6.187	1.00	16.06
	882	NE1	TRP	A	110	34.350	15.760	-7.312	1.00	29.92
	883	CZ2	TRP	A	110	35.572	14.088	-8.734	1.00	11.79
50	884	CZ3	TRP	A	110	35.260	11.817	-7.931	1.00	46.44
	885	CH2	TRP	A	110	35.812	12.748	-8.853	1.00	19.66
	886	C	TRP	A	110	34.565	14.791	-3.047	1.00	29.32
	887	O	TRP	A	110	34.162	15.708	-2.335	1.00	21.14
55	888	N	ARG	A	111	35.814	14.736	-3.559	1.00	32.25
	889	CA	ARG	A	111	36.819	15.806	-3.372	1.00	51.05
	890	CB	ARG	A	111	36.294	17.122	-3.911	1.00	55.38
	891	CG	ARG	A	111	36.335	17.249	-5.405	1.00	82.45
	892	CD	ARG	A	111	37.728	16.914	-5.919	1.00	117.48
60	893	NE	ARG	A	111	37.701	16.807	-7.377	1.00	137.24
	894	CZ	ARG	A	111	38.779	16.716	-8.149	1.00	143.04
	895	NH1	ARG	A	111	39.988	16.721	-7.601	1.00	142.25
	896	NH2	ARG	A	111	38.650	16.625	-9.468	1.00	146.91
	897	C	ARG	A	111	37.110	16.070	-1.919	1.00	61.58
65	898	O	ARG	A	111	37.239	17.225	-1.504	1.00	77.35
	899	N	ASN	A	112	37.217	15.017	-1.101	1.00	59.89
	900	CA	ASN	A	112	37.433	15.116	0.363	1.00	47.67
	901	CB	ASN	A	112	38.892	15.480	0.648	1.00	68.19
	902	CG	ASN	A	112	39.700	14.277	1.106	1.00	77.01
	903	OD1	ASN	A	112	39.474	13.725	2.188	1.00	77.39
70	904	ND2	ASN	A	112	40.669	13.866	0.282	1.00	78.90

	905	C	ASN	A	112	36.433	16.068	0.984	1.00	28.46
	906	O	ASN	A	112	36.705	16.745	1.990	1.00	47.00
	907	N	TRP	A	113	35.263	16.090	0.367	1.00	35.39
	908	CA	TRP	A	113	34.201	16.977	0.819	1.00	51.08
5	909	CB	TRP	A	113	33.208	17.136	-0.253	1.00	64.97
	910	CG	TRP	A	113	32.539	18.373	0.147	1.00	81.55
	911	CD2	TRP	A	113	32.917	19.678	-0.301	1.00	74.85
	912	CE2	TRP	A	113	32.014	20.570	0.303	1.00	85.26
	913	CE3	TRP	A	113	33.902	20.163	-1.177	1.00	61.05
10	914	CD1	TRP	A	113	31.496	18.519	0.997	1.00	83.43
	915	NE1	TRP	A	113	31.158	19.856	1.104	1.00	83.67
	916	CZ2	TRP	A	113	32.073	21.949	0.055	1.00	96.42
	917	CZ3	TRP	A	113	33.958	21.536	-1.420	1.00	72.53
15	918	CH2	TRP	A	113	33.046	22.396	-0.803	1.00	92.25
	919	C	TRP	A	113	33.482	16.590	2.066	1.00	46.75
	920	O	TRP	A	113	33.409	15.393	2.379	1.00	35.50
	921	N	ASP	A	114	32.921	17.551	2.792	1.00	63.72
	922	CA	ASP	A	114	32.243	17.173	4.025	1.00	64.61
	923	CB	ASP	A	114	32.177	18.380	4.943	1.00	86.45
20	924	CG	ASP	A	114	33.506	18.737	5.602	1.00	98.41
	925	OD1	ASP	A	114	34.402	17.872	5.707	1.00	84.34
	926	OD2	ASP	A	114	33.641	19.918	6.023	1.00	109.32
	927	C	ASP	A	114	30.871	16.558	3.829	1.00	61.40
	928	O	ASP	A	114	30.070	17.044	3.039	1.00	81.69
25	929	N	VAL	A	115	30.569	15.463	4.556	1.00	39.40
	930	CA	VAL	A	115	29.265	14.772	4.391	1.00	37.88
	931	CB	VAL	A	115	29.491	13.274	4.126	1.00	10.52
	932	CG1	VAL	A	115	28.209	12.621	3.617	1.00	5.47
	933	CG2	VAL	A	115	30.635	13.071	3.147	1.00	9.13
30	934	C	VAL	A	115	28.364	14.928	5.596	1.00	28.56
	935	O	VAL	A	115	28.807	14.733	6.740	1.00	19.72
	936	N	TYR	A	116	27.101	15.273	5.384	1.00	37.21
	937	CA	TYR	A	116	26.192	15.428	6.517	1.00	46.14
35	938	CB	TYR	A	116	25.652	16.857	6.574	1.00	61.34
	939	CG	TYR	A	116	26.725	17.921	6.689	1.00	76.00
	940	CD1	TYR	A	116	27.203	18.582	5.557	1.00	87.94
	941	CE1	TYR	A	116	28.190	19.572	5.658	1.00	91.76
	942	CD2	TYR	A	116	27.264	18.269	7.931	1.00	84.35
	943	CE2	TYR	A	116	28.255	19.255	8.041	1.00	88.13
40	944	CZ	TYR	A	116	28.709	19.897	6.899	1.00	83.79
	945	OH	TYR	A	116	29.683	20.859	6.988	1.00	79.96
	946	C	TYR	A	116	25.022	14.449	6.489	1.00	48.03
	947	O	TYR	A	116	24.764	13.805	5.461	1.00	47.24
45	948	N	LYS	A	117	24.313	14.360	7.618	1.00	49.04
	949	CA	LYS	A	117	23.175	13.455	7.754	1.00	62.64
	950	CB	LYS	A	117	21.940	14.043	7.066	1.00	84.33
	951	CG	LYS	A	117	21.382	15.296	7.713	1.00	103.44
	952	CD	LYS	A	117	20.779	15.016	9.087	1.00	122.93
	953	CE	LYS	A	117	20.018	16.235	9.606	1.00	125.37
50	954	NZ	LYS	A	117	19.408	16.006	10.942	1.00	122.53
	955	C	LYS	A	117	23.543	12.117	7.115	1.00	59.71
	956	O	LYS	A	117	22.858	11.626	6.207	1.00	73.62
	957	N	VAL	A	118	24.636	11.532	7.588	1.00	36.40
	958	CA	VAL	A	118	25.107	10.262	7.057	1.00	27.92
55	959	CB	VAL	A	118	26.612	10.090	7.262	1.00	4.59
	960	CG1	VAL	A	118	27.021	8.714	6.845	1.00	4.59
	961	CG2	VAL	A	118	27.369	11.124	6.440	1.00	27.69
	962	C	VAL	A	118	24.421	9.071	7.685	1.00	21.65
	963	O	VAL	A	118	24.371	8.943	8.897	1.00	23.38
60	964	N	ILE	A	119	23.882	8.205	6.843	1.00	29.44
	965	CA	ILE	A	119	23.222	7.008	7.313	1.00	32.32
	966	CB	ILE	A	119	21.749	7.038	7.026	1.00	15.68
	967	CG2	ILE	A	119	21.120	5.711	7.453	1.00	9.94
65	968	CG1	ILE	A	119	21.116	8.205	7.779	1.00	16.41
	969	CD1	ILE	A	119	19.568	8.203	7.722	1.00	28.41
	970	C	ILE	A	119	23.817	5.818	6.605	1.00	41.89
	971	O	ILE	A	119	24.159	5.901	5.424	1.00	51.23
	972	N	TYR	A	120	23.973	4.719	7.330	1.00	34.78
	973	CA	TYR	A	120	24.530	3.531	6.720	1.00	31.98
70	974	CB	TYR	A	120	25.732	3.013	7.510	1.00	6.64

	975	CG	TYR	A	120	26.965	3.845	7.362	1.00	4.59
	976	CD1	TYR	A	120	27.192	4.931	8.175	1.00	7.90
	977	CE1	TYR	A	120	28.354	5.687	8.055	1.00	5.34
5	978	CD2	TYR	A	120	27.912	3.527	6.413	1.00	8.49
	979	CE2	TYR	A	120	29.085	4.271	6.270	1.00	23.20
	980	CZ	TYR	A	120	29.304	5.353	7.090	1.00	24.78
	981	OH	TYR	A	120	30.467	6.077	6.927	1.00	41.99
	982	C	TYR	A	120	23.454	2.476	6.672	1.00	39.78
	983	O	TYR	A	120	22.664	2.339	7.614	1.00	25.06
10	984	N	TYR	A	121	23.406	1.748	5.564	1.00	40.70
	985	CA	TYR	A	121	22.421	0.694	5.421	1.00	43.93
	986	CB	TYR	A	121	21.497	0.982	4.248	1.00	37.43
	987	CG	TYR	A	121	20.739	2.288	4.367	1.00	49.95
	988	CD1	TYR	A	121	21.387	3.511	4.161	1.00	49.22
15	989	CE1	TYR	A	121	20.691	4.723	4.262	1.00	56.51
	990	CD2	TYR	A	121	19.369	2.303	4.678	1.00	25.20
	991	CE2	TYR	A	121	18.664	3.494	4.783	1.00	32.17
	992	CZ	TYR	A	121	19.326	4.709	4.572	1.00	58.52
	993	OH	TYR	A	121	18.632	5.904	4.685	1.00	47.56
20	994	C	TYR	A	121	23.095	-0.650	5.206	1.00	57.82
	995	O	TYR	A	121	23.997	-0.778	4.341	1.00	56.35
	996	N	LYS	A	122	22.677	-1.636	6.003	1.00	50.06
	997	CA	LYS	A	122	23.216	-2.978	5.881	1.00	54.50
	998	CB	LYS	A	122	23.790	-3.487	7.209	1.00	66.15
25	999	CG	LYS	A	122	24.742	-4.667	7.027	1.00	79.15
	1000	CD	LYS	A	122	24.992	-5.443	8.315	1.00	81.56
	1001	CE	LYS	A	122	23.821	-6.355	8.653	1.00	78.05
	1002	NZ	LYS	A	122	24.119	-7.213	9.829	1.00	89.70
	1003	C	LYS	A	122	22.040	-3.841	5.463	1.00	56.73
30	1004	O	LYS	A	122	21.202	-4.210	6.289	1.00	47.59
	1005	N	ASP	A	123	21.978	-4.138	4.168	1.00	66.50
	1006	CA	ASP	A	123	20.911	-4.951	3.599	1.00	73.31
	1007	CB	ASP	A	123	20.768	-6.270	4.365	1.00	80.64
	1008	CG	ASP	A	123	21.977	-7.186	4.190	1.00	94.21
35	1009	OD1	ASP	A	123	22.334	-7.499	3.031	1.00	103.57
	1010	OD2	ASP	A	123	22.568	-7.600	5.214	1.00	97.62
	1011	C	ASP	A	123	19.591	-4.203	3.608	1.00	74.17
	1012	O	ASP	A	123	18.616	-4.644	4.220	1.00	66.73
	1013	N	GLY	A	124	19.571	-3.062	2.928	1.00	75.26
40	1014	CA	GLY	A	124	18.362	-2.265	2.851	1.00	79.44
	1015	C	GLY	A	124	17.954	-1.637	4.166	1.00	80.57
	1016	O	GLY	A	124	17.323	-0.580	4.186	1.00	91.15
	1017	N	GLU	A	125	18.301	-2.295	5.268	1.00	74.63
	1018	CA	GLU	A	125	17.981	-1.786	6.594	1.00	61.74
45	1019	CB	GLU	A	125	18.066	-2.914	7.616	1.00	79.17
	1020	CG	GLU	A	125	17.092	-4.054	7.365	1.00	98.38
	1021	CD	GLU	A	125	15.642	-3.619	7.478	1.00	106.78
	1022	OE1	GLU	A	125	15.235	-3.167	8.570	1.00	118.36
	1023	OE2	GLU	A	125	14.907	-3.728	6.475	1.00	110.58
50	1024	C	GLU	A	125	18.947	-0.660	6.981	1.00	58.10
	1025	O	GLU	A	125	20.161	-0.897	6.664	1.00	30.38
	1026	N	ALA	A	126	18.399	0.343	7.662	1.00	50.55
	1027	CA	ALA	A	126	19.185	1.490	8.088	1.00	52.07
	1028	CB	ALA	A	126	18.322	2.732	8.098	1.00	53.61
55	1029	C	ALA	A	126	19.795	1.272	9.461	1.00	45.73
	1030	O	ALA	A	126	19.077	1.194	10.459	1.00	48.02
	1031	N	LEU	A	127	21.122	1.179	9.491	1.00	34.72
	1032	CA	LEU	A	127	21.895	0.979	10.720	1.00	30.29
	1033	CB	LEU	A	127	23.358	0.751	10.350	1.00	15.93
60	1034	CG	LEU	A	127	23.473	-0.487	9.465	1.00	4.91
	1035	CD1	LEU	A	127	24.904	-0.710	9.010	1.00	4.59
	1036	CD2	LEU	A	127	22.935	-1.692	10.260	1.00	16.61
	1037	C	LEU	A	127	21.782	2.175	11.660	1.00	21.97
	1038	O	LEU	A	127	22.724	2.962	11.801	1.00	23.95
65	1039	N	LYS	A	128	20.635	2.305	12.315	1.00	19.75
	1040	CA	LYS	A	128	20.391	3.427	13.205	1.00	29.37
	1041	CB	LYS	A	128	19.091	3.206	13.951	1.00	16.78
	1042	CG	LYS	A	128	17.911	2.993	13.019	1.00	47.56
	1043	CD	LYS	A	128	16.603	2.817	13.777	1.00	56.74
70	1044	CE	LYS	A	128	15.492	2.380	12.824	1.00	58.68

	1045	NZ	LYS	A	128	14.183	2.220	13.519	1.00	55.73
	1046	C	LYS	A	128	21.529	3.647	14.187	1.00	40.15
	1047	O	LYS	A	128	22.289	4.599	14.064	1.00	53.09
	1048	N	TYR	A	129	21.647	2.757	15.159	1.00	36.41
5	1049	CA	TYR	A	129	22.707	2.860	16.144	1.00	37.61
	1050	CB	TYR	A	129	23.134	1.465	16.629	1.00	55.67
	1051	CG	TYR	A	129	22.011	0.668	17.256	1.00	69.76
	1052	CD1	TYR	A	129	21.225	-0.184	16.491	1.00	84.41
	1053	CE1	TYR	A	129	20.152	-0.868	17.051	1.00	80.71
10	1054	CD2	TYR	A	129	21.699	0.813	18.604	1.00	78.34
	1055	CE2	TYR	A	129	20.632	0.136	19.172	1.00	85.65
	1056	CZ	TYR	A	129	19.860	-0.702	18.391	1.00	81.90
	1057	OH	TYR	A	129	18.794	-1.369	18.952	1.00	78.93
	1058	C	TYR	A	129	23.938	3.635	15.664	1.00	41.39
15	1059	O	TYR	A	129	24.414	4.513	16.379	1.00	73.88
	1060	N	TRP	A	130	24.451	3.321	14.475	1.00	21.26
	1061	CA	TRP	A	130	25.630	4.021	13.983	1.00	55.41
	1062	CB	TRP	A	130	26.227	3.270	12.798	1.00	66.63
	1063	CG	TRP	A	130	26.560	1.867	13.090	1.00	78.03
20	1064	CD2	TRP	A	130	27.747	1.387	13.717	1.00	80.17
	1065	CE2	TRP	A	130	27.652	-0.021	13.762	1.00	96.27
	1066	CE3	TRP	A	130	28.889	2.009	14.244	1.00	63.46
	1067	CD1	TRP	A	130	25.807	0.770	12.791	1.00	95.81
	1068	NE1	TRP	A	130	26.456	-0.371	13.189	1.00	93.15
25	1069	CZ2	TRP	A	130	28.657	-0.822	14.314	1.00	106.12
	1070	CZ3	TRP	A	130	29.888	1.215	14.792	1.00	70.51
	1071	CH2	TRP	A	130	29.764	-0.188	14.823	1.00	97.78
	1072	C	TRP	A	130	25.397	5.477	13.569	1.00	69.95
	1073	O	TRP	A	130	26.292	6.113	13.027	1.00	86.40
30	1074	N	TYR	A	131	24.215	6.013	13.841	1.00	75.40
	1075	CA	TYR	A	131	23.916	7.387	13.449	1.00	97.14
	1076	CB	TYR	A	131	22.479	7.739	13.825	1.00	111.94
	1077	CG	TYR	A	131	21.976	8.995	13.151	1.00	148.46
	1078	CD1	TYR	A	131	21.452	8.958	11.863	1.00	154.63
35	1079	CE1	TYR	A	131	20.988	10.111	11.242	1.00	166.01
	1080	CD2	TYR	A	131	22.025	10.223	13.800	1.00	162.09
	1081	CE2	TYR	A	131	21.566	11.383	13.187	1.00	169.95
	1082	CZ	TYR	A	131	21.046	11.320	11.909	1.00	172.27
	1083	OH	TYR	A	131	20.578	12.465	11.306	1.00	171.20
40	1084	C	TYR	A	131	24.854	8.424	14.048	1.00	107.44
	1085	O	TYR	A	131	25.432	9.238	13.326	1.00	112.84
	1086	N	GLU	A	132	24.991	8.410	15.368	1.00	111.22
	1087	CA	GLU	A	132	25.857	9.362	16.047	1.00	114.10
	1088	CB	GLU	A	132	26.071	8.954	17.505	1.00	121.12
45	1089	CG	GLU	A	132	24.802	8.888	18.342	1.00	146.81
	1090	CD	GLU	A	132	25.067	8.459	19.774	1.00	156.:0
	1091	OE1	GLU	A	132	26.243	8.195	20.104	1.00	168.06
	1092	OE2	GLU	A	132	24.100	8.386	20.565	1.00	164.60
	1093	C	GLU	A	132	27.212	9.442	15.359	1.00	112.41
50	1094	O	GLU	A	132	27.715	10.523	15.090	1.00	126.08
	1095	N	ASN	A	133	27.792	8.286	15.065	1.00	107.15
	1096	CA	ASN	A	133	29.101	8.246	14.436	1.00	110.99
	1097	CB	ASN	A	133	29.828	6.972	14.874	1.00	132.56
	1098	CG	ASN	A	133	29.903	6.843	16.381	1.00	152.00
55	1099	OD1	ASN	A	133	30.195	7.810	17.084	1.00	156.21
	1100	ND2	ASN	A	133	29.636	5.653	16.882	1.00	104.22
	1101	C	ASN	A	133	29.071	8.366	12.913	1.00	103.70
	1102	O	ASN	A	133	28.344	7.653	12.236	1.00	103.53
	1103	N	HIS	A	134	29.885	9.274	12.388	1.00	108.74
60	1104	CA	HIS	A	134	29.987	9.520	10.954	1.00	130.31
	1105	CB	HIS	A	134	30.880	10.729	10.703	1.00	148.82
	1106	CG	HIS	A	134	30.457	11.949	11.454	1.00	166.98
	1107	CD2	HIS	A	134	31.030	12.601	12.493	1.00	171.29
	1108	ND1	HIS	A	134	29.283	12.620	11.183	1.00	179.56
65	1109	CE1	HIS	A	134	29.153	13.629	12.026	1.00	185.16
	1110	NE2	HIS	A	134	30.196	13.641	12.829	1.00	183.14
	1111	C	HIS	A	134	30.572	8.320	10.242	1.00	130.17
	1112	O	HIS	A	134	30.194	8.013	9.120	1.00	144.97
	1113	N	ASN	A	135	31.506	7.668	10.891	1.00	115.50
70	1114	CA	ASN	A	135	32.133	6.470	10.351	1.00	106.66

	1115	CB	ASN	A	135	33.641	6.677	10.201	1.00	111.41
	1116	CG	ASN	A	135	34.357	6.732	11.535	1.00	121.66
	1117	OD1	ASN	A	135	33.734	6.607	12.590	1.00	137.22
	1118	ND2	ASN	A	135	35.671	6.919	11.493	1.00	131.58
5	1119	C	ASN	A	135	31.848	5.256	11.226	1.00	98.67
	1120	O	ASN	A	135	31.560	5.429	12.414	1.00	85.00
	1121	N	ILE	A	136	31.914	4.084	10.657	1.00	84.56
	1122	CA	ILE	A	136	31.590	2.901	11.441	1.00	68.70
	1123	CB	ILE	A	136	30.615	2.005	10.689	1.00	70.57
10	1124	CG2	ILE	A	136	30.242	0.824	11.556	1.00	57.24
	1125	CG1	ILE	A	136	29.371	2.809	10.308	1.00	76.41
	1126	CD1	ILE	A	136	28.315	1.994	9.607	1.00	81.35
	1127	C	ILE	A	136	32.825	2.108	11.771	1.00	67.79
	1128	O	ILE	A	136	33.484	1.575	10.879	1.00	75.89
15	1129	N	SER	A	137	33.153	2.051	13.057	1.00	64.01
	1130	CA	SER	A	137	34.327	1.314	13.512	1.00	50.08
	1131	CB	SER	A	137	35.240	2.228	14.319	1.00	42.18
	1132	OG	SER	A	137	36.435	1.547	14.654	1.00	74.65
	1133	C	SER	A	137	33.882	0.137	14.366	1.00	40.13
20	1134	O	SER	A	137	33.257	0.331	15.402	1.00	31.91
	1135	N	ILE	A	138	34.172	-1.079	13.915	1.00	47.57
	1136	CA	ILE	A	138	33.767	-2.272	14.646	1.00	55.59
	1137	CB	ILE	A	138	32.849	-3.173	13.801	1.00	45.34
	1138	CG2	ILE	A	138	32.360	-4.317	14.646	1.00	52.83
25	1139	CG1	ILE	A	138	31.640	-2.378	13.310	1.00	55.63
	1140	CD1	ILE	A	138	30.680	-3.166	12.457	1.00	59.56
	1141	C	ILE	A	138	35.014	-3.039	15.023	1.00	69.36
	1142	O	ILE	A	138	35.542	-3.824	14.243	1.00	86.80
	1143	N	THR	A	139	35.481	-2.793	16.238	1.00	80.29
30	1144	CA	THR	A	139	36.687	-3.412	16.765	1.00	71.05
	1145	CB	THR	A	139	36.824	-3.094	18.243	1.00	65.21
	1146	OG1	THR	A	139	35.584	-3.396	18.894	1.00	63.19
	1147	CG2	THR	A	139	37.152	-1.610	18.429	1.00	37.67
	1148	C	THR	A	139	36.727	-4.906	16.577	1.00	73.17
35	1149	O	THR	A	139	37.633	-5.439	15.927	1.00	72.09
	1150	N	ASN	A	140	35.731	-5.585	17.126	1.00	71.99
	1151	CA	ASN	A	140	35.689	-7.021	17.012	1.00	74.50
	1152	CB	ASN	A	140	35.704	-7.615	18.427	1.00	83.94
	1153	CG	ASN	A	140	37.023	-8.292	18.747	1.00	102.78
40	1154	OD1	ASN	A	140	37.329	-9.296	18.114	1.00	129.44
	1155	ND2	ASN	A	140	37.842	-7.797	19.666	1.00	102.21
	1156	C	ASN	A	140	34.509	-7.489	16.134	1.00	66.79
	1157	O	ASN	A	140	33.351	-7.495	16.568	1.00	67.94
	1158	N	ALA	A	141	34.834	-7.874	14.888	1.00	51.28
45	1159	CA	ALA	A	141	33.851	-8.305	13.887	1.00	50.10
	1160	CB	ALA	A	141	34.536	-8.441	12.546	1.00	44.66
	1161	C	ALA	A	141	33.037	-9.568	14.167	1.00	57.39
	1162	O	ALA	A	141	33.395	-10.379	15.013	1.00	76.44
	1163	N	THR	A	142	31.940	-9.721	13.424	1.00	63.44
50	1164	CA	THR	A	142	31.029	-10.864	13.548	1.00	68.80
	1165	CB	THR	A	142	29.830	-10.522	14.429	1.00	56.28
	1166	OG1	THR	A	142	30.292	-9.914	15.637	1.00	69.20
	1167	CG2	THR	A	142	29.038	-11.771	14.756	1.00	63.69
	1168	C	THR	A	142	30.476	-11.284	12.186	1.00	77.84
55	1169	O	THR	A	142	30.350	-10.467	11.275	1.00	84.69
	1170	N	VAL	A	143	30.133	-12.562	12.053	1.00	80.43
	1171	CA	VAL	A	143	29.594	-13.071	10.800	1.00	75.62
	1172	CB	VAL	A	143	29.347	-14.600	10.870	1.00	62.57
	1173	CG1	VAL	A	143	28.297	-14.907	11.934	1.00	69.07
60	1174	CG2	VAL	A	143	28.903	-15.123	9.516	1.00	78.52
	1175	C	VAL	A	143	28.282	-12.361	10.472	1.00	73.71
	1176	O	VAL	A	143	27.893	-12.285	9.307	1.00	85.08
	1177	N	GLU	A	144	27.593	-11.846	11.491	1.00	65.50
	1178	CA	GLU	A	144	26.347	-11.130	11.245	1.00	78.86
65	1179	CB	GLU	A	144	25.554	-10.974	12.544	1.00	88.26
	1180	CG	GLU	A	144	24.140	-10.450	12.348	1.00	123.20
	1181	CD	GLU	A	144	23.389	-10.299	13.656	1.00	142.61
	1182	OE1	GLU	A	144	23.977	-10.598	14.717	1.00	141.13
	1183	OE2	GLU	A	144	22.212	-9.883	13.620	1.00	155.89
70	1184	C	GLU	A	144	26.611	-9.767	10.616	1.00	84.50

	1185	O	GLU	A	144	25.793	-9.241	9.855	1.00	86.40
	1186	N	ASP	A	145	27.764	-9.198	10.943	1.00	83.52
	1187	CA	ASP	A	145	28.139	-7.913	10.383	1.00	73.54
5	1188	CB	ASP	A	145	29.429	-7.402	11.033	1.00	81.77
	1189	CG	ASP	A	145	29.191	-6.826	12.430	1.00	98.36
	1190	OD1	ASP	A	145	28.336	-5.914	12.559	1.00	102.22
	1191	OD2	ASP	A	145	29.856	-7.280	13.394	1.00	95.71
	1192	C	ASP	A	145	28.317	-8.028	8.875	1.00	65.16
	1193	O	ASP	A	145	28.626	-7.053	8.211	1.00	74.60
10	1194	N	SER	A	146	28.112	-9.224	8.337	1.00	63.10
	1195	CA	SER	A	146	28.246	-9.460	6.906	1.00	51.02
	1196	CB	SER	A	146	28.403	-10.959	6.619	1.00	62.55
	1197	OG	SER	A	146	29.671	-11.452	7.030	1.00	53.04
	1198	C	SER	A	146	26.997	-8.949	6.221	1.00	50.62
15	1199	O	SER	A	146	25.935	-8.865	6.848	1.00	44.95
	1200	N	GLY	A	147	27.130	-8.609	4.942	1.00	48.93
	1201	CA	GLY	A	147	25.992	-8.119	4.185	1.00	55.32
	1202	C	GLY	A	147	26.389	-7.039	3.199	1.00	60.64
	1203	O	GLY	A	147	27.587	-6.725	3.051	1.00	55.89
20	1204	N	THR	A	148	25.396	-6.477	2.510	1.00	61.14
	1205	CA	THR	A	148	25.665	-5.415	1.540	1.00	66.29
	1206	CB	THR	A	148	24.735	-5.502	0.318	1.00	67.47
	1207	OG1	THR	A	148	23.514	-4.813	0.604	1.00	89.27
	1208	CG2	THR	A	148	24.414	-6.954	-0.006	1.00	53.85
25	1209	C	THR	A	148	25.442	-4.064	2.229	1.00	60.43
	1210	O	THR	A	148	24.373	-3.805	2.793	1.00	48.98
	1211	N	TYR	A	149	26.461	-3.214	2.203	1.00	56.49
	1212	CA	TYR	A	149	26.371	-1.911	2.836	1.00	46.76
	1213	CB	TYR	A	149	27.600	-1.648	3.726	1.00	50.51
30	1214	CG	TYR	A	149	27.679	-2.436	5.010	1.00	37.62
	1215	CD1	TYR	A	149	28.197	-3.727	5.030	1.00	38.64
	1216	CE1	TYR	A	149	28.288	-4.446	6.214	1.00	21.54
	1217	CD2	TYR	A	149	27.252	-1.882	6.211	1.00	27.02
	1218	CE2	TYR	A	149	27.336	-2.589	7.393	1.00	25.84
35	1219	CZ	TYR	A	149	27.854	-3.868	7.390	1.00	22.38
	1220	OH	TYR	A	149	27.923	-4.562	8.573	1.00	47.89
	1221	C	TYR	A	149	26.329	-0.824	1.775	1.00	47.29
	1222	O	TYR	A	149	26.626	-1.059	0.590	1.00	37.99
	1223	N	TYR	A	150	25.962	0.369	2.225	1.00	35.54
40	1224	CA	TYR	A	150	25.947	1.547	1.380	1.00	37.17
	1225	CB	TYR	A	150	25.029	1.341	0.165	1.00	20.88
	1226	CG	TYR	A	150	23.546	1.438	0.440	1.00	11.30
	1227	CD1	TYR	A	150	22.897	2.667	0.465	1.00	12.45
	1228	CE1	TYR	A	150	21.518	2.751	0.712	1.00	32.37
45	1229	CD2	TYR	A	150	22.789	0.299	0.668	1.00	24.35
	1230	CE2	TYR	A	150	21.412	0.374	0.909	1.00	20.64
	1231	CZ	TYR	A	150	20.784	1.599	0.933	1.00	30.87
	1232	OH	TYR	A	150	19.428	1.673	1.174	1.00	44.40
	1233	C	TYR	A	150	25.492	2.711	2.250	1.00	39.54
50	1234	O	TYR	A	15:	24.661	2.544	3.170	1.00	10.94
	1235	N	CYS	A	151	26.062	3.882	1.987	1.00	36.69
	1236	CA	CYS	A	151	25.705	5.052	2.757	1.00	45.12
	1237	C	CYS	A	151	25.007	6.072	1.908	1.00	51.21
	1238	O	CYS	A	151	25.146	6.112	0.686	1.00	60.75
55	1239	CB	CYS	A	151	26.931	5.677	3.410	1.00	44.14
	1240	SG	CYS	A	151	28.208	6.239	2.230	1.00	79.82
	1241	N	THR	A	152	24.258	6.891	2.606	1.00	48.42
	1242	CA	THR	A	152	23.500	7.959	1.949	1.00	39.06
	1243	CB	THR	A	152	22.068	7.517	1.650	1.00	43.65
60	1244	OG1	THR	A	152	21.399	8.531	0.891	1.00	41.96
	1245	CG2	THR	A	152	21.310	7.257	2.942	1.00	52.65
	1246	C	THR	A	152	23.555	9.204	2.825	1.00	38.12
	1247	O	THR	A	152	23.025	9.224	3.943	1.00	25.44
	1248	N	GLY	A	153	24.215	10.236	2.307	1.00	56.51
65	1249	CA	GLY	A	153	24.377	11.477	3.048	1.00	57.72
	1250	C	GLY	A	153	24.335	12.680	2.112	1.00	54.16
	1251	O	GLY	A	153	24.362	12.540	0.903	1.00	50.60
	1252	N	LYS	A	154	24.309	13.842	2.706	1.00	38.84
	1253	CA	LYS	A	154	24.227	14.969	1.840	1.00	51.33
70	1254	CB	LYS	A	154	23.115	15.878	2.356	1.00	63.30

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1255	CG	LYS	A	154	23.445	17.360	2.388	1.00	72.63
1256	CD	LYS	A	154	22.595	18.054	3.439	1.00	102.12
1257	CE	LYS	A	154	23.004	19.508	3.589	1.00	114.39
1258	NZ	LYS	A	154	22.404	20.128	4.797	1.00	116.75
1259	C	LYS	A	154	25.591	15.650	1.647	1.00	43.23
1260	O	LYS	A	154	26.393	15.769	2.565	1.00	25.84
1261	N	VAL	A	155	25.799	16.110	0.410	1.00	50.07
1262	CA	VAL	A	155	27.053	16.754	0.017	1.00	48.54
1263	CB	VAL	A	155	27.920	15.801	-0.810	1.00	44.27
1264	CG1	VAL	A	155	29.142	16.517	-1.363	1.00	33.53
1265	CG2	VAL	A	155	28.341	14.619	0.032	1.00	57.29
1266	C	VAL	A	155	26.752	18.008	-0.791	1.00	67.17
1267	O	VAL	A	155	26.127	17.926	-1.839	1.00	75.50
1268	N	TRP	A	156	27.200	19.158	-0.290	1.00	71.27
1269	CA	TRP	A	156	26.950	20.433	-0.941	1.00	74.25
1270	CB	TRP	A	156	27.792	20.531	-2.227	1.00	82.77
1271	CG	TRP	A	156	27.663	21.880	-2.856	1.00	95.08
1272	CD2	TRP	A	156	27.991	23.118	-2.237	1.00	99.06
1273	CE2	TRP	A	156	27.707	24.146	-3.172	1.00	109.06
1274	CE3	TRP	A	156	28.499	23.466	-0.981	1.00	92.83
1275	CD1	TRP	A	156	27.202	22.187	-4.115	1.00	103.95
1276	NE1	TRP	A	156	27.226	23.548	-4.308	1.00	101.14
1277	CZ2	TRP	A	156	27.915	25.505	-2.883	1.00	117.16
1278	CZ3	TRP	A	156	28.708	24.820	-0.691	1.00	111.82
1279	CH2	TRP	A	156	28.415	25.823	-1.644	1.00	117.54
1280	C	TRP	A	156	25.451	20.622	-1.252	1.00	77.62
1281	O	TRP	A	156	25.074	20.840	-2.391	1.00	86.35
1282	N	GLN	A	157	24.612	20.526	-0.216	1.00	65.28
1283	CA	GLN	A	157	23.148	20.731	-0.292	1.00	81.65
1284	CB	GLN	A	157	22.904	22.189	-0.665	1.00	97.92
1285	CG	GLN	A	157	23.502	23.199	0.312	1.00	117.66
1286	CD	GLN	A	157	23.208	24.631	-0.086	1.00	136.93
1287	OE1	GLN	A	157	22.533	24.882	-1.084	1.00	146.04
1288	NE2	GLN	A	157	23.616	25.725	0.549	1.00	141.98
1289	C	GLN	A	157	22.274	19.790	-1.165	1.00	79.89
1290	O	GLN	A	157	21.156	20.148	-1.533	1.00	84.84
1291	N	LEU	A	158	22.779	18.632	-1.485	1.00	73.68
1292	CA	LEU	A	158	22.000	17.633	-2.253	1.00	79.20
1293	CB	LEU	A	158	22.364	17.659	-3.749	1.00	79.50
1294	CG	LEU	A	158	22.096	18.967	-4.507	1.00	86.09
1295	CD1	LEU	A	158	22.474	18.815	-5.972	1.00	76.62
1296	CD2	LEU	A	158	20.647	19.379	-4.373	1.00	92.41
1297	C	LEU	A	158	22.262	16.262	-1.673	1.00	70.21
1298	O	LEU	A	158	23.390	15.914	-1.325	1.00	65.09
1299	N	ASP	A	159	21.236	15.470	-1.538	1.00	60.67
1300	CA	ASP	A	159	21.404	14.148	-0.999	1.00	55.55
1301	CB	ASP	A	159	20.088	13.617	-0.446	1.00	67.04
1302	CG	ASP	A	159	19.493	14.534	0.596	1.00	100.18
1303	OD1	ASP	A	159	20.141	14.767	1.640	1.00	107.25
1304	OD2	ASP	A	159	18.375	15.034	0.368	1.00	120.77
1305	C	ASP	A	159	21.937	13.199	-2.057	1.00	59.79
1306	O	ASP	A	159	21.662	13.379	-3.258	1.00	71.48
1307	N	TYR	A	160	22.692	12.198	-1.619	1.00	46.99
1308	CA	TYR	A	160	23.237	11.218	-2.545	1.00	36.10
1309	CB	TYR	A	160	24.620	11.639	-3.026	1.00	27.20
1310	CG	TYR	A	160	24.661	13.032	-3.599	1.00	48.59
1311	CD1	TYR	A	160	24.780	14.143	-2.770	1.00	67.84
1312	CE1	TYR	A	160	24.805	15.440	-3.297	1.00	85.53
1313	CD2	TYR	A	160	24.570	13.246	-4.970	1.00	46.32
1314	CE2	TYR	A	160	24.592	14.538	-5.507	1.00	59.84
1315	CZ	TYR	A	160	24.713	15.630	-4.665	1.00	78.07
1316	OH	TYR	A	160	24.740	16.912	-5.178	1.00	80.23
1317	C	TYR	A	160	23.314	9.852	-1.881	1.00	41.50
1318	O	TYR	A	160	23.085	9.729	-0.675	1.00	33.36
1319	N	GLU	A	161	23.623	8.830	-2.675	1.00	46.21
1320	CA	GLU	A	161	23.725	7.469	-2.173	1.00	42.10
1321	CB	GLU	A	161	22.425	6.733	-2.462	1.00	40.63
1322	CG	GLU	A	161	22.451	5.247	-2.195	1.00	72.70
1323	CD	GLU	A	161	21.042	4.640	-2.132	1.00	87.13
1324	OE1	GLU	A	161	20.932	3.391	-2.193	1.00	96.87

	1325	OE2	GLU	A	161	20.049	5.405	-2.006	1.00	69.68
	1326	C	GLU	A	161	24.898	6.793	-2.864	1.00	48.06
	1327	O	GLU	A	161	25.040	6.878	-4.080	1.00	53.65
5	1328	N	SER	A	162	25.750	6.146	-2.079	1.00	55.15
	1329	CA	SER	A	162	26.933	5.475	-2.612	1.00	57.03
	1330	CB	SER	A	162	27.868	5.246	-1.498	1.00	68.17
	1331	OG	SER	A	162	27.499	4.339	-0.501	1.00	46.93
	1332	C	SER	A	162	26.572	4.138	-3.230	1.00	58.42
	1333	O	SER	A	162	25.476	3.615	-3.020	1.00	48.37
10	1334	N	GLU	A	163	27.498	3.587	-4.002	1.00	65.57
	1335	CA	GLU	A	163	27.268	2.290	-4.619	1.00	70.23
	1336	CB	GLU	A	163	28.356	1.990	-5.650	1.00	87.77
	1337	CG	GLU	A	163	28.293	2.834	-6.909	1.00	103.75
	1338	CD	GLU	A	163	27.121	2.453	-7.797	1.00	115.27
15	1339	OE1	GLU	A	163	27.060	1.281	-8.229	1.00	111.84
	1340	OE2	GLU	A	163	26.262	3.323	-8.062	1.00	129.74
	1341	C	GLU	A	163	27.366	1.282	-3.491	1.00	70.72
	1342	O	GLU	A	163	28.244	1.387	-2.645	1.00	89.57
	1343	N	PRO	A	164	26.460	0.300	-3.448	1.00	55.48
20	1344	CD	PRO	A	164	25.401	-0.737	-4.397	1.00	62.15
	1345	CA	PRO	A	164	26.538	-0.684	-2.369	1.00	41.51
	1346	CB	PRO	A	164	25.363	-1.606	-2.663	1.00	42.71
	1347	CG	PRO	A	164	25.250	-1.532	-4.128	1.00	64.09
	1348	C	PRO	A	164	27.877	-1.409	-2.399	1.00	38.62
25	1349	O	PRO	A	164	28.585	-1.386	-3.426	1.00	31.41
	1350	N	LEU	A	165	28.234	-2.022	-1.268	1.00	33.57
	1351	CA	LEU	A	165	29.498	-2.753	-1.151	1.00	25.38
	1352	CB	LEU	A	165	30.540	-1.879	-0.490	1.00	26.45
	1353	CG	LEU	A	165	31.924	-2.483	-0.322	1.00	25.16
30	1354	CD1	LEU	A	165	32.619	-2.579	-1.655	1.00	29.84
	1355	CD2	LEU	A	165	32.736	-1.587	0.602	1.00	42.13
	1356	C	LEU	A	165	29.278	-3.983	-0.306	1.00	26.10
	1357	O	LEU	A	165	28.794	-3.876	0.815	1.00	33.23
	1358	N	ASN	A	166	29.618	-5.152	-0.838	1.00	40.53
35	1359	CA	ASN	A	166	29.400	-6.398	-0.106	1.00	50.87
	1360	CB	ASN	A	166	29.257	-7.595	-1.049	1.00	69.69
	1361	CG	ASN	A	166	27.875	-7.698	-1.649	1.00	86.10
	1362	OD1	ASN	A	166	26.895	-7.260	-1.034	1.00	58.55
	1363	ND2	ASN	A	166	27.799	-8.292	-2.839	1.00	110.79
40	1364	C	ASN	A	166	30.537	-6.664	0.833	1.00	48.09
	1365	O	ASN	A	166	31.703	-6.667	0.416	1.00	40.29
	1366	N	ILE	A	167	30.193	-6.908	2.094	1.00	46.84
	1367	CA	ILE	A	167	31.191	-7.165	3.119	1.00	53.30
	1368	CB	ILE	A	167	31.192	-6.039	4.156	1.00	54.88
45	1369	CG2	ILE	A	167	31.949	-6.458	5.383	1.00	47.53
	1370	CG1	ILE	A	167	31.816	-4.791	3.545	1.00	48.70
	1371	CD1	ILE	A	167	31.781	-3.603	4.447	1.00	54.75
	1372	C	ILE	A	167	30.945	-8.492	3.815	1.00	59.98
	1373	O	ILE	A	167	29.862	-8.731	4.388	1.00	39.94
50	1374	N	THR	A	168	31.957	-9.353	3.777	1.00	61.65
	1375	CA	THR	A	168	31.835	-10.666	4.386	1.00	68.33
	1376	CB	THR	A	168	32.052	-11.774	3.343	1.00	80.46
	1377	OG1	THR	A	168	31.627	-11.306	2.058	1.00	92.03
	1378	CG2	THR	A	168	31.239	-13.010	3.704	1.00	94.56
55	1379	C	THR	A	168	32.829	-10.891	5.515	1.00	60.61
	1380	O	THR	A	168	34.031	-10.670	5.346	1.00	54.25
	1381	N	VAL	A	169	32.313	-11.331	6.660	1.00	57.24
	1382	CA	VAL	A	169	33.143	-11.638	7.820	1.00	64.14
	1383	CB	VAL	A	169	32.567	-11.028	9.083	1.00	54.63
60	1384	CG1	VAL	A	169	33.436	-11.381	10.261	1.00	75.25
	1385	CG2	VAL	A	169	32.470	-9.533	8.929	1.00	61.93
	1386	C	VAL	A	169	33.112	-13.156	7.950	1.00	73.51
	1387	O	VAL	A	169	32.044	-13.739	8.173	1.00	77.56
	1388	N	ILE	A	170	34.268	-13.801	7.815	1.00	75.88
65	1389	CA	ILE	A	170	34.312	-15.259	7.873	1.00	80.16
	1390	CB	ILE	A	170	35.341	-15.815	6.866	1.00	75.70
	1391	CG2	ILE	A	170	34.778	-15.807	5.465	1.00	70.82
	1392	CG1	ILE	A	170	36.633	-15.007	6.932	1.00	90.89
	1393	CD1	ILE	A	170	37.719	-15.518	6.004	1.00	107.17
70	1394	C	ILE	A	170	34.568	-15.879	9.246	1.00	87.00

	1395	O	ILE	A	170	35.373	-15.415	10.042	1.00	96.41
	1396	N	LYS	A	171	33.843	-16.956	9.475	1.00	84.91
	1397	CA	LYS	A	171	34.002	-17.747	10.684	1.00	77.44
	1398	CB	LYS	A	171	32.777	-18.646	10.912	1.00	69.57
5	1399	CG	LYS	A	171	32.895	-19.571	12.108	1.00	99.45
	1400	CD	LYS	A	171	32.836	-18.812	13.422	1.00	104.18
	1401	CE	LYS	A	171	32.865	-19.773	14.611	1.00	104.74
	1402	NZ	LYS	A	171	32.737	-19.061	15.914	1.00	93.90
	1403	C	LYS	A	171	35.260	-18.572	.10.523	1.00	84.98
10	1404	O	LYS	A	171	35.628	-18.860	9.376	1.00	94.71
	1405	N	ALA	A	172	35.970	-19.012	11.575	1.00	87.21
	1406	CA	ALA	A	172	37.223	-19.690	11.278	1.00	95.69
	1407	CB	ALA	A	172	38.361	-18.758	11.670	1.00	93.23
	1408	C	ALA	A	172	37.489	-21.071	11.877	1.00	105.19
15	1409	O	ALA	A	172	37.954	-21.216	13.004	1.00	112.63
	1410	N	PRO	A	173	37.149	-22.090	11.058	1.00	110.62
	1411	CD	PRO	A	173	35.763	-22.015	10.625	1.00	99.89
	1412	CA	PRO	A	173	37.466	-23.510	11.384	1.00	115.87
	1413	CB	PRO	A	173	36.690	-24.249	10.308	1.00	108.18
20	1414	CG	PRO	A	173	35.438	-23.407	10.162	1.00	104.37
	1415	C	PRO	A	173	38.974	-23.790	11.504	1.00	128.43
	1416	O	PRO	A	173	39.763	-23.104	10.878	1.00	141.54
	1417	N	ARG	A	174	39.371	-24.790	12.289	1.00	133.44
	1418	CA	ARG	A	174	40.784	-25.147	12.416	1.00	142.76
25	1419	CB	ARG	A	174	41.404	-24.373	13.578	1.00	151.84
	1420	CG	ARG	A	174	40.646	-24.535	14.896	1.00	162.79
	1421	CD	ARG	A	174	40.099	-23.221	15.420	1.00	169.70
	1422	NE	ARG	A	174	38.922	-23.410	16.282	1.00	176.81
	1423	CZ	ARG	A	174	38.907	-23.284	17.609	1.00	177.27
30	1424	NH1	ARG	A	174	40.007	-22.942	18.271	1.00	174.36
	1425	NH2	ARG	A	174	37.770	-23.499	18.277	1.00	178.48
	1426	C	ARG	A	174	40.973	-26.657	12.620	1.00	148.93
	1427	O	ARG	A	174	40.343	-27.476	11.946	1.00	150.68
	1428	C1	NAG	A	221	48.150	13.699	-5.031	1.00	63.44
35	1429	C2	NAG	A	221	47.709	15.109	-4.571	1.00	53.07
	1430	N2	NAG	A	221	46.282	15.294	-4.715	1.00	54.52
	1431	C7	NAG	A	221	45.470	14.819	-3.771	1.00	67.27
	1432	O7	NAG	A	221	45.884	14.210	-2.774	1.00	51.25
	1433	C8	NAG	A	221	43.972	15.033	-3.951	1.00	58.18
40	1434	C3	NAG	A	221	48.484	16.177	-5.342	1.00	64.80
	1435	O3	NAG	A	221	48.035	17.468	-4.966	1.00	76.76
	1436	C4	NAG	A	221	49.919	15.918	-4.908	1.00	84.55
	1437	O4	NAG	A	221	50.874	16.976	-5.150	1.00	121.48
	1438	C5	NAG	A	221	50.354	14.610	-5.540	1.00	75.06
45	1439	O5	NAG	A	221	49.589	13.531	-4.944	1.00	65.34
	1440	C6	NAG	A	221	51.837	14.319	-5.314	1.00	72.88
	1441	O6	NAG	A	221	52.240	13.109	-5.940	1.00	79.15
	1442	C1	NAG	A	222	50.797	17.958	-6.068	1.00	145.53
	1443	C2	NAG	A	222	50.822	19.497	-5.910	1.00	155.10
50	1444	N2	NAG	A	222	49.525	20.056	-6.240	1.00	159.26
	1445	C7	NAG	A	222	48.710	20.465	-5.270	1.00	165.01
	1446	O7	NAG	A	222	48.999	20.393	-4.072	1.00	169.69
	1447	C8	NAG	A	222	47.367	21.040	-5.688	1.00	162.00
	1448	C3	NAG	A	222	51.905	20.174	-6.746	1.00	158.11
55	1449	O3	NAG	A	222	51.976	21.552	-6.412	1.00	158.38
	1450	C4	NAG	A	222	53.236	19.510	-6.450	1.00	161.49
	1451	O4	NAG	A	222	54.266	20.119	-7.216	1.00	161.28
	1452	C5	NAG	A	222	53.108	18.028	-6.799	1.00	162.76
	1453	O5	NAG	A	222	52.123	17.403	-5.946	1.00	157.35
60	1454	C6	NAG	A	222	54.409	17.273	-6.600	1.00	163.69
	1455	O6	NAG	A	222	54.197	15.869	-6.619	1.00	157.92
	1456	C1	NAG	A	242	43.365	-3.262	-14.810	1.00	13.23
	1457	C2	NAG	A	242	43.041	-2.260	-15.917	1.00	5.53
	1458	N2	NAG	A	242	44.141	-1.343	-16.143	1.00	9.70
65	1459	C7	NAG	A	242	45.252	-1.749	-16.754	1.00	29.25
	1460	O7	NAG	A	242	45.439	-2.917	-17.133	1.00	32.16
	1461	C8	NAG	A	242	46.337	-0.695	-16.957	1.00	12.96
	1462	C3	NAG	A	242	41.783	-1.489	-15.507	1.00	4.59
	1463	O3	NAG	A	242	41.435	-0.559	-16.510	1.00	15.24
70	1464	C4	NAG	A	242	40.615	-2.416	-15.249	1.00	11.27

1465	O4	NAG	A	242	39.565	-1.641	-14.619	1.00	13.74
1466	C5	NAG	A	242	41.027	-3.581	-14.306	1.00	16.30
1467	O5	NAG	A	242	42.281	-4.195	-14.704	1.00	7.58
1468	C6	NAG	A	242	40.007	-4.698	-14.278	1.00	28.55
1469	O6	NAG	A	242	39.736	-5.116	-12.948	1.00	38.66
1470	C1	NAG	A	243	38.610	-1.048	-15.431	1.00	38.51
1471	C2	NAG	A	243	37.449	-0.610	-14.570	1.00	39.03
1472	N2	NAG	A	243	36.919	-1.742	-13.845	1.00	47.25
1473	C7	NAG	A	243	36.991	-1.735	-12.517	1.00	62.38
1474	O7	NAG	A	243	37.502	-0.806	-11.885	1.00	63.20
1475	C8	NAG	A	243	36.416	-2.926	-11.769	1.00	77.74
1476	C3	NAG	A	243	36.389	0.062	-15.450	1.00	52.71
1477	O3	NAG	A	243	35.272	0.474	-14.669	1.00	54.98
1478	C4	NAG	A	243	37.029	1.275	-16.133	1.00	40.14
1479	O4	NAG	A	243	36.079	1.889	-17.033	1.00	74.71
1480	C5	NAG	A	243	38.284	0.828	-16.909	1.00	29.29
1481	O5	NAG	A	243	39.196	0.104	-16.046	1.00	36.06
1482	C6	NAG	A	243	39.063	2.012	-17.448	1.00	35.70
1483	O6	NAG	A	243	40.407	1.653	-17.751	1.00	34.26
1484	C1	MAN	A	244	35.717	3.208	-16.771	1.00	75.57
1485	C2	MAN	A	244	35.709	4.009	-18.090	1.00	81.10
1486	O2	MAN	A	244	34.884	3.345	-19.043	1.00	66.91
1487	C3	MAN	A	244	35.181	5.431	-17.820	1.00	79.87
1488	O3	MAN	A	244	35.162	6.216	-19.009	1.00	58.10
1489	C4	MAN	A	244	33.782	5.322	-17.211	1.00	73.02
1490	O4	MAN	A	244	33.238	6.611	-16.994	1.00	79.27
1491	C5	MAN	A	244	33.918	4.560	-15.890	1.00	70.92
1492	O5	MAN	A	244	34.401	3.215	-16.159	1.00	80.43
1493	C6	MAN	A	244	32.626	4.463	-15.080	1.00	62.83
1494	O6	MAN	A	244	31.720	3.523	-15.638	1.00	93.61
1495	C1	NAG	A	274	56.076	-21.009	-1.119	1.00	118.55
1496	C2	NAG	A	274	57.346	-21.243	-0.277	1.00	122.52
1497	N2	NAG	A	274	58.518	-20.916	-1.059	1.00	104.98
1498	C7	NAG	A	274	59.434	-20.096	-0.559	1.00	87.55
1499	O7	NAG	A	274	59.341	-19.596	0.555	1.00	87.40
1500	C8	NAG	A	274	60.642	-19.783	-1.417	1.00	88.80
1501	C3	NAG	A	274	57.521	-22.673	0.320	1.00	134.44
1502	O3	NAG	A	274	58.252	-22.494	1.568	1.00	158.45
1503	C4	NAG	A	274	56.155	-23.387	0.619	1.00	135.00
1504	O4	NAG	A	274	56.251	-24.825	0.491	1.00	133.45
1505	C5	NAG	A	274	55.035	-22.969	-0.345	1.00	136.04
1506	O5	NAG	A	274	54.951	-21.543	-0.442	1.00	130.02
1507	C6	NAG	A	274	53.668	-23.483	0.076	1.00	139.67
1508	O6	NAG	A	274	52.628	-22.635	-0.387	1.00	144.24
1509	C1	FCA	A	275	59.339	-23.324	1.916	1.00	166.18
1510	C2	FCA	A	275	59.905	-22.923	3.289	1.00	176.23
1511	C3	FCA	A	275	60.762	-21.695	3.251	1.00	178.46
1512	C4	FCA	A	275	61.991	-21.833	2.283	1.00	172.76
1513	C5	FCA	A	275	61.389	-22.191	0.896	1.00	176.96
1514	C6	FCA	A	275	62.389	-22.620	-0.196	1.00	180.24
1515	O2	FCA	A	275	58.772	-22.721	4.211	1.00	187.28
1516	O3	FCA	A	275	61.269	-21.376	4.553	1.00	178.44
1517	O4	FCA	A	275	62.910	-22.849	2.754	1.00	169.66
1518	O5	FCA	A	275	60.459	-23.282	0.968	1.00	169.81
1519	C1	NAG	A	276	57.235	-25.594	1.103	1.00	98.00
1520	C2	NAG	A	276	56.691	-27.020	1.226	1.00	98.05
1521	N2	NAC	A	276	55.572	27.066	2.154	1.00	97.91
1522	C7	NAG	A	276	54.356	-27.358	1.694	1.00	98.05
1523	O7	NAG	A	276	54.123	-27.596	0.498	1.00	98.12
1524	C8	NAG	A	276	53.223	-27.391	2.716	1.00	97.73
1525	C3	NAG	A	276	57.782	-28.020	1.658	1.00	98.00
1526	O3	NAG	A	276	57.292	-29.346	1.498	1.00	98.03
1527	C4	NAG	A	276	59.057	-27.855	0.815	1.00	97.83
1528	O4	NAG	A	276	60.118	-28.595	1.409	1.00	98.08
1529	C5	NAG	A	276	59.467	-26.388	0.717	1.00	97.92
1530	O5	NAG	A	276	58.367	-25.586	0.218	1.00	98.07
1531	C6	NAG	A	276	60.628	-26.186	-0.248	1.00	97.94
1532	O6	NAG	A	276	60.565	-24.929	-0.904	1.00	97.99
1533	C1	NAG	A	340	39.040	-8.595	19.969	1.00	100.93
1534	C2	NAG	A	340	39.952	-9.673	19.363	1.00	110.08

	1535	N2	NAG A	340	39.319	-10.976	19.455	1.00	124.78
	1536	C7	NAG A	340	39.582	-11.912	18.542	1.00	135.15
	1537	O7	NAG A	340	40.340	-11.731	17.581	1.00	143.28
	1538	C8	NAG A	340	38.887	-13.255	18.716	1.00	133.94
5	1539	C3	NAG A	340	41.289	-9.672	20.154	1.00	111.41
	1540	O3	NAG A	340	42.244	-10.545	19.553	1.00	102.38
	1541	C4	NAG A	340	41.892	-8.253	20.277	1.00	118.52
	1542	O4	NAG A	340	42.980	-8.268	21.194	1.00	138.80
10	1543	C5	NAG A	340	40.818	-7.251	20.750	1.00	112.80
	1544	O5	NAG A	340	39.674	-7.325	19.890	1.00	95.92
	1545	C6	NAG A	340	41.276	-5.810	20.749	1.00	115.39
	1546	O6	NAG A	340	40.167	-4.937	20.919	1.00	113.34
	1547	C1	NAG A	366	26.559	-8.481	-3.518	1.00	137.03
15	1548	C2	NAG A	366	25.744	-9.771	-3.450	1.00	148.09
	1549	N2	NAG A	366	26.028	-10.464	-2.209	1.00	155.02
	1550	C7	NAG A	366	25.085	-10.564	-1.276	1.00	162.56
	1551	O7	NAG A	366	23.951	-10.097	-1.415	1.00	164.09
	1552	C8	NAG A	366	25.455	-11.299	0.005	1.00	163.28
20	1553	C3	NAG A	366	26.084	-10.660	-4.651	1.00	155.95
	1554	O3	NAG A	366	25.247	-11.807	-4.658	1.00	159.81
	1555	C4	NAG A	366	25.893	-9.878	-5.955	1.00	160.49
	1556	O4	NAG A	366	26.355	-10.659	-7.048	1.00	169.57
	1557	C5	NAG A	366	26.666	-8.550	-5.904	1.00	155.12
25	1558	O5	NAG A	366	26.272	-7.789	-4.739	1.00	140.93
	1559	C6	NAG A	366	26.413	-7.679	-7.123	1.00	152.76
	1560	O6	NAG A	366	26.023	-6.364	-6.753	1.00	149.51
	1561	CB	VAL B	1	4.752	40.855	51.137	1.00	126.57
	1562	CG1	VAL B	1	5.003	40.880	49.633	1.00	131.97
30	1563	CG2	VAL B	1	3.866	42.021	51.535	1.00	130.09
	1564	C	VAL B	1	5.086	38.381	51.284	1.00	100.44
	1565	O	VAL B	1	6.179	38.608	50.764	1.00	97.65
	1566	N	VAL B	1	3.657	39.534	52.971	1.00	122.36
	1567	CA	VAL B	1	4.091	39.511	51.550	1.00	110.89
35	1568	N	PRO B	2	4.743	37.150	51.681	1.00	91.57
	1569	CD	PRO B	2	3.715	36.682	52.617	1.00	86.81
	1570	CA	PRO B	2	5.701	36.083	51.401	1.00	92.03
	1571	CB	PRO B	2	5.219	34.937	52.280	1.00	92.13
	1572	CG	PRO B	2	4.469	35.618	53.356	1.00	98.41
40	1573	C	PRO B	2	5.482	35.783	49.928	1.00	104.42
	1574	O	PRO B	2	4.381	35.956	49.405	1.00	108.80
	1575	N	GLN B	3	6.522	35.337	49.251	1.00	115.31
	1576	CA	GLN B	3	6.395	35.044	47.839	1.00	118.75
	1577	CB	GLN B	3	7.319	35.945	47.050	1.00	132.23
45	1578	CG	GLN B	3	6.978	37.381	47.261	1.00	134.41
	1579	CD	GLN B	3	5.850	37.837	46.374	1.00	126.94
	1580	OE1	GLN B	3	4.815	37.173	46.271	1.00	124.90
	1581	NE2	GLN B	3	6.038	38.982	45.724	1.00	122.46
	1582	C	GLN B	3	6.793	33.624	47.639	1.00	113.83
50	1583	O	GLN B	3	7.983	33.320	47.488	1.00	116.50
	1584	N	LYS B	4	5.812	32.736	47.641	1.00	104.77
	1585	CA	LYS B	4	6.188	31.357	47.465	1.00	92.78
	1586	CB	LYS B	4	4.972	30.448	47.319	1.00	100.70
	1587	CG	LYS B	4	3.816	31.031	46.558	1.00	119.63
55	1588	CD	LYS B	4	2.912	29.900	46.094	1.00	129.60
	1589	CE	LYS B	4	1.591	30.427	45.556	1.00	131.81
	1590	NZ	LYS B	4	0.528	29.403	45.762	1.00	129.85
	1591	C	LYS B	4	7.093	31.230	46.253	1.00	81.27
	1592	O	LYS B	4	6.904	31.908	45.239	1.00	74.91
60	1593	N	PRO B	5	8.133	30.392	46.370	1.00	75.63
	1594	CD	PRO B	5	8.529	29.619	47.557	1.00	71.19
	1595	CA	PRO B	5	9.074	30.177	45.271	1.00	65.65
	1596	CB	PRO B	5	10.020	29.110	45.820	1.00	54.74
	1597	CG	PRO B	5	9.982	29.343	47.268	1.00	65.46
65	1598	C	PRO B	5	8.255	29.650	44.097	1.00	64.33
	1599	O	PRO B	5	7.090	29.277	44.255	1.00	65.82
	1600	N	LYS B	6	8.858	29.608	42.923	1.00	65.65
	1601	CA	LYS B	6	8.152	29.109	41.762	1.00	62.04
	1602	CB	LYS B	6	7.636	30.279	40.927	1.00	55.18
	1603	CG	LYS B	6	6.697	29.866	39.817	1.00	89.38
70	1604	CD	LYS B	6	5.394	30.661	39.855	1.00	97.54

1605	CE	LYS	B	6	4.431	30.196	38.756	1.00	92.63
1606	NZ	LYS	B	6	3.107	30.872	38.837	1.00	79.21
1607	C	LYS	B	6	9.121	28.262	40.961	1.00	65.56
1608	O	LYS	B	6	10.042	28.789	40.325	1.00	67.90
1609	N	VAL	B	7	8.931	26.946	41.015	1.00	70.60
1610	CA	VAL	B	7	9.803	26.041	40.280	1.00	65.28
1611	CB	VAL	B	7	9.507	24.560	40.595	1.00	57.35
1612	CG1	VAL	B	7	10.356	23.663	39.694	1.00	39.82
1613	CG2	VAL	B	7	9.806	24.266	42.064	1.00	63.76
1614	C	VAL	B	7	9.621	26.268	38.785	1.00	60.19
1615	O	VAL	B	7	8.498	26.325	38.280	1.00	56.68
1616	N	SER	B	8	10.736	26.423	38.087	1.00	44.71
1617	CA	SER	B	8	10.719	26.639	36.656	1.00	31.26
1618	CB	SER	B	8	11.396	27.952	36.318	1.00	41.26
1619	OG	SER	B	8	12.802	27.750	36.214	1.00	36.80
1620	C	SER	B	8	11.540	25.504	36.055	1.00	48.76
1621	O	SER	B	8	12.480	25.002	36.675	1.00	52.73
1622	N	LEU	B	9	11.202	25.094	34.844	1.00	48.97
1623	CA	LEU	B	9	11.947	24.009	34.225	1.00	39.06
1624	CB	LEU	B	9	11.000	22.902	33.735	1.00	33.73
1625	CG	LEU	B	9	9.752	22.521	34.533	1.00	40.03
1626	CD1	LEU	B	9	9.198	21.252	33.933	1.00	39.96
1627	CD2	LEU	B	9	10.071	22.302	35.993	1.00	58.00
1628	C	LEU	B	9	12.764	24.506	33.041	1.00	33.09
1629	O	LEU	B	9	12.353	25.413	32.317	1.00	31.06
1630	N	ASN	B	10	13.930	23.908	32.848	1.00	19.95
1631	CA	ASN	B	10	14.768	24.262	31.721	1.00	20.51
1632	CB	ASN	B	10	15.833	25.276	32.096	1.00	41.33
1633	CG	ASN	B	10	16.763	25.559	30.942	1.00	52.07
1634	OD1	ASN	B	10	16.325	26.031	29.890	1.00	83.63
1635	ND2	ASN	B	10	18.048	25.263	31.119	1.00	49.68
1636	C	ASN	B	10	15.446	23.008	31.211	1.00	34.87
1637	O	ASN	B	10	16.375	22.497	31.843	1.00	40.39
1638	N	PRO	B	11	15.025	22.518	30.034	1.00	43.40
1639	CD	PRO	B	11	15.817	21.532	29.277	1.00	30.44
1640	CA	PRO	B	11	13.956	23.087	29.197	1.00	20.84
1641	CB	PRO	B	11	14.085	22.307	27.918	1.00	36.80
1642	CG	PRO	B	11	15.604	21.988	27.879	1.00	28.71
1643	C	PRO	B	11	12.572	22.964	29.819	1.00	34.02
1644	O	PRO	B	11	12.312	22.023	30.566	1.00	49.37
1645	N	PRO	B	12	11.663	23.896	29.482	1.00	30.69
1646	CD	PRO	B	12	11.938	24.837	28.384	1.00	30.68
1647	CA	PRO	B	12	10.268	24.026	29.945	1.00	24.81
1648	CB	PRO	B	12	9.668	25.062	28.995	1.00	34.63
1649	CG	PRO	B	12	10.861	25.893	28.607	1.00	49.64
1650	C	PRO	B	12	9.452	22.761	29.981	1.00	29.55
1651	O	PRO	B	12	8.465	22.654	30.716	1.00	28.29
1652	N	TRP	B	13	9.873	21.802	29.176	1.00	38.99
1653	CA	TRP	B	13	9.188	20.527	29.057	1.00	44.73
1654	CB	TRP	B	13	9.904	19.706	27.996	1.00	44.13
1655	CG	TRP	B	13	10.282	20.578	26.874	1.00	32.01
1656	CD2	TRP	B	13	9.428	21.507	26.210	1.00	33.06
1657	CE2	TRP	B	13	10.213	22.177	25.247	1.00	37.35
1658	CE3	TRP	B	13	8.069	21.841	26.335	1.00	32.11
1659	CD1	TRP	B	13	11.520	20.712	26.306	1.00	30.68
1660	NE1	TRP	B	13	11.487	21.675	25.330	1.00	32.77
1661	CZ2	TRP	B	13	9.686	23.160	24.411	1.00	42.92
1662	CZ3	TRP	B	13	7.545	22.816	25.507	1.00	36.94
1663	CH2	TRP	B	13	8.354	23.466	24.553	1.00	51.15
1664	C	TRP	B	13	9.079	19.747	30.356	1.00	42.74
1665	O	TRP	B	13	10.070	19.236	30.866	1.00	27.87
1666	N	ASN	B	14	7.862	19.660	30.879	1.00	39.20
1667	CA	ASN	B	14	7.609	18.933	32.107	1.00	42.44
1668	CB	ASN	B	14	6.354	19.469	32.774	1.00	50.46
1669	CG	ASN	B	14	5.119	19.130	32.010	1.00	49.15
1670	OD1	ASN	B	14	4.967	19.509	30.852	1.00	79.01
1671	ND2	ASN	B	14	4.221	18.402	32.649	1.00	57.09
1672	C	ASN	B	14	7.427	17.455	31.790	1.00	43.98
1673	O	ASN	B	14	7.263	16.635	32.683	1.00	61.67
1674	N	ARG	B	15	7.443	17.126	30.507	1.00	44.77

	1675	CA	ARG	B	15	7.293	15.749	30.065	1.00	37.62
	1676	CB	ARG	B	15	6.053	15.588	29.197	1.00	37.39
	1677	CG	ARG	B	15	4.972	16.603	29.455	1.00	44.80
	1678	CD	ARG	B	15	3.826	16.330	28.510	1.00	56.59
5	1679	NE	ARG	B	15	3.226	15.032	28.781	1.00	41.31
	1680	CZ	ARG	B	15	2.570	14.311	27.883	1.00	40.12
	1681	NH1	ARG	B	15	2.435	14.759	26.639	1.00	57.43
	1682	NH2	ARG	B	15	2.033	13.155	28.246	1.00	28.82
	1683	C	ARG	B	15	8.522	15.500	29.221	1.00	31.33
10	1684	O	ARG	B	15	8.737	16.159	28.202	1.00	34.58
	1685	N	ILE	B	16	9.328	14.535	29.621	1.00	29.80
	1686	CA	ILE	B	16	10.540	14.286	28.872	1.00	46.54
	1687	CB	ILE	B	16	11.728	14.912	29.604	1.00	56.61
	1688	CG2	ILE	B	16	11.405	16.370	29.929	1.00	58.31
15	1689	CG1	ILE	B	16	11.988	14.150	30.912	1.00	61.86
	1690	CD1	ILE	B	16	13.106	14.716	31.753	1.00	58.95
	1691	C	ILE	B	16	10.813	12.811	28.652	1.00	43.09
	1692	O	ILE	B	16	10.303	11.952	29.383	1.00	46.04
	1693	N	PHE	B	17	11.619	12.532	27.634	1.00	34.79
20	1694	CA	PHE	B	17	12.001	11.967	27.303	1.00	46.60
	1695	CB	PHE	B	17	12.605	11.118	25.894	1.00	38.91
	1696	CG	PHE	B	17	11.585	11.032	24.793	1.00	49.23
	1697	CD1	PHE	B	17	11.845	11.607	23.549	1.00	47.72
	1698	CD2	PHE	B	17	10.387	10.354	24.982	1.00	39.73
25	1699	CE1	PHE	B	17	10.931	11.520	22.512	1.00	39.05
	1700	CE2	PHE	B	17	9.465	10.258	23.957	1.00	33.44
	1701	CZ	PHE	B	17	9.736	10.840	22.713	1.00	50.08
	1702	C	PHE	B	17	13.028	10.639	28.305	1.00	53.02
	1703	O	PHE	B	17	13.828	11.405	28.859	1.00	46.68
30	1704	N	LYS	B	18	12.996	9.330	28.536	1.00	49.36
	1705	CA	LYS	B	18	13.942	8.691	29.439	1.00	46.09
	1706	CB	LYS	B	18	13.694	7.183	29.470	1.00	30.09
	1707	CG	LYS	B	18	14.791	6.380	30.134	1.00	62.01
	1708	CD	LYS	B	18	14.541	4.890	29.967	1.00	69.67
35	1709	CE	LYS	B	18	15.591	4.051	30.696	1.00	79.54
	1710	NZ	LYS	B	18	16.966	4.233	30.147	1.00	74.39
	1711	C	LYS	B	18	15.363	8.964	28.946	1.00	45.81
	1712	O	LYS	B	18	15.641	8.877	27.761	1.00	48.24
	1713	N	GLY	B	19	16.261	9.305	29.860	1.00	54.24
40	1714	CA	GLY	B	19	17.634	9.564	29.470	1.00	48.03
	1715	C	GLY	B	19	17.942	11.011	29.142	1.00	57.65
	1716	O	GLY	B	19	19.110	11.364	28.984	1.00	57.96
	1717	N	GLU	B	20	16.916	11.855	29.050	1.00	59.66
	1718	CA	GLU	B	20	17.142	13.269	28.754	1.00	58.50
45	1719	CB	GLU	B	20	15.900	13.889	28.106	1.00	70.52
	1720	CG	GLU	B	20	15.444	13.180	26.834	1.00	82.41
	1721	CD	GLU	B	20	14.502	14.026	25.992	1.00	79.78
	1722	OE1	GLU	B	20	13.490	14.527	26.550	1.00	67.98
	1723	OE2	GLU	B	20	14.786	14.176	24.776	1.00	80.75
50	1724	C	GLU	B	20	17.474	14.021	30.046	1.00	52.56
	1725	O	GLU	B	20	17.266	13.492	31.143	1.00	35.18
	1726	N	ASN	B	21	17.999	15.244	29.920	1.00	59.52
	1727	CA	ASN	B	21	18.344	16.072	31.085	1.00	47.35
	1728	CB	ASN	B	21	19.753	16.640	30.956	1.00	30.47
55	1729	CG	ASN	B	21	20.784	15.572	30.658	1.00	55.82
	1730	OD1	ASN	B	21	20.688	14.447	31.168	1.00	46.16
	1731	ND2	ASN	B	21	21.772	15.924	29.835	1.00	67.36
	1732	C	ASN	B	21	17.383	17.239	31.261	1.00	40.95
	1733	O	ASN	B	21	16.866	17.784	30.292	1.00	70.03
60	1734	N	VAL	B	22	17.152	17.619	32.507	1.00	25.27
	1735	CA	VAL	B	22	16.276	18.735	32.829	1.00	32.44
	1736	CB	VAL	B	22	14.824	18.247	33.003	1.00	20.08
	1737	CG1	VAL	B	22	14.692	17.429	34.270	1.00	24.18
	1738	CG2	VAL	B	22	13.882	19.426	33.061	1.00	36.02
65	1739	C	VAL	B	22	16.775	19.385	34.139	1.00	43.21
	1740	O	VAL	B	22	17.327	18.710	35.003	1.00	49.24
	1741	N	THR	B	23	16.583	20.689	34.289	1.00	39.88
	1742	CA	THR	B	23	17.030	21.383	35.489	1.00	33.49
	1743	CB	THR	B	23	18.165	22.352	35.174	1.00	34.45
70	1744	OG1	THR	B	23	19.216	21.655	34.493	1.00	42.02

	1745	CG2	THR	B	23	18.693	22.967	36.456	1.00	52.09
	1746	C	THR	B	23	15.931	22.180	36.167	1.00	43.19
	1747	O	THR	B	23	15.405	23.157	35.608	1.00	46.71
	1748	N	LEU	B	24	15.591	21.797	37.383	1.00	44.29
5	1749	CA	LEU	B	24	14.581	22.521	38.131	1.00	54.45
	1750	CB	LEU	B	24	13.911	21.596	39.141	1.00	48.21
	1751	CG	LEU	B	24	13.237	20.376	38.519	1.00	51.83
	1752	CD1	LEU	B	24	12.426	19.622	39.562	1.00	56.70
	1753	CD2	LEU	B	24	12.329	20.835	37.415	1.00	69.70
10	1754	C	LEU	B	24	15.255	23.676	38.858	1.00	60.50
	1755	O	LEU	B	24	16.299	23.494	39.482	1.00	84.20
	1756	N	THR	B	25	14.669	24.865	38.771	1.00	56.15
	1757	CA	THR	B	25	15.238	26.025	39.439	1.00	48.18
	1758	CB	THR	B	25	15.715	27.055	38.435	1.00	36.73
15	1759	OG1	THR	B	25	16.498	26.395	37.429	1.00	43.20
	1760	CG2	THR	B	25	16.584	28.095	39.134	1.00	58.01
	1761	C	THR	B	25	14.228	26.659	40.374	1.00	55.18
	1762	O	THR	B	25	13.051	26.810	40.019	1.00	39.05
	1763	N	CYS	B	26	14.700	27.010	41.571	1.00	69.20
20	1764	C	CYS	B	26	13.866	27.603	42.608	1.00	77.69
	1765	C	CYS	B	26	14.115	29.091	42.752	1.00	84.84
	1766	O	CYS	B	26	15.186	29.501	43.193	1.00	95.13
	1767	CB	CYS	B	26	14.146	26.925	43.947	1.00	70.99
	1768	SG	CYS	B	26	12.878	27.161	45.240	1.00	87.46
25	1769	N	ASN	B	27	13.127	29.898	42.378	1.00	94.31
	1770	CA	ASN	B	27	13.234	31.349	42.491	1.00	97.02
	1771	CB	ASN	B	27	14.182	31.917	41.409	1.00	104.76
	1772	CG	ASN	B	27	13.616	31.796	39.988	1.00	106.25
	1773	OD1	ASN	B	27	12.599	31.141	39.748	1.00	109.42
30	1774	ND2	ASN	B	27	14.293	32.434	39.035	1.00	104.71
	1775	C	ASN	B	27	11.848	31.975	42.388	1.00	95.21
	1776	O	ASN	B	27	10.979	31.462	41.684	1.00	83.43
	1777	N	GLY	B	28	11.639	33.069	43.112	1.00	106.07
	1778	CA	GLY	B	28	10.354	33.753	43.101	1.00	127.70
35	1779	C	GLY	B	28	10.461	34.992	43.966	1.00	138.06
	1780	O	GLY	B	28	10.631	34.879	45.182	1.00	143.08
	1781	N	ASN	B	29	10.341	36.173	43.362	1.00	142.87
	1782	CA	ASN	B	29	10.498	37.424	44.099	1.00	153.48
	1783	CB	ASN	B	29	9.350	37.669	45.082	1.00	152.59
40	1784	CG	ASN	B	29	9.535	38.959	45.876	1.00	158.12
	1785	OD1	ASN	B	29	10.508	39.679	45.675	1.00	156.21
	1786	ND2	ASN	B	29	8.607	39.253	46.772	1.00	158.95
	1787	C	ASN	B	29	11.787	37.198	44.865	1.00	161.65
	1788	O	ASN	B	29	11.820	37.250	46.094	1.00	164.05
45	1789	N	ASN	B	30	12.842	36.920	44.109	1.00	173.43
	1790	CA	ASN	B	30	14.136	36.629	44.690	1.00	183.92
	1791	CB	ASN	B	30	15.174	36.378	43.593	1.00	190.23
	1792	CG	ASN	B	30	16.451	35.752	44.136	1.00	197.43
	1793	OD1	ASN	B	30	16.552	35.442	45.325	1.00	203.09
50	1794	ND2	ASN	B	30	17.431	35.555	43.262	1.00	200.85
	1795	C	ASN	B	30	14.653	37.685	45.639	1.00	186.26
	1796	O	ASN	B	30	14.262	38.855	45.593	1.00	185.38
	1797	N	PHE	B	31	15.547	37.235	46.501	1.00	188.59
	1798	CA	PHE	B	31	16.173	38.036	47.500	1.00	194.52
55	1799	CB	PHE	B	31	15.485	37.780	48.8·11	1.00	203.03
	1800	CG	PHE	B	31	15.971	38.766	49.886	1.00	210.47
	1801	CD1	PHE	B	31	15.408	40.027	49.940	1.00	216.06
	1802	CD2	PHE	B	31	16.993	38.456	50.730	1.00	211.10
	1803	CE1	PHE	B	31	15.861	40.961	50.804	1.00	222.00
60	1804	CE2	PHE	B	31	17.485	39.387	51.600	1.00	215.51
	1805	CZ	PHE	B	31	16.924	40.643	51.640	1.00	219.04
	1806	C	PHE	B	31	17.649	37.672	47.559	1.00	191.71
	1807	O	PHE	B	31	18.344	37.980	48.535	1.00	197.27
	1808	N	PHE	B	32	18.115	36.994	46.528	1.00	183.37
65	1809	CA	PHE	B	32	19.516	36.543	46.471	1.00	176.18
	1810	CB	PHE	B	32	20.457	37.696	46.108	1.00	171.85
	1811	CG	PHE	B	32	20.693	38.668	47.204	1.00	170.32
	1812	CD1	PHE	B	32	21.637	38.396	48.187	1.00	169.89
	1813	CD2	PHE	B	32	19.977	39.859	47.276	1.00	168.03
70	1814	CE1	PHE	B	32	21.868	39.298	49.221	1.00	164.25

	1815	CE2	PHE	B	32	20.201	40.765	48.308	1.00	160.78
	1816	CZ	PHE	B	32	21.145	40.483	49.282	1.00	159.57
	1817	C	PHE	B	32	19.870	35.945	47.824	1.00	175.68
	1818	O	PHE	B	32	21.029	35.946	48.235	1.00	173.43
5	1819	N	GLU	B	33	18.872	35.409	48.474	1.00	177.15
	1820	CA	GLU	B	33	19.012	34.712	49.721	1.00	177.13
	1821	CB	GLU	B	33	17.859	35.035	50.674	1.00	179.86
	1822	CG	GLU	B	33	18.021	34.459	52.073	1.00	176.70
	1823	CD	GLU	B	33	19.050	35.206	52.898	1.00	173.43
10	1824	OE1	GLU	B	33	19.758	36.067	52.334	1.00	173.17
	1825	OE2	GLU	B	33	19.151	34.929	54.111	1.00	172.06
	1826	C	GLU	B	33	18.966	33.237	49.329	1.00	175.21
	1827	O	GLU	B	33	18.622	32.361	50.122	1.00	174.80
	1828	N	VAL	B	34	19.311	32.998	48.071	1.00	172.32
15	1829	CA	VAL	B	34	19.336	31.679	47.454	1.00	166.26
	1830	CB	VAL	B	34	20.040	31.769	46.083	1.00	167.66
	1831	CG1	VAL	B	34	20.242	30.393	45.487	1.00	171.78
	1832	CG2	VAL	B	34	19.234	32.658	45.147	1.00	170.77
	1833	C	VAL	B	34	19.997	30.573	48.274	1.00	160.12
20	1834	O	VAL	B	34	19.643	29.405	48.137	1.00	161.37
	1835	N	SER	B	35	20.953	30.940	49.117	1.00	154.76
	1836	CA	SER	B	35	21.668	29.962	49.933	1.00	144.31
	1837	CB	SER	B	35	22.442	30.673	51.049	1.00	145.69
	1838	OG	SER	B	35	21.565	31.183	52.038	1.00	143.47
25	1839	C	SER	B	35	20.772	28.897	50.555	1.00	136.95
	1840	O	SER	B	35	21.184	27.749	50.708	1.00	135.37
	1841	N	SER	B	36	19.547	29.269	50.912	1.00	130.67
	1842	CA	SER	B	36	18.623	28.328	51.542	1.00	127.00
	1843	CB	SER	B	36	17.944	28.990	52.748	1.00	133.26
30	1844	OG	SER	B	36	17.047	30.017	52.345	1.00	123.80
	1845	C	SER	B	36	17.545	27.766	50.615	1.00	123.00
	1846	O	SER	B	36	16.620	28.481	50.222	1.00	128.61
	1847	N	THR	B	37	17.657	26.480	50.282	1.00	107.86
	1848	CA	THR	B	37	16.675	25.821	49.426	1.00	88.91
35	1849	CB	THR	B	37	17.089	25.793	47.928	1.00	87.15
	1850	OG1	THR	B	37	17.358	27.116	47.445	1.00	64.20
	1851	CG2	THR	B	37	15.955	25.213	47.103	1.00	90.90
	1852	C	THR	B	37	16.469	24.376	49.854	1.00	86.86
	1853	O	THR	B	37	17.427	23.669	50.168	1.00	83.90
40	1854	N	LYS	B	38	15.212	23.948	49.845	1.00	82.11
	1855	CA	LYS	B	38	14.835	22.596	50.224	1.00	83.86
	1856	CB	LYS	B	38	13.885	22.630	51.427	1.00	86.79
	1857	CG	LYS	B	38	14.442	22.010	52.699	1.00	100.07
	1858	CD	LYS	B	38	15.694	22.734	53.185	1.00	104.27
45	1859	CE	LYS	B	38	16.039	22.305	54.602	1.00	97.90
	1860	NZ	LYS	B	38	14.882	22.578	55.510	1.00	91.89
	1861	C	LYS	B	38	14.115	21.953	49.051	1.00	82.06
	1862	O	LYS	B	38	13.147	22.520	48.545	1.00	72.96
	1863	N	TRP	B	39	14.579	20.784	48.613	1.00	82.25
50	1864	CA	TRP	B	39	13.915	20.097	47.508	1.00	66.31
	1865	CB	TRP	B	39	14.922	19.675	46.449	1.00	58.26
	1866	CG	TRP	B	39	15.429	20.832	45.665	1.00	63.66
	1867	CD2	TRP	B	39	14.789	21.453	44.542	1.00	65.27
	1868	CE2	TRP	B	39	15.607	22.534	44.139	1.00	67.87
55	1869	CE3	TRP	B	39	13.605	21.201	43.841	1.00	51.05
	1870	CD1	TRP	B	39	16.574	21.541	45.891	1.00	62.46
	1871	NE1	TRP	B	39	16.690	22.565	44.977	1.00	57.52
	1872	CZ2	TRP	B	39	15.277	23.364	43.061	1.00	59.34
	1873	CZ3	TRP	B	39	13.280	22.023	42.775	1.00	59.55
60	1874	CH2	TRP	B	39	14.114	23.093	42.395	1.00	51.52
	1875	C	TRP	B	39	13.113	18.888	47.971	1.00	57.60
	1876	O	TRP	B	39	13.484	18.191	48.920	1.00	57.66
	1877	N	PHE	B	40	11.993	18.652	47.304	1.00	54.42
	1878	CA	PHE	B	40	11.149	17.534	47.671	1.00	62.19
65	1879	CB	PHE	B	40	9.926	18.018	48.449	1.00	54.85
	1880	CG	PHE	B	40	10.262	18.678	49.745	1.00	59.54
	1881	CD1	PHE	B	40	10.602	20.025	49.783	1.00	63.79
	1882	CD2	PHE	B	40	10.310	17.934	50.920	1.00	65.98
	1883	CE1	PHE	B	40	10.988	20.623	50.981	1.00	81.46
70	1884	CE2	PHE	B	40	10.696	18.518	52.122	1.00	72.69

	1885	CZ	PHE	B	40	11.039	19.863	52.154	1.00	78.47
	1886	C	PHE	B	40	10.688	16.728	46.476	1.00	68.64
	1887	O	PHE	B	40	9.920	17.217	45.650	1.00	78.19
	1888	N	HIS	B	41	11.157	15.487	46.396	1.00	72.46
5	1889	CA	HIS	B	41	10.778	14.593	45.314	1.00	69.06
	1890	CB	HIS	B	41	11.988	13.804	44.833	1.00	61.71
	1891	CG	HIS	B	41	11.706	12.972	43.630	1.00	66.30
	1892	CD2	HIS	B	41	12.491	12.132	42.921	1.00	62.70
	1893	ND1	HIS	B	41	10.476	12.970	43.011	1.00	68.58
10	1894	CE1	HIS	B	41	10.517	12.161	41.967	1.00	82.82
	1895	NE2	HIS	B	41	11.728	11.640	41.890	1.00	79.59
	1896	C	HIS	B	41	9.713	13.641	45.839	1.00	66.17
	1897	O	HIS	B	41	9.971	12.842	46.727	1.00	64.30
	1898	N	ASN	B	42	8.511	13.726	45.288	1.00	75.54
15	1899	CA	ASN	B	42	7.423	12.877	45.751	1.00	79.71
	1900	CB	ASN	B	42	7.739	11.397	45.530	1.00	78.21
	1901	CG	ASN	B	42	7.203	10.871	44.210	1.00	78.51
	1902	OD1	ASN	B	42	6.080	11.203	43.803	1.00	76.64
	1903	ND2	ASN	B	42	8.001	10.027	43.560	1.00	77.12
20	1904	C	ASN	B	42	7.183	13.113	47.236	1.00	79.13
	1905	O	ASN	B	42	6.754	12.203	47.958	1.00	64.42
	1906	N	GLY	B	43	7.478	14.330	47.692	1.00	81.21
	1907	CA	GLY	B	43	7.276	14.662	49.091	1.00	80.48
	1908	C	GLY	B	43	8.459	14.460	50.020	1.00	64.04
25	1909	O	GLY	B	43	8.452	14.985	51.123	1.00	63.95
	1910	N	SER	B	44	9.472	13.719	49.573	1.00	59.76
	1911	CA	SER	B	44	10.655	13.449	50.387	1.00	64.76
	1912	CB	SER	B	44	11.191	12.034	50.114	1.00	70.69
	1913	OG	SER	B	44	10.248	11.045	50.502	1.00	89.71
30	1914	C	SER	B	44	11.758	14.454	50.134	1.00	65.31
	1915	O	SER	B	44	12.038	14.802	48.993	1.00	76.25
	1916	N	LEU	B	45	12.386	14.914	51.209	1.00	65.35
	1917	CA	LEU	B	45	13.471	15.877	51.100	1.00	61.98
	1918	CB	LEU	B	45	13.917	16.337	52.496	1.00	65.46
35	1919	CG	LEU	B	45	15.182	17.202	52.529	1.00	79.05
	1920	CD1	LEU	B	45	14.971	18.471	51.691	1.00	77.35
	1921	CD2	LEU	B	45	15.526	17.548	53.971	1.00	72.35
	1922	C	LEU	B	45	14.663	15.278	50.351	1.00	60.60
	1923	O	LEU	B	45	15.109	14.168	50.638	1.00	63.58
40	1924	N	SER	B	46	15.167	16.015	49.374	1.00	61.57
	1925	CA	SER	B	46	16.315	15.564	48.608	1.00	73.03
	1926	CB	SER	B	46	16.247	16.120	47.186	1.00	77.22
	1927	OG	SER	B	46	17.386	15.737	46.432	1.00	90.60
	1928	C	SER	B	46	17.569	16.083	49.302	1.00	80.37
45	1929	O	SER	B	46	17.499	16.999	50.129	1.00	76.01
	1930	N	GLU	B	47	18.710	15.493	48.969	1.00	84.85
	1931	CA	GLU	B	47	19.974	15.930	49.548	1.00	84.12
	1932	CB	GLU	B	47	21.027	14.827	49.429	1.00	87.82
	1933	CG	GLU	B	47	20.659	13.538	50.145	1.00	101.06
50	1934	CD	GLU	B	47	20.468	13.733	51.637	1.00	111.75
	1935	OE1	GLU	B	47	20.638	14.876	52.113	1.00	115.76
	1936	OE2	GLU	B	47	20.148	12.744	52.329	1.00	122.59
	1937	C	GLU	B	47	20.468	17.212	48.886	1.00	82.42
	1938	O	GLU	B	47	21.259	17.951	49.455	1.00	91.17
55	1939	N	GLU	B	48	19.971	17.458	47.675	1.00	78.36
	1940	CA	GLU	B	48	20.339	18.649	46.918	1.00	77.76
	1941	CB	GLU	B	48	19.624	18.652	45.569	1.00	83.13
	1942	CG	GLU	B	48	19.832	19.876	44.726	1.00	92.74
	1943	CD	GLU	B	48	21.376	19.914	44.265	1.00	101.93
60	1944	OE1	GLU	B	48	21.677	19.317	43.203	1.00	102.91
	1945	OE2	GLU	B	48	22.204	20.531	44.975	1.00	108.55
	1946	C	GLU	B	48	19.970	19.916	47.686	1.00	77.31
	1947	O	GLU	B	48	18.853	20.040	48.204	1.00	74.82
	1948	N	THR	B	49	20.900	20.864	47.749	1.00	78.12
65	1949	CA	THR	B	49	20.659	22.107	48.475	1.00	81.85
	1950	CB	THR	B	49	21.526	22.184	49.748	1.00	83.91
	1951	OG1	THR	B	49	22.684	21.353	49.593	1.00	88.24
	1952	CG2	THR	B	49	20.726	21.743	50.961	1.00	75.28
	1953	C	THR	B	49	20.871	23.390	47.680	1.00	82.91
70	1954	O	THR	B	49	20.664	24.481	48.208	1.00	84.53

	1955	N	ASN	B	50	21.296	23.273	46.425	1.00	89.01
	1956	CA	ASN	B	50	21.491	24.455	45.592	1.00	90.45
	1957	CB	ASN	B	50	22.483	24.139	44.463	1.00	96.17
	1958	CG	ASN	B	50	22.910	25.375	43.697	1.00	111.81
5	1959	OD1	ASN	B	50	22.449	26.482	43.971	1.00	112.79
	1960	ND2	ASN	B	50	23.798	25.190	42.727	1.00	110.81
	1961	C	ASN	B	50	20.123	24.856	45.013	1.00	89.21
	1962	O	ASN	B	50	19.208	24.033	44.942	1.00	94.63
	1963	N	SER	B	51	19.976	26.118	44.625	1.00	84.28
10	1964	CA	SER	B	51	18.724	26.613	44.045	1.00	84.66
	1965	CB	SER	B	51	18.820	28.123	43.846	1.00	90.77
	1966	OG	SER	B	51	20.000	28.461	43.134	1.00	104.30
	1967	C	SER	B	51	18.387	25.940	42.699	1.00	77.58
	1968	O	SER	B	51	17.312	26.150	42.126	1.00	52.63
15	1969	N	SER	B	52	19.313	25.133	42.195	1.00	74.45
	1970	CA	SER	B	52	19.108	24.441	40.934	1.00	62.55
	1971	CB	SER	B	52	20.120	24.930	39.907	1.00	56.77
	1972	OG	SER	B	52	20.003	26.329	39.742	1.00	76.18
	1973	C	SER	B	52	19.243	22.934	41.098	1.00	61.53
20	1974	O	SER	B	52	20.327	22.425	41.391	1.00	66.28
	1975	N	LEU	B	53	18.133	22.229	40.915	1.00	56.00
	1976	CA	LEU	B	53	18.102	20.778	41.014	1.00	42.82
	1977	CB	LEU	B	53	16.789	20.323	41.642	1.00	35.21
	1978	CG	LEU	B	53	16.530	18.816	41.653	1.00	46.47
25	1979	CD1	LEU	B	53	17.775	18.057	42.111	1.00	51.40
	1980	CD2	LEU	B	53	15.337	18.539	42.565	1.00	29.95
	1981	C	LEU	B	53	18.236	20.189	39.627	1.00	40.92
	1982	O	LEU	B	53	17.347	20.336	38.801	1.00	59.69
	1983	N	ASN	B	54	19.353	19.524	39.372	1.00	53.72
30	1984	CA	ASN	B	54	19.583	18.921	38.068	1.00	63.37
	1985	CB	ASN	B	54	21.064	19.074	37.686	1.00	66.79
	1986	CG	ASN	B	54	21.475	20.516	37.562	1.00	81.16
	1987	OD1	ASN	B	54	20.985	21.239	36.691	1.00	89.84
	1988	ND2	ASN	B	54	22.372	20.952	38.439	1.00	99.57
35	1989	C	ASN	B	54	19.205	17.444	37.989	1.00	68.27
	1990	O	ASN	B	54	19.398	16.681	38.935	1.00	72.52
	1991	N	ILE	B	55	18.643	17.061	36.849	1.00	66.50
	1992	CA	ILE	B	55	18.242	15.689	36.596	1.00	55.12
	1993	CB	ILE	B	55	16.744	15.574	36.310	1.00	34.50
40	1994	CG2	ILE	B	55	16.431	14.175	35.822	1.00	22.09
	1995	CG1	ILE	B	55	15.952	15.909	37.577	1.00	32.78
	1996	CD1	ILE	B	55	14.466	15.688	37.459	1.00	38.73
	1997	C	ILE	B	55	19.012	15.235	35.371	1.00	57.07
	1998	O	ILE	B	55	18.806	15.751	34.276	1.00	69.88
45	1999	N	VAL	B	56	19.910	14.277	35.560	1.00	58.62
	2000	CA	VAL	B	56	20.719	13.795	34.450	1.00	65.98
	2001	CB	VAL	B	56	22.202	13.797	34.826	1.00	58.88
	2002	CG1	VAL	B	56	23.047	13.490	33.609	1.00	54.44
	2003	CG2	VAL	B	56	22.573	15.146	35.401	1.00	58.22
50	2004	C	VAL	B	56	20.326	12.401	33.984	1.00	71.96
	2005	O	VAL	B	56	20.232	11.468	34.782	1.00	82.07
	2006	N	ASN	B	57	20.103	12.272	32.678	1.00	70.61
	2007	CA	ASN	B	57	19.704	11.006	32.081	1.00	79.87
	2008	CB	ASN	B	57	20.879	10.028	32.084	1.00	88.09
55	2009	CG	ASN	B	57	22.082	10.573	31.331	1.00	104.06
	2010	OD1	ASN	B	57	21.990	10.934	30.151	1.00	109.39
	2011	ND2	ASN	B	57	23.220	10.640	32.013	1.00	110.76
	2012	C	ASN	B	57	18.532	10.441	32.865	1.00	77.25
	2013	O	ASN	B	57	18.597	9.335	33.403	1.00	83.22
60	2014	N	ALA	B	58	17.463	11.229	32.916	1.00	69.58
	2015	CA	ALA	B	58	16.246	10.872	33.629	1.00	67.83
	2016	CB	ALA	B	58	15.101	11.748	33.155	1.00	70.80
	2017	C	ALA	B	58	15.854	9.399	33.519	1.00	66.71
	2018	O	ALA	B	58	15.912	8.790	32.455	1.00	63.76
65	2019	N	LYS	B	59	15.472	8.837	34.655	1.00	62.18
	2020	CA	LYS	B	59	15.035	7.452	34.742	1.00	62.15
	2021	CB	LYS	B	59	15.688	6.774	35.943	1.00	77.31
	2022	CG	LYS	B	59	17.214	6.849	35.933	1.00	89.39
	2023	CD	LYS	B	59	17.816	6.471	37.277	1.00	86.69
70	2024	CE	LYS	B	59	19.320	6.717	37.280	1.00	83.05

	2025	NZ	LYS	B	59	19.914	6.523	38.630	1.00	80.45
	2026	C	LYS	B	59	13.548	7.589	34.978	1.00	56.91
	2027	O	LYS	B	59	13.062	8.707	35.128	1.00	72.49
5	2028	N	PHE	B	60	12.813	6.486	35.016	1.00	42.51
	2029	CA	PHE	B	60	11.380	6.608	35.244	1.00	48.10
	2030	CB	PHE	B	60	10.657	5.310	34.915	1.00	48.50
	2031	CG	PHE	B	60	10.808	4.884	33.480	1.00	64.06
	2032	CD1	PHE	B	60	11.919	4.149	33.072	1.00	63.95
10	2033	CD2	PHE	B	60	9.837	5.216	32.533	1.00	74.15
	2034	CE1	PHE	B	60	12.068	3.753	31.739	1.00	62.10
	2035	CE2	PHE	B	60	9.977	4.826	31.196	1.00	74.92
	2036	CZ	PHE	B	60	11.092	4.089	30.801	1.00	69.78
15	2037	C	PHE	B	60	11.166	6.962	36.693	1.00	55.02
	2038	O	PHE	B	60	10.203	7.639	37.058	1.00	61.86
	2039	N	GLU	B	61	12.097	6.503	37.517	1.00	75.45
	2040	CA	GLU	B	61	12.044	6.763	38.944	1.00	83.97
20	2041	CB	GLU	B	61	13.190	6.038	39.668	1.00	96.33
	2042	CG	GLU	B	61	13.077	4.505	39.705	1.00	106.00
	2043	CD	GLU	B	61	13.368	3.847	38.362	1.00	110.30
	2044	OE1	GLU	B	61	14.506	3.988	37.861	1.00	109.44
	2045	OE2	GLU	B	61	12.459	3.187	37.811	1.00	111.21
25	2046	C	GLU	B	61	12.136	8.267	39.188	1.00	78.63
	2047	O	GLU	B	61	11.814	8.747	40.277	1.00	79.41
	2048	N	ASP	B	62	12.579	9.007	38.174	1.00	64.96
	2049	CA	ASP	B	62	12.698	10.452	38.299	1.00	56.09
30	2050	CB	ASP	B	62	13.720	11.010	37.306	1.00	58.67
	2051	CG	ASP	B	62	15.152	10.763	37.744	1.00	72.63
	2052	OD1	ASP	B	62	15.467	11.068	38.916	1.00	85.98
	2053	OD2	ASP	B	62	15.963	10.277	36.923	1.00	71.52
	2054	C	ASP	B	62	11.366	11.151	38.094	1.00	52.65
35	2055	O	ASP	B	62	11.227	12.325	38.442	1.00	50.83
	2056	N	SER	B	63	10.391	10.440	37.533	1.00	47.35
	2057	CA	SER	B	63	9.076	11.029	37.311	1.00	51.69
	2058	CB	SER	B	63	8.157	10.038	36.609	1.00	59.14
	2059	OG	SER	B	63	8.676	9.676	35.341	1.00	76.77
40	2060	C	SER	B	63	8.511	11.353	38.669	1.00	48.98
	2061	O	SER	B	63	9.048	10.900	39.666	1.00	55.63
	2062	N	GLY	B	64	7.439	12.135	38.717	1.00	50.75
	2063	CA	GLY	B	64	6.846	12.460	39.998	1.00	54.90
45	2064	C	GLY	B	64	6.550	13.922	40.254	1.00	57.89
	2065	O	GLY	B	64	6.405	14.721	39.327	1.00	65.67
	2066	N	GLU	B	65	6.456	14.260	41.536	1.00	63.70
	2067	CA	GLU	B	65	6.161	15.619	41.982	1.00	62.19
	2068	CB	GLU	B	65	5.036	15.576	43.009	1.00	58.85
50	2069	CG	GLU	B	65	4.715	16.899	43.646	1.00	74.39
	2070	CD	GLU	B	65	3.957	16.719	44.960	1.00	96.38
	2071	OE1	GLU	B	65	4.578	16.285	45.968	1.00	90.14
	2072	OE2	GLU	B	65	2.734	17.002	44.976	1.00	104.83
	2073	C	GLU	B	65	7.386	16.301	42.598	1.00	58.45
55	2074	O	GLU	B	65	8.084	15.716	43.424	1.00	57.76
	2075	N	TYR	B	66	7.647	17.533	42.176	1.00	49.99
	2076	CA	TYR	B	66	8.768	18.291	42.696	1.00	34.15
	2077	CB	TYR	B	66	9.797	18.547	41.614	1.00	10.05
	2078	CG	TYR	B	66	10.595	17.338	41.213	1.00	33.40
60	2079	CD1	TYR	B	66	10.185	16.517	40.173	1.00	44.03
	2080	CE1	TYR	B	66	10.957	15.427	39.766	1.00	55.60
	2081	CD2	TYR	B	66	11.794	17.042	41.841	1.00	51.50
	2082	CE2	TYR	B	66	12.574	15.951	41.445	1.00	59.78
	2083	CZ	TYR	B	66	12.154	15.150	40.405	1.00	62.67
65	2084	OH	TYR	B	66	12.927	14.073	40.013	1.00	60.36
	2085	C	TYR	B	66	8.311	19.623	43.246	1.00	44.11
	2086	O	TYR	B	66	7.440	20.275	42.671	1.00	50.42
	2087	N	LYS	B	67	8.888	20.006	44.380	1.00	55.20
	2088	CA	LYS	B	67	8.577	21.275	45.043	1.00	54.38
70	2089	CB	LYS	B	67	7.289	21.199	45.879	1.00	37.10
	2090	CG	LYS	B	67	7.088	19.925	46.675	1.00	40.24
	2091	CD	LYS	B	67	5.836	20.053	47.546	1.00	55.82
	2092	CE	LYS	B	67	5.362	18.702	48.076	1.00	71.24
	2093	NZ	LYS	B	67	4.355	18.855	49.172	1.00	79.55
	2094	C	LYS	B	67	9.725	21.684	45.931	1.00	61.59

2095	O	LYS	B	67	10.222	20.891	46.730	1.00	80.11
2096	N	CYS	B	68	10.161	22.924	45.761	1.00	69.06
2097	CA	CYS	B	68	11.261	23.443	46.547	1.00	75.09
2098	C	CYS	B	68	10.728	24.348	47.641	1.00	76.08
2099	O	CYS	B	68	9.543	24.682	47.671	1.00	78.03
2100	CB	CYS	B	68	12.231	24.217	45.665	1.00	71.35
2101	SG	CYS	B	68	11.523	25.691	44.866	1.00	75.66
2102	N	GLN	B	69	11.625	24.756	48.527	1.00	80.08
2103	CA	GLN	B	69	11.233	25.600	49.635	1.00	74.62
2104	CB	GLN	B	69	10.612	24.728	50.712	1.00	70.96
2105	CG	GLN	B	69	10.067	25.488	51.859	1.00	72.60
2106	CD	GLN	B	69	9.343	24.592	52.818	1.00	88.38
2107	OE1	GLN	B	69	9.406	23.363	52.720	1.00	85.19
2108	NE2	GLN	B	69	8.656	25.199	53.760	1.00	98.27
2109	C	GLN	B	69	12.418	26.356	50.212	1.00	78.27
2110	O	GLN	B	69	13.519	25.819	50.311	1.00	81.84
2111	N	HIS	B	70	12.193	27.611	50.577	1.00	82.10
2112	CA	HIS	B	70	13.252	28.390	51.183	1.00	85.15
2113	CB	HIS	B	70	13.822	29.437	50.192	1.00	82.03
2114	CG	HIS	B	70	12.892	30.565	49.860	1.00	93.26
2115	CD2	HIS	B	70	12.763	31.800	50.398	1.00	95.48
2116	ND1	HIS	B	70	11.997	30.515	48.812	1.00	109.66
2117	CE1	HIS	B	70	11.361	31.671	48.721	1.00	109.26
2118	NE2	HIS	B	70	11.804	32.468	49.672	1.00	109.02
2119	C	HIS	B	70	12.735	29.044	52.469	1.00	85.57
2120	O	HIS	B	70	11.549	29.350	52.598	1.00	85.74
2121	N	GLN	B	71	13.635	29.213	53.431	1.00	79.77
2122	CA	GLN	B	71	13.312	29.777	54.740	1.00	80.82
2123	CB	GLN	B	71	14.619	30.126	55.465	1.00	89.59
2124	CG	GLN	B	71	14.460	30.447	56.945	1.00	103.30
2125	CD	GLN	B	71	15.762	30.921	57.585	1.00	109.00
2126	OE1	GLN	B	71	16.789	30.220	57.542	1.00	100.56
2127	NE2	GLN	B	71	15.726	32.120	58.184	1.00	102.47
2128	C	GLN	B	71	12.365	30.993	54.763	1.00	67.00
2129	O	GLN	B	71	12.486	31.913	53.953	1.00	42.78
2130	N	GLN	B	72	11.432	30.978	55.715	1.00	69.70
2131	CA	GLN	B	72	10.460	32.063	55.922	1.00	70.51
2132	CB	GLN	B	72	11.188	33.388	56.149	1.00	78.43
2133	CG	GLN	B	72	11.812	33.551	57.509	1.00	78.98
2134	CD	GLN	B	72	12.598	34.838	57.593	1.00	95.13
2135	OE1	GLN	B	72	13.532	35.065	56.807	1.00	97.37
2136	NE2	GLN	B	72	12.223	35.700	58.540	1.00	98.58
2137	C	GLN	B	72	9.398	32.282	54.840	1.00	66.32
2138	O	GLN	B	72	8.737	33.329	54.816	1.00	61.96
2139	N	VAL	B	73	9.227	31.302	53.960	1.00	63.38
2140	CA	VAL	B	73	8.249	31.414	52.884	1.00	57.15
2141	CB	VAL	B	73	8.933	31.810	51.592	1.00	31.26
2142	CG1	VAL	B	73	9.710	30.646	51.074	1.00	36.55
2143	CG2	VAL	B	73	7.918	32.256	50.585	1.00	50.56
2144	C	VAL	B	73	7.552	30.075	52.663	1.00	59.51
2145	O	VAL	B	73	8.148	29.022	52.896	1.00	77.00
2146	N	ASN	B	74	6.300	30.115	52.210	1.00	61.46
2147	CA	ASN	B	74	5.534	28.892	51.965	1.00	68.17
2148	CB	ASN	B	74	4.195	29.223	51.312	1.00	73.30
2149	CG	ASN	B	74	3.211	29.829	52.267	1.00	72.42
2150	OD1	ASN	B	74	2.787	29.182	53.225	1.00	62.22
2151	ND2	ASN	B	74	2.831	31.081	52.014	1.00	85.31
2152	C	ASN	B	74	6.251	27.885	51.066	1.00	73.92
2153	O	ASN	B	74	7.342	28.142	50.543	1.00	73.43
2154	N	GLU	B	75	5.612	26.732	50.891	1.00	82.35
2155	CA	GLU	B	75	6.138	25.682	50.029	1.00	88.01
2156	CB	GLU	B	75	5.450	24.338	50.297	1.00	88.41
2157	CG	GLU	B	75	5.962	23.548	51.490	1.00	102.21
2158	CD	GLU	B	75	5.673	22.053	51.358	1.00	103.43
2159	OE1	GLU	B	75	4.497	21.692	51.118	1.00	95.26
2160	OE2	GLU	B	75	6.622	21.242	51.493	1.00	104.69
2161	C	GLU	B	75	5.844	26.073	48.592	1.00	85.00
2162	O	GLU	B	75	4.760	26.580	48.287	1.00	92.66
2163	N	SER	B	76	6.799	25.830	47.705	1.00	74.73
2164	CA	SER	B	76	6.597	26.136	46.299	1.00	64.93

	2165	CB	SER	B	76	7.811	25.716	45.474	1.00	65.57
	2166	OG	SER	B	76	7.884	24.300	45.366	1.00	53.84
	2167	C	SER	B	76	5.392	25.350	45.802	1.00	64.12
	2168	O	SER	B	76	4.920	24.425	46.467	1.00	55.19
5	2169	N	GLU	B	77	4.891	25.745	44.639	1.00	73.18
	2170	CA	GLU	B	77	3.779	25.015	44.046	1.00	69.69
	2171	CB	GLU	B	77	3.077	25.874	42.993	1.00 ·	59.63
	2172	CG	GLU	B	77	2.498	27.169	43.535	1.00	89.51
	2173	CD	GLU	B	77	1.820	28.000	42.462	1.00	107.00
10	2174	OE1	GLU	B	77	1.798	27.557	41.295	1.00	103.77
	2175	OE2	GLU	B	77	1.312	29.093	42.789	1.00	116.96
	2176	C	GLU	B	77	4.246	23.698	43.437	1.00	63.68
	2177	O	GLU	B	77	5.367	23.648	42.922	1.00	69.58
	2178	N	PRO	B	78	3.458	22.659	43.542	1.00	56.73
15	2179	CD	PRO	B	78	2.145	22.518	44.185	1.00	60.28
	2180	CA	PRO	B	78	3.910	21.387	42.987	1.00	49.00
	2181	CB	PRO	B	78	2.760	20.438	43.304	1.00	42.75
	2182	CG	PRO	B	78	2.141	21.046	44.534	1.00	68.49
	2183	C	PRO	B	78	4.155	21.509	41.497	1.00	44.78
20	2184	O	PRO	B	78	3.483	22.260	40.795	1.00	52.51
	2185	N	VAL	B	79	5.137	20.766	41.024	1.00	34.40
	2186	CA	VAL	B	79	5.486	20.745	39.616	1.00	23.08
	2187	CB	VAL	B	79	6.779	21.527	39.364	1.00	17.91
	2188	CG1	VAL	B	79	7.636	20.834	38.297	1.00	4.69
25	2189	CG2	VAL	B	79	6.413	22.948	38.961	1.00	17.83
	2190	C	VAL	B	79	5.674	19.278	39.257	1.00	40.76
	2191	O	VAL	B	79	6.573	18.609	39.783	1.00	37.75
	2192	N	TYR	B	80	4.831	18.773	38.362	1.00	43.38
	2193	CA	TYR	B	80	4.912	17.375	37.992	1.00	37.05
30	2194	CB	TYR	B	80	3.510	16.807	37.858	1.00	19.64
	2195	CG	TYR	B	80	2.736	16.988	39.122	1.00	52.81
	2196	CD1	TYR	B	80	1.881	18.084	39.293	1.00	64.76
	2197	CE1	TYR	B	80	1.205	18.294	40.505	1.00	83.30
	2198	CD2	TYR	B	80	2.901	16.098	40.186	1.00	64.99
35	2199	CE2	TYR	B	80	2.235	16.294	41.404	1.00	80.87
	2200	CZ	TYR	B	80	1.390	17.394	41.559	1.00	84.40
	2201	OH	TYR	B	80	0.754	17.609	42.767	1.00	76.06
	2202	C	TYR	B	80	5.723	17.083	36.752	1.00	42.78
	2203	O	TYR	B	80	5.472	17.622	35.674	1.00	56.71
40	2204	N	LEU	B	81	6.716	16.223	36.937	1.00	42.87
	2205	CA	LEU	B	81	7.615	15.798	35.878	1.00	47.81
	2206	CB	LEU	B	81	9.049	15.953	36.360	1.00	39.60
	2207	CG	LEU	B	81	10.151	15.383	35.481	1.00	53.84
	2208	CD1	LEU	B	81	10.118	16.055	34.119	1.00	61.99
45	2209	CD2	LEU	B	81	11.494	15.611	36.160	1.00	65.74
	2210	C	LEU	B	81	7.312	14.328	35.562	1.00	60.00
	2211	O	LEU	B	81	7.172	13.508	36.467	1.00	72.⌣ :
	2212	N	GLU	B	82	7.208	13.992	34.282	1.00	60.42
	2213	CA	GLU	B	82	6.888	12.623	33.895	1.00	51.18
50	2214	CB	GLU	B	82	5.425	12.559	33.475	1.00	60.43
	2215	CG	GLU	B	82	4.967	11.207	32.988	1.00	75.17
	2216	CD	GLU	B	82	3.453	11.151	32.824	1.00	92.83
	2217	OE1	GLU	B	82	2.880	12.091	32.219	1.00	98.53
	2218	OE2	GLU	B	82	2.839	·10.166	33.301	1.00	97.49
55	2219	C	GLU	B	82	7.778	12.089	32.780	1.00	49.31
	2220	O	GLU	B	82	7.734	12.564	31.645	1.00	54.46
	2221	N	VAL	B	83	8.590	11.095	33.116	1.00	44.1:
	2222	CA	VAL	B	83	9.512	10.492	32.158	1.00	51.30
	2223	CB	VAL	B	83	10.656	9.749	32.862	1.00	44.14
60	2224	CG1	VAL	B	83	11.654	9.218	31.812	1.00	45.56
	2225	CG2	VAL	B	83	11.334	10.669	33.861	1.00	46.11
	2226	C	VAL	B	83	8.820	9.488	31.246	1.00	55.74
	2227	O	VAL	B	83	8.110	8.609	31.713	1.00	73.69
	2228	N	PHE	B	84	9.051	9.608	29.945	1.00	53.23
65	2229	CA	PHE	B	84	8.431	8.707	28.981	1.00	49.95
	2230	CB	PHE	B	84	7.631	9.481	27.929	1.00	49.58
	2231	CG	PHE	B	84	6.436	10.200	28.462	1.00	35.11
	2232	CD1	PHE	B	84	6.570	11.175	29.423	1.00	52.71
	2233	CD2	PHE	B	84	5.176	9.913	27.982	1.00	56.24
70	2234	CE1	PHE	B	84	5.463	11.859	29.898	1.00	63.67

	2235	CE2	PHE	B	84	4.062	10.595	28.453	1.00	57.29
	2236	CZ	PHE	B	84	4.210	11.568	29.414	1.00	52.51
	2237	C	PHE	B	84	9.495	7.935	28.238	1.00	56.77
	2238	O	PHE	B	84	10.696	8.144	28.444	1.00	51.00
5	2239	N	SER	B	85	9.021	7.056	27.360	1.00	59.31
	2240	CA	SER	B	85	9.856	6.236	26.496	1.00	53.43
	2241	CB	SER	B	85	10.382	5.014	27.230	1.00	52.20
	2242	OG	SER	B	85	11.313	4.342	26.403	1.00	68.06
	2243	C	SER	B	85	8.929	5.799	25.372	1.00	61.23
10	2244	O	SER	B	85	8.107	4.897	25.547	1.00	56.17
	2245	N	ASP	B	86	9.053	6.474	24.234	1.00	68.29
	2246	CA	ASP	B	86	8.228	6.219	23.064	1.00	57.51
	2247	CB	ASP	B	86	6.812	6.736	23.321	1.00	51.72
	2248	CG	ASP	B	86	5.802	6.181	22.336	1.00	90.19
15	2249	OD1	ASP	B	86	6.002	6.371	21.113	1.00	100.01
	2250	OD2	ASP	B	86	4.811	5.554	22.788	1.00	98.70
	2251	C	ASP	B	86	8.868	6.974	21.897	1.00	57.18
	2252	O	ASP	B	86	9.851	7.701	22.080	1.00	62.75
	2253	N	TRP	B	87	8.330	6.799	20.699	1.00	51.37
20	2254	CA	TRP	B	87	8.896	7.483	19.543	1.00	50.71
	2255	CB	TRP	B	87	8.415	6.811	18.264	1.00	58.25
	2256	CG	TRP	B	87	8.811	5.379	18.134	1.00	53.11
	2257	CD2	TRP	B	87	10.032	4.880	17.562	1.00	52.15
	2258	CE2	TRP	B	87	9.945	3.476	17.552	1.00	60.06
25	2259	CE3	TRP	B	87	11.187	5.489	17.054	1.00	60.86
	2260	CD1	TRP	B	87	8.060	4.285	18.452	1.00	44.63
	2261	NE1	TRP	B	87	8.734	3.138	18.096	1.00	23.48
	2262	CZ2	TRP	B	87	10.964	2.672	17.056	1.00	78.55
	2263	CZ3	TRP	B	87	12.197	4.691	16.561	1.00	84.54
30	2264	CH2	TRP	B	87	12.077	3.294	16.565	1.00	87.37
	2265	C	TRP	B	87	8.545	8.982	19.495	1.00	42.37
	2266	O	TRP	B	87	9.367	9.839	19.123	1.00	23.61
	2267	N	LEU	B	88	7.308	9.296	19.849	1.00	29.09
	2268	CA	LEU	B	88	6.893	10.682	19.837	1.00	31.21
35	2269	CB	LEU	B	88	5.817	10.944	18.777	1.00	33.13
	2270	CG	LEU	B	88	6.167	10.869	17.290	1.00	18.54
	2271	CD1	LEU	B	88	5.021	11.506	16.542	1.00	25.10
	2272	CD2	LEU	B	88	7.449	11.594	16.959	1.00	4.59
	2273	C	LEU	B	88	6.348	11.083	21.182	1.00	40.21
40	2274	O	LEU	B	88	5.517	10.381	21.783	1.00	42.92
	2275	N	LEU	B	89	6.815	12.234	21.644	1.00	40.58
	2276	CA	LEU	B	89	6.369	12.780	22.912	1.00	31.34
	2277	CB	LEU	B	89	7.514	12.805	23.921	1.00	33.17
	2278	CG	LEU	B	89	7.202	13.378	25.299	1.00	42.18
45	2279	CD1	LEU	B	89	5.821	12.933	25.763	1.00	52.47
	2280	CD2	LEU	B	89	8.282	12.923	26.264	1.00	49.06
	2281	C	LEU	b	89	5.899	14.194	22.621	1.00	27.75
	2282	O	LEU	B	89	6.617	14.973	21.947	1.00	5.35
	2283	N	LEU	B	90	4.703	14.517	23.109	1.00	4.73
50	2284	CA	LEU	B	90	4.149	15.830	22.883	1.00	7.84
	2285	CB	LEU	B	90	2.634	15.775	22.724	1.00	21.81
	2286	CG	LEU	B	90	2.032	17.148	22.410	1.00	21.45
	2287	CD1	LEU	B	90	2.511	17.587	21.026	1.00	29.29
	2288	CD2	LEU	B	90	0.521	17.103	22.464	1.00	15.21
55	2289	C	LEU	B	90	4.473	16.654	24.087	1.00	25.07
	2290	O	LEU	B	90	3.901	16.441	25.149	1.00	44.25
	2291	N	GLN	B	91	5.382	17.603	23.924	1.00	35.94
	2292	CA	GLN	B	91	5.768	18.461	25.028	1.00	35.91
	2293	CB	GLN	B	91	7.273	18.707	24.955	1.00	17.00
60	2294	CG	GLN	B	91	8.061	17.428	25.129	1.00	13.88
	2295	CD	GLN	B	91	9.547	17.637	25.066	1.00	35.42
	2296	OE1	GLN	B	91	10.092	18.074	24.040	1.00	18.59
	2297	NE2	GLN	B	91	10.226	17.318	26.165	1.00	42.81
	2298	C	GLN	B	91	4.995	19.781	25.025	1.00	36.56
65	2299	O	GLN	B	91	4.606	20.285	23.966	1.00	49.74
	2300	N	ALA	B	92	4.761	20.335	26.212	1.00	35.59
	2301	CA	ALA	B	92	4.054	21.607	26.313	1.00	43.59
	2302	CB	ALA	B	92	2.628	21.377	26.734	1.00	28.50
	2303	C	ALA	B	92	4.719	22.580	27.283	1.00	53.87
70	2304	O	ALA	B	92	5.250	22.184	28.318	1.00	69.37

	2305	N	SER	B	93	4.684	23.860	26.832	1.00	68.52
	2306	CA	SER	B	93	5.252	24.923	27.761	1.00	64.18
	2307	CB	SER	B	93	4.947	26.287	27.133	1.00	72.74
	2308	OG	SER	B	93	3.537	26.475	26.986	1.00	77.53
5	2309	C	SER	B	93	4.593	24.849	29.128	1.00	56.86
	2310	O	SER	B	93	5.200	25.163	30.143	1.00	67.19
	2311	N	ALA	B	94	3.336	24.430	29.131	1.00	36.84
	2312	CA	ALA	B	94	2.560	24.304	30.346	1.00	46.61
	2313	CB	ALA	B	94	2.296	25.671	30.923	1.00	39.28
10	2314	C	ALA	B	94	1.248	23.611	29.999	1.00	57.58
	2315	O	ALA	B	94	0.553	24.008	29.063	1.00	64.68
	2316	N	GLU	B	95	0.912	22.571	30.754	1.00	65.01
	2317	CA	GLU	B	95	-0.311	21.824	30.510	1.00	66.91
	2318	CB	GLU	B	95	-0.290	20.535	31.329	1.00	69.50
15	2319	CG	GLU	B	95	0.872	19.619	30.950	1.00	64.00
	2320	CD	GLU	B	95	0.886	18.326	31.738	1.00	82.38
	2321	OE1	GLU	B	95	1.716	17.452	31.415	1.00	86.38
	2322	OE2	GLU	B	95	0.075	18.181	32.678	1.00	93.94
	2323	C	GLU	B	95	-1.540	22.669	30.831	1.00	68.95
20	2324	O	GLU	B	95	-2.644	22.394	30.346	1.00	67.01
	2325	N	VAL	B	96	-1.345	23.703	31.644	1.00	72.58
	2326	CA	VAL	B	96	-2.442	24.603	31.996	1.00	72.17
	2327	CB	VAL	B	96	-3.012	24.282	33.374	1.00	56.87
25	2328	CG1	VAL	B	96	-4.277	25.079	33.592	1.00	54.83
	2329	CG2	VAL	B	96	-3.280	22.788	33.489	1.00	38.14
	2330	C	VAL	B	96	-1.980	26.059	31.988	1.00	76.73
	2331	O	VAL	B	96	-1.079	26.441	32.738	1.00	76.80
	2332	N	VAL	B	97	-2.611	26.867	31.141	1.00	80.52
30	2333	CA	VAL	B	97	-2.258	28.271	30.996	1.00	82.56
	2334	CB	VAL	B	97	-1.740	28.546	29.562	1.00	85.79
	2335	CG1	VAL	B	97	-1.543	30.029	29.341	1.00	102.89
	2336	CG2	VAL	B	97	-0.429	27.803	29.334	1.00	95.31
	2337	C	VAL	B	97	-3.420	29.216	31.283	1.00	82.63
35	2338	O	VAL	B	97	-4.591	28.885	31.041	1.00	75.81
	2339	N	MET	B	98	-3.073	30.394	31.807	1.00	84.13
	2340	CA	MET	B	98	-4.050	31.442	32.112	1.00	91.67
	2341	CB	MET	B	98	-3.430	32.509	33.020	1.00	102.42
	2342	CG	MET	B	98	-3.324	32.120	34.480	1.00	120.32
40	2343	SD	MET	B	98	-4.951	31.748	35.181	1.00	137.79
	2344	CE	MET	B	98	-5.607	33.383	35.438	1.00	124.64
	2345	C	MET	B	98	-4.488	32.107	30.808	1.00	86.05
	2346	O	MET	B	98	-3.637	32.555	30.027	1.00	83.23
	2347	N	GLU	B	99	-5.797	32.193	30.571	1.00	75.14
45	2348	CA	GLU	B	99	-6.266	32.803	29.334	1.00	80.10
	2349	CB	GLU	B	99	-7.745	33.156	29.408	1.00	83.15
	2350	CG	GLU	B	99	-8.228	33.862	28.144	1.00	109.03
	2351	CD	GLU	B	99	-9.693	34.250	28.204	1.00	121.43
	2352	OE1	GLU	B	99	-10.084	34.917	29.189	1.00	131.12
50	2353	OE2	GLU	B	99	-10.446	33.893	27.265	1.00	120.08
	2354	C	GLU	B	99	-5.477	34.059	29.019	1.00	76.85
	2355	O	GLU	B	9:	-5.371	34.955	29.846	1.00	76.94
	2356	N	GLY	B	100	-4.915	34.113	27.818	1.00	81.06
	2357	CA	GLY	B	100	-4.139	35.273	27.429	1.00	80.78
55	2358	C	GLY	B	100	-2.644	35.015	27.460	1.00	77.00
	2359	O	GLY	B	100	-1.877	35.674	26.752	1.00	79.67
	2360	N	GLN	B	101	-2.220	34.062	28.284	1.00	75.05
	2361	CA	GLN	B	101	-0.798	33.729	28.370	1.00	78.99
	2362	CB	GLN	B	101	-0.494	32.996	29.682	1.00	84.76
60	2363	CG	GLN	B	101	-0.561	33.870	30.924	1.00	92.38
	2364	CD	GLN	B	101	0.340	35.097	30.817	1.00	98.22
	2365	OE1	GLN	B	101	-0.007	36.083	30.156	1.00	100.31
	2366	NE2	GLN	B	101	1.509	35.036	31.456	1.00	92.08
	2367	C	GLN	B	101	-0.351	32.876	27.178	1.00	65.25
65	2368	O	GLN	B	101	-1.169	32.375	26.414	1.00	57.39
	2369	N	PRO	B	102	0.963	32.708	26.997	1.00	59.88
	2370	CD	PRO	B	102	2.093	33.382	27.653	1.00	62.83
	2371	CA	PRO	B	102	1.422	31.801	25.868	1.00	59.94
	2372	CB	PRO	B	102	2.864	32.365	25.683	1.00	48.67
70	2373	CG	PRO	B	102	3.284	32.645	27.070	1.00	63.93
	2374	C	PRO	B	102	1.313	30.411	26.120	1.00	60.51

	2375	O	PRO	B	102	1.559	29.938	27.220	1.00	71.07
	2376	N	LEU	B	103	0.926	29.686	25.081	1.00	66.31
	2377	CA	LEU	B	103	0.780	28.238	25.119	1.00	56.78
	2378	CB	LEU	B	103	-0.664	27.880	24.821	1.00	50.78
5	2379	CG	LEU	B	103	-0.974	26.402	24.666	1.00	77.35
	2380	CD1	LEU	B	103	-0.629	25.680	25.955	1.00	76.88
	2381	CD2	LEU	B	103	-2.450	26.229	24.318	1.00	77.48
	2382	C	LEU	B	103	1.703	27.688	24.030	1.00	54.03
	2383	O	LEU	B	103	1.554	28.025	22.857	1.00	55.72
10	2384	N	PHE	B	104	2.655	26.842	24.402	1.00	48.78
	2385	CA	PHE	B	104	3.607	26.332	23.414	1.00	45.32
	2386	CB	PHE	B	104	4.979	26.893	23.748	1.00	32.16
	2387	CG	PHE	B	104	5.976	26.705	22.677	1.00	32.32
	2388	CD1	PHE	B	104	6.158	27.689	21.717	1.00	39.73
15	2389	CD2	PHE	B	104	6.770	25.566	22.641	1.00	39.96
	2390	CE1	PHE	B	104	7.123	27.544	20.708	1.00	55.96
	2391	CE2	PHE	B	104	7.744	25.404	21.638	1.00	63.91
	2392	CZ	PHE	B	104	7.923	26.404	20.673	1.00	61.86
	2393	C	PHE	B	104	3.700	24.805	23.299	1.00	42.46
20	2394	O	PHE	B	104	4.206	24.140	24.199	1.00	46.85
	2395	N	LEU	B	105	3.223	24.250	22.190	1.00	35.08
	2396	CA	LEU	B	105	3.277	22.811	22.006	1.00	22.82
	2397	CB	LEU	B	105	1.999	22.311	21.356	1.00	37.29
	2398	CG	LEU	B	105	0.804	22.355	22.298	1.00	42.12
25	2399	CD1	LEU	B	105	-0.404	21.635	21.660	1.00	56.32
	2400	CD2	LEU	B	105	1.196	21.673	23.579	1.00	54.72
	2401	C	LEU	B	105	4.468	22.421	21.165	1.00	23.23
	2402	O	LEU	B	105	5.055	23.250	20.476	1.00	30.46
	2403	N	ARG	B	106	4.833	21.149	21.226	1.00	15.51
30	2404	CA	ARG	B	106	5.990	20.674	20.475	1.00	30.48
	2405	CB	ARG	B	106	7.249	21.056	21.243	1.00	25.17
	2406	CG	ARG	B	106	8.540	20.446	20.746	1.00	50.57
	2407	CD	ARG	B	106	9.631	20.546	21.842	1.00	51.15
	2408	NE	ARG	B	106	10.970	20.223	21.346	1.00	50.88
35	2409	CZ	ARG	B	106	12.013	19.938	22.120	1.00	42.48
	2410	NH1	ARG	B	106	11.875	19.937	23.436	1.00	52.91
	2411	NH2	ARG	B	106	13.191	19.650	21.581	1.00	40.82
	2412	C	ARG	B	106	5.913	19.143	20.289	1.00	37.36
	2413	O	ARG	B	106	5.488	18.406	21.199	1.00	26.46
40	2414	N	CYS	B	107	6.304	18.660	19.113	1.00	28.15
	2415	CA	CYS	B	107	6.250	17.231	18.860	1.00	29.34
	2416	C	CYS	B	107	7.669	16.735	18.872	1.00	42.87
	2417	O	CYS	B	107	8.280	16.584	17.812	1.00	35.58
	2418	CB	CYS	B	107	5.617	16.945	17.502	1.00	38.81
45	2419	SG	CYS	B	107	5.072	15.220	17.305	1.00	55.53
	2420	N	HIS	B	108	8.173	16.481	20.081	1.00	42.37
	2421	CA	HIS	B	108	9.544	16.022	20.296	1.00	43.07
	2422	CB	HIS	B	108	9.947	16.267	21.751	1.00	59.40
	2423	CG	HIS	B	108	11.374	15.931	22.052	1.00	55.40
50	2424	CD2	HIS	B	108	11.925	15.232	23.068	1.00	55.98
	2425	ND1	HIS	B	108	12.421	16.349	21.259	1.00	54.99
	2426	CE1	HIS	B	108	13.558	15.919	21.776	1.00	62.39
	2427	NE2	HIS	B	108	13.286	15.239	22.874	1.00	62.88
	2428	C	HIS	B	108	9.739	14.563	19.946	1.00	36.76
55	2429	O	HIS	B	108	9.008	13.698	20.440	1.00	16.46
	2430	N	GLY	B	109	10.733	14.307	19.097	1.00	27.59
	2431	CA	GLY	B	109	11.001	12.953	18.656	1.00	39.81
	2432	C	GLY	B	109	12.066	12.233	19.446	1.00	36.02
	2433	O	GLY	B	109	13.025	12.841	19.903	1.00	45.53
60	2434	N	TRP	B	110	11.902	10.925	19.589	1.00	45.09
	2435	CA	TRP	B	110	12.842	10.094	20.328	1.00	42.50
	2436	CB	TRP	B	110	12.456	8.614	20.147	1.00	42.85
	2437	CG	TRP	B	110	13.388	7.739	20.893	1.00	47.55
	2438	CD2	TRP	B	110	13.360	7.449	22.295	1.00	54.18
65	2439	CE2	TRP	B	110	14.455	6.601	22.586	1.00	43.50
	2440	CE3	TRP	B	110	12.518	7.855	23.339	1.00	57.45
	2441	CD1	TRP	B	110	14.459	7.056	20.399	1.00	51.38
	2442	NE1	TRP	B	110	15.108	6.357	21.409	1.00	48.13
	2443	CZ2	TRP	B	110	14.729	6.151	23.872	1.00	33.15
70	2444	CZ3	TRP	B	110	12.793	7.403	24.629	1.00	55.46

	2445	CH2	TRP	B	110	13.894	6.557	24.877	1.00	49.35
	2446	C	TRP	B	110	14.276	10.354	19.886	1.00	45.65
	2447	O	TRP	B	110	14.544	10.511	18.680	1.00	34.73
	2448	N	ARG	B	111	15.182	10.388	20.866	1.00	55.00
5	2449	CA	ARG	B	111	16.604	10.644	20.631	1.00	60.99
	2450	CB	ARG	B	111	17.254	9.438	19.949	1.00	56.42
	2451	CG	ARG	B	111	17.586	8.319	20.926	1.00	78.50
	2452	CD	ARG	B	111	18.140	7.100	20.224	1.00	104.44
	2453	NE	ARG	B	111	18.757	6.157	21.154	1.00	117.08
10	2454	CZ	ARG	B	111	19.996	6.272	21.628	1.00	124.78
	2455	NH1	ARG	B	111	20.766	7.291	21.261	1.00	125.05
	2456	NH2	ARG	B	111	20.463	5.363	22.473	1.00	126.10
	2457	C	ARG	B	111	16.813	11.896	19.790	1.00	67.62
	2458	O	ARG	B	111	17.751	11.974	19.000	1.00	74.03
15	2459	N	ASN	B	112	15.934	12.876	19.978	1.00	69.44
	2460	CA	ASN	B	112	16.039	14.116	19.228	1.00	76.51
	2461	CB	ASN	B	112	17.207	14.964	19.725	1.00	84.90
	2462	CG	ASN	B	112	17.150	16.373	19.160	1.00	106.45
	2463	OD1	ASN	B	112	16.253	16.734	18.385	1.00	105.76
20	2464	ND2	ASN	B	112	18.134	17.183	19.546	1.00	117.72
	2465	C	ASN	B	112	16.155	13.785	17.751	1.00	79.76
	2466	O	ASN	B	112	16.695	14.568	16.973	1.00	88.06
	2467	N	TRP	B	113	15.686	12.614	17.372	1.00	76.72
	2468	CA	TRP	B	113	15.721	12.245	15.953	1.00	59.95
25	2469	CB	TRP	B	113	15.222	10.811	15.765	1.00	54.79
	2470	CG	TRP	B	113	16.236	9.821	16.180	1.00	40.29
	2471	CD2	TRP	B	113	16.046	8.442	16.523	1.00	18.18
	2472	CE2	TRP	B	113	17.312	7.914	16.846	1.00	22.19
	2473	CE3	TRP	B	113	14.930	7.603	16.587	1.00	12.77
30	2474	CD1	TRP	B	113	17.574	10.060	16.308	1.00	42.86
	2475	NE1	TRP	B	113	18.226	8.922	16.707	1.00	25.08
	2476	CZ2	TRP	B	113	17.493	6.587	17.228	1.00	22.94
	2477	CZ3	TRP	B	113	15.111	6.286	16.966	1.00	28.48
	2478	CH2	TRP	B	113	16.383	5.790	17.281	1.00	24.73
35	2479	C	TRP	B	113	14.836	13.224	15.194	1.00	65.32
	2480	O	TRP	B	113	13.836	13.822	15.777	1.00	68.76
	2481	N	ASP	B	114	15.057	13.403	13.912	1.00	50.94
	2482	CA	ASP	B	114	14.164	14.252	13.145	1.00	52.09
	2483	CB	ASP	B	114	14.767	14.536	11.768	1.00	52.20
40	2484	CG	ASP	B	114	16.039	15.346	11.830	1.00	66.27
	2485	OD1	ASP	B	114	16.065	16.368	12.546	1.00	80.90
	2486	OD2	ASP	B	114	17.011	14.967	11.147	1.00	65.81
	2487	C	ASP	B	114	12.798	13.615	13.004	1.00	54.32
	2488	O	ASP	B	114	12.676	12.397	13.005	1.00	49.44
45	2489	N	VAL	B	115	11.762	14.429	12.886	1.00	59.65
	2490	CA	VAL	B	115	10.408	13.936	12.713	1.00	44.63
	2491	CB	VAL	B	115	9.542	14.291	13.899	1.00	43.22
	2492	CG1	VAL	B	115	8.162	13.697	13.715	1.00	33.45
	2493	CG2	VAL	B	115	10.192	13.802	15.156	1.00	33.33
50	2494	C	VAL	B	115	9.876	14.672	11.497	1.00	60.55
	2495	O	VAL	B	115	10.254	15.827	11.261	1.00	71.83
	2496	N	TYR	B	116	9.023	14.021	10.715	1.00	48.40
	2497	CA	TYR	B	116	8.490	14.684	9.543	1.00	29.55
	2498	CB	TYR	B	116	9.214	14.204	8.299	1.00	25.24
55	2499	CG	TYR	B	116	10.708	14.436	8.299	1.00	28.14
	2500	CD1	TYR	B	116	11.582	13.475	8.783	1.00	40.15
	2501	CE1	TYR	B	116	12.956	13.645	8.691	1.00	52.64
	2502	CD2	TYR	B	116	11.250	15.590	7.745	1.00	41.11
	2503	CE2	TYR	B	116	12.635	15.770	7.651	1.00	48.69
60	2504	CZ	TYR	B	116	13.478	14.797	8.127	1.00	44.88
	2505	OH	TYR	B	116	14.841	14.957	8.017	1.00	54.67
	2506	C	TYR	B	116	6.991	14.501	9.377	1.00	27.78
	2507	O	TYR	B	116	6.383	13.681	10.051	1.00	28.35
	2508	N	LYS	B	117	6.409	15.265	8.460	1.00	38.88
65	2509	CA	LYS	B	117	4.976	15.213	8.227	1.00	37.83
	2510	CB	LYS	B	117	4.567	13.922	7.508	1.00	47.24
	2511	CG	LYS	B	117	4.732	13.956	5.998	1.00	69.83
	2512	CD	LYS	B	117	4.053	12.743	5.350	1.00	93.57
	2513	CE	LYS	B	117	2.549	12.716	5.644	1.00	101.93
70	2514	NZ	LYS	B	117	1.865	11.498	5.113	1.00	91.83

	2515	C	LYS	B	117	4.347	15.264	9.603	1.00	25.37
	2516	O	LYS	B	117	3.695	14.319	10.041	1.00	28.98
	2517	N	VAL	B	118	4.568	16.374	10.296	1.00	23.24
	2518	CA	VAL	B	118	4.014	16.513	11.629	1.00	23.69
5	2519	CB	VAL	B	118	4.919	17.367	12.545	1.00	38.59
	2520	CG1	VAL	B	118	4.205	17.627	13.868	1.00	45.19
	2521	CG2	VAL	B	118	6.254	16.648	12.795	1.00	18.15
	2522	C	VAL	B	118	2.650	17.152	11.593	1.00	18.84
	2523	O	VAL	B	118	2.462	18.227	11.006	1.00	8.55
10	2524	N	ILE	B	119	1.700	16.503	12.250	1.00	12.98
	2525	CA	ILE	B	119	0.355	17.026	12.293	1.00	30.22
	2526	CB	ILE	B	119	-0.627	16.130	11.498	1.00	46.31
	2527	CG2	ILE	B	119	-2.064	16.621	11.688	1.00	42.76
	2528	CG1	ILE	B	119	-0.236	16.112	10.019	1.00	21.93
15	2529	CD1	ILE	B	119	-1.236	15.436	9.133	1.00	51.60
	2530	C	ILE	B	119	-0.076	17.038	13.734	1.00	38.62
	2531	O	ILE	B	119	0.261	16.123	14.483	1.00	47.55
	2532	N	TYR	B	120	-0.818	18.068	14.125	1.00	32.69
	2533	CA	TYR	B	120	-1.312	18.148	15.489	1.00	32.47
20	2534	CB	TYR	B	120	-0.950	19.474	16.123	1.00	16.42
	2535	CG	TYR	B	120	0.503	19.596	16.455	1.00	25.56
	2536	CD1	TYR	B	120	1.419	20.056	15.515	1.00	35.91
	2537	CE1	TYR	B	120	2.771	20.205	15.844	1.00	51.47
	2538	CD2	TYR	B	120	0.966	19.275	17.728	1.00	32.05
25	2539	CE2	TYR	B	120	2.311	19.412	18.070	1.00	29.56
	2540	CZ	TYR	B	120	3.209	19.883	17.123	1.00	44.13
	2541	OH	TYR	B	120	4.537	20.063	17.438	1.00	29.40
	2542	C	TYR	B	120	-2.806	18.001	15.490	1.00	33.00
	2543	O	TYR	B	120	-3.484	18.535	14.625	1.00	54.53
30	2544	N	TYR	B	121	-3.322	17.277	16.467	1.00	31.54
	2545	CA	TYR	B	121	-4.744	17.066	16.544	1.00	38.10
	2546	CB	TYR	B	121	-5.068	15.570	16.402	1.00	34.72
	2547	CG	TYR	B	121	-4.635	14.953	15.087	1.00	45.90
	2548	CD1	TYR	B	121	-3.293	14.656	14.855	1.00	43.35
35	2549	CE1	TYR	B	121	-2.878	14.083	13.654	1.00	44.63
	2550	CD2	TYR	B	121	-5.570	14.659	14.076	1.00	45.04
	2551	CE2	TYR	B	121	-5.169	14.078	12.874	1.00	37.76
	2552	CZ	TYR	B	121	-3.822	13.796	12.675	1.00	47.75
	2553	OH	TYR	B	121	-3.411	13.225	11.502	1.00	43.41
40	2554	C	TYR	B	121	-5.272	17.579	17.864	1.00	51.86
	2555	O	TYR	B	121	-4.735	17.246	18.927	1.00	65.44
	2556	N	LYS	B	122	-6.314	18.403	17.794	1.00	51.19
	2557	CA	LYS	B	122	-6.957	18.914	18.992	1.00	60.52
	2558	CB	LYS	B	122	-7.037	20.435	18.969	1.00	58.03
45	2559	CG	LYS	B	122	-7.268	21.024	20.357	1.00	76.69
	2560	CD	LYS	B	122	-7.727	22.472	20.312	1.00	76.94
	2561	CE	LYS	B	122	-9.203	22.561	19.973	1.00	78.85
	2562	NZ	LYS	B	122	-9.694	23.961	20.057	1.00	78.17
	2563	C	LYS	B	122	-8.368	18.331	19.016	1.00	69.22
50	2564	O	LYS	B	122	-9.259	18.817	18.314	1.00	71.75
	2565	N	ASP	B	123	-8.554	17.283	19.814	1.00	75.25
	2566	CA	ASP	B	123	-9.840	16.611	19.936	1.00	81.83
	2567	CB	ASP	B	123	-10.952	17.623	20.242	1.00	85.33
	2568	CG	ASP	B	123	-10.809	18.253	21.618	1.00	86.97
55	2569	OD1	ASP	B	123	-10.750	17.499	22.613	1.00	97.59
	2570	OD2	ASP	B	123	-10.764	19.501	21.703	1.00	80.57
	2571	C	ASP	B	:23	-10.172	15.841	18.660	1.00	85.87
	2572	O	ASP	B	123	-11.183	16.107	18.002	1.00	90.87
	2573	N	GLY	B	124	-9.310	14.889	18.314	1.00	83.44
60	2574	CA	GLY	B	124	-9.538	14.080	17.131	1.00	83.47
	2575	C	GLY	B	124	-9.383	14.835	15.826	1.00	82.06
	2576	O	GLY	B	124	-9.053	14.236	14.804	1.00	80.62
	2577	N	GLU	B	125	-9.615	16.144	15.847	1.00	76.60
	2578	CA	GLU	B	125	-9.479	16.951	14.640	1.00	69.95
65	2579	CB	GLU	B	125	-10.431	18.146	14.697	1.00	83.15
	2580	CG	GLU	B	125	-11.903	17.778	14.854	1.00	99.12
	2581	CD	GLU	B	125	-12.808	19.009	14.961	1.00	110.18
	2582	OE1	GLU	B	125	-12.287	20.153	14.909	1.00	115.12
	2583	OE2	GLU	B	125	-14.041	18.828	15.099	1.00	112.68
70	2584	C	GLU	B	125	-8.043	17.452	14.501	1.00	59.20

	2585	O	GLU	B	125	-7.370	17.681	15.493	1.00	68.90
	2586	N	ALA	B	126	-7.574	17.609	13.269	1.00	55.84
	2587	CA	ALA	B	126	-6.221	18.112	13.032	1.00	49.26
5	2588	CB	ALA	B	126	-5.783	17.788	11.636	1.00	37.55
	2589	C	ALA	B	126	-6.229	19.623	13.229	1.00	55.35
	2590	O	ALA	B	126	-7.288	20.251	13.192	1.00	62.37
	2591	N	LEU	B	127	-5.053	20.211	13.425	1.00	58.36
	2592	CA	LEU	B	127	-4.968	21.648	13.652	1.00	56.69
10	2593	CB	LEU	B	127	-4.821	21.938	15.148	1.00	64.48
	2594	CG	LEU	B	127	-4.606	23.411	15.496	1.00	71.37
	2595	CD1	LEU	B	127	-5.705	24.262	14.864	1.00	76.49
	2596	CD2	LEU	B	127	-4.590	23.573	17.012	1.00	74.87
	2597	C	LEU	B	127	-3.837	22.314	12.895	1.00	59.25
15	2598	O	LEU	B	127	-3.979	23.463	12.449	1.00	65.52
	2599	N	LYS	B	128	-2.710	21.619	12.760	1.00	39.64
	2600	CA	LYS	B	128	-1.583	22.176	12.022	1.00	49.21
	2601	CB	LYS	B	128	-0.695	23.067	12.911	1.00	55.50
	2602	CG	LYS	B	128	-1.370	24.362	13.365	1.00	77.67
20	2603	CD	LYS	B	128	-0.363	25.479	13.615	1.00	85.20
	2604	CE	LYS	B	128	-1.085	26.778	13.981	1.00	95.26
	2605	NZ	LYS	B	128	-0.159	27.945	14.093	1.00	94.69
	2606	C	LYS	B	128	-0.743	21.091	11.397	1.00	47.41
	2607	O	LYS	B	128	-0.639	19.967	11.917	1.00	56.27
25	2608	N	TYR	B	129	-0.181	21.412	10.277	1.00	25.40
	2609	CA	TYR	B	129	0.682	20.491	9.551	1.00	31.17
	2610	CB	TYR	B	129	-0.094	19.800	8.429	1.00	9.94
	2611	CG	TYR	B	129	0.773	18.963	7.516	1.00	7.68
	2612	CD1	TYR	B	129	0.995	17.618	7.780	1.00	13.54
	2613	CE1	TYR	B	129	1.788	16.850	6.948	1.00	15.62
30	2614	CD2	TYR	B	129	1.370	19.519	6.393	1.00	9.74
	2615	CE2	TYR	B	129	2.164	18.759	5.558	1.00	6.56
	2616	CZ	TYR	B	129	2.369	17.425	5.839	1.00	23.46
	2617	OH	TYR	B	129	3.160	16.667	5.007	1.00	29.69
	2618	C	TYR	B	129	1.905	21.203	8.987	1.00	18.84
35	2619	O	TYR	B	129	1.810	22.418	8.723	1.00	20.48
	2620	N	TRP	B	130	2.983	20.508	8.856	1.00	10.01
	2621	CA	TRP	B	130	4.195	21.121	8.376	1.00	26.80
	2622	CB	TRP	B	130	4.621	22.248	9.331	1.00	24.97
	2623	CG	TRP	B	130	5.657	23.141	8.763	1.00	34.86
40	2624	CD2	TRP	B	130	5.463	24.474	8.258	1.00	19.75
	2625	CE2	TRP	B	130	6.718	24.833	7.789	1.00	18.96
	2626	CE3	TRP	B	130	4.338	25.321	8.160	1.00	4.59
	2627	CD1	TRP	B	130	6.995	22.854	8.577	1.00	46.79
	2628	NE1	TRP	B	130	7.637	23.935	7.990	1.00	33.27
45	2629	CZ2	TRP	B	130	6.887	26.195	7.230	1.00	7.20
	2630	CZ3	TRP	B	130	4.513	26.582	7.599	1.00	26.73
	2631	CH2	TRP	B	130	5.778	27.003	7.141	1.00	33.91
	2632	C	TRP	B	130	5.204	19.990	8.359	1.00	28.67
	2633	O	TRP	B	130	5.511	19.385	9.388	1.00	37.85
50	2634	N	TYR	B	131	5.686	19.697	7.164	1.00	25.88
	2635	CA	TYR	B	131	6.639	18.631	6.919	1.00	25.53
	2636	CB	TYR	B	131	7.327	18.864	5.599	1.00	12.69
	2637	CG	TYR	B	131	8.003	17.638	5.076	1.00	27.25
	2638	CD1	TYR	B	131	7.258	16.534	4.672	1.00	27.89
55	2639	CE1	TYR	B	131	7.893	15.406	4.143	1.00	37.49
	2640	CD2	TYR	B	131	9.385	17.589	4.949	1.00	47.62
	2641	CE2	TYR	B	131	10.030	16.477	4.424	1.00	47.79
	2642	CZ	TYR	B	131	9.287	15.394	4.023	1.00	46.72
	2643	OH	TYR	B	131	9.948	14.315	3.487	1.00	44.87
60	2644	C	TYR	B	131	7.699	18.490	7.988	1.00	41.53
	2645	O	TYR	B	131	7.730	17.491	8.714	1.00	45.44
	2646	N	GLU	B	132	8.584	19.481	8.058	1.00	41.35
	2647	CA	GLU	B	132	9.651	19.477	9.045	1.00	23.47
	2648	CB	GLU	B	132	10.631	20.595	8.746	1.00	26.69
65	2649	CG	GLU	B	132	11.512	20.343	7.517	1.00	30.91
	2650	CD	GLU	B	132	12.674	19.419	7.819	1.00	59.01
	2651	OE1	GLU	B	132	12.695	18.835	8.933	1.00	78.14
	2652	OE2	GLU	B	132	13.555	19.276	6.939	1.00	45.30
	2653	C	GLU	B	132	9.017	19.678	10.410	1.00	30.80
70	2654	O	GLU	B	132	7.926	20.252	10.503	1.00	15.18

	2655	N	ASN	B	133	9.673	19.198	11.466	1.00	38.68
	2656	CA	ASN	B	133	9.078	19.340	12.785	1.00	35.69
	2657	CB	ASN	B	133	9.969	18.765	13.884	1.00	24.76
	2658	CG	ASN	B	133	9.165	18.350	15.126	1.00	52.21
5	2659	OD1	ASN	B	133	8.183	19.018	15.524	1.00	35.03
	2660	ND2	ASN	B	133	9.582	17.243	15.745	1.00	43.95
	2661	C	ASN	B	133	8.857	20.813	13.030	1.00	29.20
	2662	O	ASN	B	133	9.651	21.644	12.587	1.00	43.35
	2663	N	HIS	B	134	7.770	21.132	13.718	1.00	15.66
10	2664	CA	HIS	B	134	7.435	22.506	14.022	1.00	21.19
	2665	CB	HIS	B	134	6.522	23.054	12.927	1.00	41.57
	2666	CG	HIS	B	134	5.268	22.256	12.734	1.00	45.84
	2667	CD2	HIS	B	134	3.972	22.543	12.990	1.00	30.22
	2668	ND1	HIS	B	134	5.280	20.969	12.228	1.00	29.02
15	2669	CE1	HIS	B	134	4.037	20.507	12.183	1.00	45.78
	2670	NE2	HIS	B	134	3.230	21.443	12.640	1.00	39.55
	2671	C	HIS	B	134	6.733	22.587	15.380	1.00	30.10
	2672	O	HIS	B	134	6.072	21.631	15.826	1.00	22.57
	2673	N	ASN	B	135	6.871	23.731	16.043	1.00	35.59
20	2674	CA	ASN	B	135	6.263	23.933	17.355	1.00	43.05
	2675	CB	ASN	B	135	7.182	24.741	18.303	1.00	49.56
	2676	CG	ASN	B	135	8.585	24.138	18.481	1.00	62.83
	2677	OD1	ASN	B	135	8.717	22.936	18.749	1.00	59.97
	2678	ND2	ASN	B	135	9.614	24.991	18.356	1.00	50.35
25	2679	C	ASN	B	135	5.006	24.761	17.162	1.00	31.65
	2680	O	ASN	B	135	5.024	25.700	16.384	1.00	53.46
	2681	N	ILE	B	136	3.910	24.406	17.820	1.00	39.40
	2682	CA	ILE	B	136	2.720	25.244	17.749	1.00	46.75
	2683	CB	ILE	B	136	1.440	24.484	18.081	1.00	51.16
30	2684	CG2	ILE	B	136	0.254	25.448	18.105	1.00	27.02
	2685	CG1	ILE	B	136	1.232	23.368	17.065	1.00	48.68
	2686	CD1	ILE	B	136	-0.057	22.599	17.259	1.00	57.62
	2687	C	ILE	B	136	2.922	26.304	18.834	1.00	57.38
	2688	O	ILE	B	136	2.996	25.995	20.026	1.00	38.50
35	2689	N	SER	B	137	3.035	27.554	18.409	1.00	62.66
	2690	CA	SER	B	137	3.238	28.653	19.333	1.00	62.59
	2691	CB	SER	B	137	4.495	29.443	18.941	1.00	62.06
	2692	OG	SER	B	137	4.789	30.448	19.899	1.00	70.77
	2693	C	SER	B	137	2.015	29.557	19.314	1.00	54.31
40	2694	O	SER	B	137	1.675	30.140	18.295	1.00	61.87
	2695	N	ILE	B	138	1.344	29.665	20.450	1.00	57.19
	2696	CA	ILE	B	138	0.167	30.511	20.551	1.00	64.51
	2697	CB	ILE	B	138	-1.060	29.702	20.970	1.00	66.59
	2698	CG2	ILE	B	138	-2.289	30.588	20.965	1.00	62.45
45	2699	CG1	ILE	B	138	-1.244	28.528	20.011	1.00	72.23
	2700	CD1	ILE	B	138	-2.439	27.657	20.338	1.00	72.19
	2701	C	ILE	B	138	0.409	31.600	21.581	1.00	70.00
	2702	O	ILE	B	138	0.207	31.396	22.777	1.00	80.22
	2703	N	THR	B	139	0.846	32.760	21.100	1.00	75.14
50	2704	CA	THR	B	139	1.143	33.914	21.951	1.00	76.04
	2705	CB	THR	B	139	1.419	35.149	21.086	1.00	66.84
	2706	OG1	THR	B	139	0.347	35.322	20.153	1.00	70.10
	2707	CG2	THR	B	139	2.720	34.969	20.312	1.00	62.07
	2708	C	THR	B	139	0.064	34.246	22.993	1.00	77.29
55	2709	O	THR	B	139	0.333	34.206	24.190	1.00	88.78
	2710	N	ASN	B	140	-1.142	34.598	22.553	1.00	78.71
	2711	CA	ASN	B	140	-2.244	34.893	23.485	1.00	86.24
	2712	CB	ASN	B	140	-2.994	36.169	23.082	1.00	96.34
	2713	CG	ASN	B	140	-2.195	37.465	23.304	1.00	113.86
60	2714	OD1	ASN	B	140	-2.591	38.486	22.747	1.00	123.78
	2715	ND2	ASN	B	140	-1.120	37.473	24.100	1.00	121.56
	2716	C	ASN	B	140	-3.245	33.716	23.456	1.00	84.41
	2717	O	ASN	B	140	-3.962	33.521	22.474	1.00	92.35
	2718	N	ALA	B	141	-3.298	32.944	24.536	1.00	74.85
65	2719	CA	ALA	B	141	-4.186	31.781	24.642	1.00	70.00
	2720	CB	ALA	B	141	-3.768	30.931	25.819	1.00	60.72
	2721	C	ALA	B	141	-5.679	32.080	24.744	1.00	73.54
	2722	O	ALA	B	141	-6.083	33.215	25.000	1.00	71.12
	2723	N	THR	B	142	-6.486	31.033	24.557	1.00	79.19
70	2724	CA	THR	B	142	-7.945	31.135	24.602	1.00	81.65

	2725	CB	THR	B	142	-8.550	31.294	23.191	1.00	87.55
	2726	OG1	THR	B	142	-7.856	32.324	22.475	1.00	87.31
	2727	CG2	THR	B	142	-10.032	31.647	23.292	1.00	80.50
5	2728	C	THR	B	142	-8.556	29.872	25.196	1.00	81.42
	2729	O	THR	B	142	-8.001	28.782	25.063	1.00	80.47
	2730	N	VAL	B	143	-9.716	30.022	25.828	1.00	79.19
	2731	CA	VAL	B	143	-10.385	28.881	26.430	1.00	80.64
	2732	CB	VAL	B	143	-11.681	29.314	27.154	1.00	85.23
	2733	CG1	VAL	B	143	-12.667	29.899	26.146	1.00	91.61
10	2734	CG2	VAL	B	143	-12.293	28.123	27.880	1.00	91.42
	2735	C	VAL	B	143	-10.728	27.848	25.370	1.00	78.44
	2736	O	VAL	B	143	-10.878	26.659	25.659	1.00	67.92
	2737	N	GLU	B	144	-10.847	28.317	24.132	1.00	87.88
	2738	CA	GLU	B	144	-11.173	27.438	23.019	1.00	94.42
15	2739	CB	GLU	B	144	-11.546	28.261	21.775	1.00	103.89
	2740	CG	GLU	B	144	-12.116	27.439	20.605	1.00	127.47
	2741	CD	GLU	B	144	-13.460	26.781	20.925	1.00	145.47
	2742	OE1	GLU	B	144	-14.018	27.052	22.011	1.00	154.66
	2743	OE2	GLU	B	144	-13.960	25.995	20.087	1.00	153.18
20	2744	C	GLU	B	144	-9.977	26.546	22.721	1.00	87.49
	2745	O	GLU	B	144	-10.137	25.385	22.328	1.00	92.98
	2746	N	ASP	B	145	-8.777	27.086	22.919	1.00	73.99
	2747	CA	ASP	B	145	-7.557	26.336	22.674	1.00	73.40
	2748	CB	ASP	B	145	-6.348	27.253	22.815	1.00	76.84
25	2749	CG	ASP	B	145	-6.159	28.159	21.614	1.00	84.39
	2750	OD1	ASP	B	145	-6.061	27.632	20.481	1.00	89.54
	2751	OD2	ASP	B	145	-6.101	29.394	21.801	1.00	78.78
	2752	C	ASP	B	145	-7.434	25.135	23.618	1.00	72.65
	2753	O	ASP	B	145	-6.468	24.371	23.546	1.00	66.12
30	2754	N	SER	B	146	-8.423	24.971	24.496	1.00	68.40
	2755	CA	SER	B	146	-8.445	23.857	25.441	1.00	59.96
	2756	CB	SER	B	146	-9.433	24.128	26.579	1.00	59.40
	2757	OG	SER	B	146	-8.959	25.158	27.435	1.00	82.76
	2758	C	SER	B	146	-8.862	22.590	24.725	1.00	55.02
35	2759	O	SER	B	146	-9.531	22.649	23.703	1.00	74.05
	2760	N	GLY	B	147	-8.462	21.447	25.267	1.00	55.86
	2761	CA	GLY	B	147	-8.811	20.174	24.662	1.00	55.22
	2762	C	GLY	B	147	-7.680	19.168	24.739	1.00	55.94
	2763	O	GLY	B	147	-6.624	19.453	25.308	1.00	65.07
40	2764	N	THR	B	148	-7.895	17.984	24.173	1.00	51.77
	2765	CA	THR	B	148	-6.871	16.945	24.186	1.00	56.97
	2766	CB	THR	B	148	-7.493	15.537	24.299	1.00	62.53
	2767	OG1	THR	B	148	-7.822	15.054	22.992	1.00	93.22
	2768	CG2	THR	B	148	-8.769	15.581	25.130	1.00	61.98
45	2769	C	THR	B	148	-6.061	17.028	22.895	1.00	50.21
	2770	O	THR	B	148	-6.605	16.990	21.803	1.00	61.31
	2771	N	TYR	B	149	-4.752	17.167	23.026	1.00	47.96
	2772	CA	TYR	B	149	-3.873	17.263	21.870	1.00	36.15
	2773	CB	TYR	B	149	-2.907	18.438	22.008	1.00	39.15
50	2774	CG	TYR	B	149	-3.504	19.814	21.873	1.00	32.57
	2775	CD1	TYR	B	149	-4.170	20.418	22.932	1.00	43.98
	2776	CE1	TYR	B	149	-4.695	21.704	22.815	1.00	43.58
	2777	CD2	TYR	B	149	-3.382	20.525	20.687	1.00	33.74
	2778	CE2	TYR	B	149	-3.909	21.810	20.553	1.00	35.76
55	2779	CZ	TYR	B	149	-4.564	22.396	21.621	1.00	41.82
	2780	OH	TYR	B	149	-5.089	23.668	21.494	1.00	40.18
	2781	C	TYR	B	149	-3.028	16.013	21.730	1.00	38.28
	2782	O	TYR	B	149	-2.944	15.191	22.651	1.00	37.42
	2783	N	TYR	B	150	-2.386	15.893	20.573	1.00	28.35
60	2784	CA	TYR	B	150	-1.500	14.776	20.287	1.00	32.70
	2785	CB	TYR	B	150	-2.226	13.421	20.440	1.00	46.79
	2786	CG	TYR	B	150	-3.180	13.018	19.328	1.00	40.91
	2787	CD1	TYR	B	150	-2.710	12.397	18.168	1.00	38.70
	2788	CE1	TYR	B	150	-3.588	12.007	17.150	1.00	49.78
65	2789	CD2	TYR	B	150	-4.556	13.245	19.447	1.00	29.49
	2790	CE2	TYR	B	150	-5.440	12.862	18.436	1.00	54.83
	2791	CZ	TYR	B	150	-4.950	12.245	17.294	1.00	51.46
	2792	OH	TYR	B	150	-5.828	11.857	16.310	1.00	68.38
	2793	C	TYR	B	150	-1.002	14.971	18.880	1.00	30.40
70	2794	O	TYR	B	150	-1.718	15.477	18.028	1.00	49.73

2795	N	CYS B	151	0.241	14.596	18.645	1.00	25.26
2796	CA	CYS B	151	0.808	14.746	17.326	1.00	39.72
2797	C	CYS B	151	1.175	13.410	16.699	1.00	37.05
2798	O	CYS B	151	1.270	12.395	17.383	1.00	49.88
2799	CB	CYS B	151	2.040	15.652	17.399	1.00	44.87
2800	SG	CYS B	151	3.415	15.099	18.482	1.00	47.69
2801	N	THR B	152	1.380	13.419	15.387	1.00	34.36
2802	CA	THR B	152	1.753	12.217	14.648	1.00	40.90
2803	CB	THR B	152	0.641	11.715	13.712	1.00	46.04
2804	OG1	THR B	152	0.435	12.666	12.656	1.00	59.44
2805	CG2	THR B	152	-0.652	11.514	14.487	1.00	54.68
2806	C	THR B	152	2.906	12.646	13.784	1.00	39.86
2807	O	THR B	152	3.063	13.845	13.500	1.00	42.60
2808	N	GLY B	153	3.707	11.680	13.155	1.00	28.17
2809	CA	GLY B	153	4.846	12.024	12.340	1.00	26.12
2810	C	GLY B	153	5.647	10.818	12.112	1.00	33.14
2811	O	GLY B	153	5.622	9.753	12.734	1.00	34.08
2812	N	LYS B	154	6.365	10.998	11.021	1.00	17.31
2813	CA	LYS B	154	7.188	9.959	10.471	1.00	31.41
2814	CB	LYS B	154	7.185	10.086	8.949	1.00	56.81
2815	CG	LYS B	154	8.472	9.671	8.248	1.00	78.50
2816	CD	LYS B	154	8.399	10.064	6.771	1.00	85.12
2817	CE	LYS B	154	9.733	9.881	6.064	1.00	88.41
2818	NZ	LYS B	154	9.649	10.343	4.653	1.00	64.75
2819	C	LYS B	154	8.597	10.101	11.028	1.00	44.08
2820	O	LYS B	154	9.266	11.116	10.811	1.00	51.89
2821	N	VAL B	155	9.027	9.078	11.762	1.00	46.05
2822	CA	VAL B	155	10.362	9.047	12.345	1.00	43.86
2823	CB	VAL B	155	10.321	8.903	13.878	1.00	37.35
2824	CG1	VAL B	155	11.732	8.926	14.416	1.00	21.63
2825	CG2	VAL B	155	9.487	10.030	14.499	1.00	48.98
2826	C	VAL B	155	11.035	7.823	11.779	1.00	41.23
2827	O	VAL B	155	10.560	6.716	11.989	1.00	37.63
2828	N	TRP B	156	12.129	8.012	11.057	1.00	52.20
2829	CA	TRP B	156	12.824	6.880	10.454	1.00	74.29
2830	CB	TRP B	156	13.196	5.838	11.510	1.00	65.13
2831	CG	TRP B	156	14.467	6.147	12.211	1.00	70.49
2832	CD2	TRP B	156	15.771	6.221	11.629	1.00	54.80
2833	CE2	TRP B	156	16.670	6.585	12.646	1.00	64.98
2834	CE3	TRP B	156	16.252	6.012	10.334	1.00	50.71
2835	CD1	TRP B	156	14.631	6.458	13.539	1.00	71.39
2836	NE1	TRP B	156	15.954	6.725	13.804	1.00	63.30
2837	CZ2	TRP B	156	18.051	6.752	12.415	1.00	62.21
2838	CZ3	TRP B	156	17.624	6.179	10.101	1.00	67.16
2839	CH2	TRP B	156	18.500	6.545	11.141	1.00	53.68
2840	C	TRP B	156	12.015	6.201	9.347	1.00	90.81
2841	O	TRP B	156	11.962	4.971	9.263	1.00	111.59
2842	N	GLN B	157	11.389	7.013	8.506	1.00	88.48
2843	CA	GLN B	157	10.608	6.526	7.382	1.00	85.04
2844	CB	GLN B	157	11.461	5.575	6.536	1.00	110.53
2845	CG	GLN B	157	10.830	5.324	5.138	1.00	124.62
2846	CD	GLN B	157	11.824	4.383	4.337	1.00	129.56
2847	OE1	GLN B	157	12.951	4.080	4.749	1.00	127.90
2848	NE2	GLN B	157	11.329	3.926	3.183	1.00	123.80
2849	C	GLN B	157	9.311	5.842	7.816	1.00	78.48
2850	O	GLN B	157	8.544	5.392	6.977	1.00	77.35
2851	N	LEU B	158	9.074	5.760	9.122	1.00	70.67
2852	CA	LEU B	158	7.849	5.147	9.635	1.00	70.41
2853	CB	LEU B	158	8.170	4.049	10.637	1.00	81.95
2854	CG	LEU B	158	8.646	2.722	10.055	1.00	86.23
2855	CD1	LEU B	158	8.865	1.715	11.174	1.00	105.28
2856	CD2	LEU B	158	7.602	2.204	9.081	1.00	94.27
2857	C	LEU B	158	6.998	6.203	10.313	1.00	70.44
2858	O	LEU B	158	7.499	7.275	10.632	1.00	80.05
2859	N	ASP B	159	5.721	5.904	10.537	1.00	67.41
2860	CA	ASP B	159	4.837	6.880	11.171	1.00	82.00
2861	CB	ASP B	159	3.519	7.001	10.392	1.00	86.28
2862	CG	ASP B	159	3.736	7.375	8.938	1.00	106.10
2863	OD1	ASP B	159	4.285	8.469	8.664	1.00	117.95
2864	OD2	ASP B	159	3.361	6.564	8.067	1.00	115.39

2865	C	ASP	B	159	4.547	6.495	12.611	1.00	77.19
2866	O	ASP	B	159	4.590	5.316	12.962	1.00	77.19
2867	N	TYR	B	160	4.274	7.492	13.448	1.00	65.57
2868	CA	TYR	B	160	3.972	7.232	14.842	1.00	48.77
2869	CB	TYR	B	160	5.244	7.273	15.670	1.00	37.12
2870	CG	TYR	B	160	6.332	6.371	15.148	1.00	34.46
2871	CD1	TYR	B	160	7.199	6.797	14.134	1.00	37.79
2872	CE1	TYR	B	160	8.195	5.961	13.645	1.00	56.87
2873	CD2	TYR	B	160	6.490	5.086	15.661	1.00	19.69
2874	CE2	TYR	B	160	7.486	4.233	15.179	1.00	40.99
2875	CZ	TYR	B	160	8.341	4.674	14.172	1.00	60.40
2876	OH	TYR	B	160	9.343	3.841	13.702	1.00	70.89
2877	C	TYR	B	160	3.000	8.266	15.364	1.00	54.13
2878	O	TYR	B	160	2.718	9.265	14.687	1.00	60.44
2879	N	GLU	B	161	2.496	8.022	16.569	1.00	47.74
2880	CA	GLU	B	161	1.546	8.926	17.193	1.00	48.57
2881	CB	GLU	B	161	0.133	8.387	16.988	1.00	55.17
2882	CG	GLU	B	161	-0.965	9.106	17.748	1.00	80.84
2883	CD	GLU	B	161	-2.360	8.757	17.226	1.00	93.70
2884	OE1	GLU	B	161	-3.352	9.054	17.932	1.00	99.33
2885	OE2	GLU	B	161	-2.465	8.198	16.106	1.00	101.86
2886	C	GLU	B	161	1.872	9.038	18.671	1.00	56.41
2887	O	GLU	B	161	2.080	8.028	19.340	1.00	58.09
2888	N	SER	B	162	1.928	10.268	19.173	1.00	61.15
2889	CA	SER	B	162	2.240	10.515	20.578	1.00	70.01
2890	CB	SER	B	162	2.700	11.965	20.771	1.00	82.47
2891	OG	SER	B	162	1.646	12.889	20.523	1.00	75.43
2892	C	SER	B	162	1.046	10.258	21.481	1.00	69.94
2893	O	SER	B	162	-0.083	10.163	21.017	1.00	70.40
2894	N	GLU	B	163	1.301	10.133	22.776	1.00	76.24
2895	CA	GLU	B	163	0.223	9.924	23.728	1.00	74.01
2896	CB	GLU	B	163	0.785	9.585	25.106	1.00	83.42
2897	CG	GLU	B	163	1.437	8.222	25.201	1.00	108.95
2898	CD	GLU	B	163	0.421	7.096	25.165	1.00	124.63
2899	OE1	GLU	B	163	-0.463	7.070	26.051	1.00	126.10
2900	OE2	GLU	B	163	0.507	6.239	24.255	1.00	137.68
2901	C	GLU	B	163	-0.517	11.246	23.809	1.00	64.66
2902	O	GLU	B	163	0.096	12.303	23.836	1.00	78.89
2903	N	PRO	B	164	-1.848	11.211	23.829	1.00	49.91
2904	CD	PRO	B	164	-2.763	10.066	23.886	1.00	45.53
2905	CA	PRO	B	164	-2.580	12.477	23.912	1.00	49.79
2906	CB	PRO	B	164	-4.040	12.042	23.913	1.00	50.14
2907	CG	PRO	B	164	-3.988	10.692	24.532	1.00	54.43
2908	C	PRO	B	164	-2.210	13.229	25.177	1.00	52.68
2909	O	PRO	B	164	-1.676	12.650	26.121	1.00	55.25
2910	N	LEU	B	165	-2.496	14.523	25.187	1.00	46.01
2911	CA	LEU	B	165	-2.195	15.363	26.330	1.00	38.63
2912	CB	LEU	B	165	-0.862	16.080	26.112	1.00	42.39
2913	CG	LEU	B	165	-0.390	17.012	27.232	1.00	34.72
2914	CD1	LEU	B	165	0.058	16.181	28.423	1.00	36.79
2915	CD2	LEU	B	165	0.765	17.879	26.732	1.00	31.18
2916	C	LEU	B	165	-3.306	16.390	26.491	1.00	41.11
2917	O	LEU	B	165	-3.561	17.181	25.597	1.00	47.00
2918	N	ASN	B	166	-3.983	16.369	27.626	1.00	47.91
2919	CA	ASN	B	166	-5.044	17.332	27.952	1.00	62.56
2920	CB	ASN	B	166	-5.919	16.892	29.031	1.00	89.42
2921	CG	ASN	B	166	-6.897	15.795	28.644	1.00	111.40
2922	OD1	ASN	B	166	-7.511	15.874	27.581	1.00	117.56
2923	ND2	ASN	B	166	-7.069	14.782	29.490	1.00	128.12
2924	C	ASN	B	166	-4.419	18.685	28.139	1.00	63.19
2925	O	ASN	B	166	-3.385	18.758	28.798	1.00	75.62
2926	N	ILE	B	167	-5.028	19.743	27.614	1.00	55.85
2927	CA	ILE	B	167	-4.547	21.103	27.837	1.00	50.63
2928	CB	ILE	B	167	-3.775	21.642	26.625	1.00	41.65
2929	CG2	ILE	B	167	-3.644	23.158	26.704	1.00	27.67
2930	CG1	ILE	B	167	-2.398	20.981	26.572	1.00	49.69
2931	CD1	ILE	B	167	-1.576	21.401	25.373	1.00	71.73
2932	C	ILE	B	167	-5.719	22.018	28.127	1.00	52.51
2933	O	ILE	B	167	-6.636	22.141	27.328	1.00	54.25
2934	N	THR	B	168	-5.677	22.669	29.279	1.00	62.54

	2935	CA	THR	B	168	-6.762	23.552	29.672	1.00	73.12
	2936	CB	THR	B	168	-7.371	23.090	30.995	1.00	77.82
	2937	OG1	THR	B	168	-7.229	21.668	31.116	1.00	71.03
	2938	CG2	THR	B	168	-8.847	23.472	31.049	1.00	80.41
5	2939	C	THR	B	168	-6.329	25.002	29.841	1.00	79.24
	2940	O	THR	B	168	-5.347	25.294	30.526	1.00	81.73
	2941	N	VAL	B	169	-7.070	25.907	29.214	1.00	81.68
	2942	CA	VAL	B	169	-6.792	27.336	29.302	1.00	82.56
	2943	CB	VAL	B	169	-6.787	27.996	27.916	1.00	80.42
10	2944	CG1	VAL	B	169	-6.538	29.487	28.048	1.00	71.55
	2945	CG2	VAL	B	169	-5.731	27.352	27.041	1.00	82.46
	2946	C	VAL	B	169	-7.937	27.908	30.115	1.00	89.49
	2947	O	VAL	B	169	-9.098	27.841	29.696	1.00	87.82
	2948	N	ILE	B	170	-7.625	28.469	31.277	1.00	94.48
15	2949	CA	ILE	B	170	-8.668	28.995	32.143	1.00	101.94
	2950	CB	ILE	B	170	-8.332	28.730	33.631	1.00	98.82
	2951	CG2	ILE	B	170	-8.574	27.262	33.966	1.00	99.33
	2952	CG1	ILE	B	170	-6.876	29.092	33.912	1.00	103.85
	2953	CD1	ILE	B	170	-6.453	28.836	35.347	1.00	102.26
20	2954	C	ILE	B	170	-9.027	30.467	31.967	1.00	106.09
	2955	O	ILE	B	170	-8.162	31.307	31.727	1.00	103.79
	2956	N	LYS	B	171	-10.326	30.715	32.066	1.00	115.25
	2957	CA	LYS	B	171	-10.870	32.069	32.000	1.00	116.92
	2958	CB	LYS	B	171	-12.374	32.030	31.674	1.00	111.37
25	2959	CG	LYS	B	171	-13.021	33.402	31.721	1.00	106.02
	2960	CD	LYS	B	171	-12.523	34.293	30.594	1.00	110.98
	2961	CE	LYS	B	171	-13.256	35.629	30.587	1.00	109.27
	2962	NZ	LYS	B	171	-12.673	36.579	29.609	1.00	99.03
	2963	C	LYS	B	171	-10.606	32.682	33.357	1.00	122.05
30	2964	O	LYS	B	171	-10.455	31.952	34.327	1.00	122.45
	2965	N	ALA	B	172	-10.550	34.004	33.492	1.00	121.93
	2966	CA	ALA	B	172	-10.154	34.550	34.807	1.00	124.78
	2967	CB	ALA	B	172	-8.778	35.182	34.669	1.00	110.24
	2968	C	ALA	B	172	-11.069	35.577	35.528	1.00	131.95
35	2969	O	ALA	B	172	-11.006	36.782	35.303	1.00	136.47
	2970	N	PRO	B	173	-11.911	35.025	36.361	1.00	138.57
	2971	CD	PRO	B	173	-12.775	34.002	35.754	1.00	133.76
	2972	CA	PRO	B	173	-12.781	35.842	37.272	1.00	145.56
	2973	CB	PRO	B	173	-13.714	34.799	37.872	1.00	143.51
40	2974	CG	PRO	B	173	-13.935	33.894	36.705	1.00	139.83
	2975	C	PRO	B	173	-12.008	36.690	38.273	1.00	152.09
	2976	O	PRO	B	173	-10.896	36.332	38.614	1.00	158.41
	2977	N	ARG	B	174	-12.559	37.804	38.749	1.00	156.36
	2978	CA	ARG	B	174	-11.852	38.646	39.733	1.00	159.88
45	2979	CB	ARG	B	174	-10.934	39.640	39.008	1.00	160.37
	2980	CG	ARG	B	174	-11.660	40.518	38.000	1.00	164.23
	2981	CD	ARG	B	174	-11.074	40.350	36.593	1.00	169.49
	2982	NE	ARG	B	174	-12.049	40.638	35.539	1.00	176.01
	2983	CZ	ARG	B	174	-12.039	41.731	34.773	1.00	180.58
50	2984	NH1	ARG	B	174	-11.100	42.655	34.956	1.00	179.79
	2985	NH2	ARG	B	174	-12.954	41.882	33.824	1.00	181.42
	2986	C	ARG	B	174	-12.853	39.368	40.639	1.00	160.54
	2987	O	ARG	B	174	-13.891	38.809	41.006	1.00	159.92
	2988	C1	NAG	B	221	22.996	15.148	29.775	1.00	90.21
55	2989	C2	NAG	B	221	23.132	14.494	28.397	1.00	106.23
	2990	N2	NAG	B	221	21.968	13.691	28.083	1.00	110.50
	2991	C7	NAG	B	221	21.087	14.132	27.187	1.00	109.71
	2992	O7	NAG	B	221	21.209	15.211	26.594	1.00	98.37
	2993	C8	NAG	B	221	19.888	13.243	26.902	1.00	105.30
60	2994	C3	NAG	B	221	24.395	13.644	28.376	1.00	115.44
	2995	O3	NAG	B	221	24.547	13.046	27.097	1.00	116.65
	2996	C4	NAG	B	221	25.598	14.538	28.682	1.00	118.34
	2997	O4	NAG	B	221	26.785	13.757	28.731	1.00	122.24
	2998	C5	NAG	B	221	25.393	15.264	30.022	1.00	113.54
65	2999	O5	NAG	B	221	24.136	15.989	30.028	1.00	102.61
	3000	C6	NAG	B	221	26.494	16.278	30.269	1.00	108.41
	3001	O6	NAG	B	221	26.454	16.766	31.601	1.00	119.03
	3002	C1	NAG	B	242	7.596	9.421	42.304	1.00	89.99
	3003	C2	NAG	B	242	8.393	8.151	42.040	1.00	87.43
70	3004	N2	NAG	B	242	9.815	8.410	42.148	1.00	86.29

	3005	C7	NAG	B	242	10.433	8.308	43.321	1.00	82.76
	3006	O7	NAG	B	242	9.852	7.998	44.367	1.00	76.22
	3007	C8	NAG	B	242	11.928	8.599	43.333	1.00	77.25
	3008	C3	NAG	B	242	8.059	7.652	40.641	1.00	90.08
5	3009	O3	NAG	B	242	8.693	6.400	40.436	1.00	97.55
	3010	C4	NAG	B	242	6.539	7.501	40.426	1.00	91.14
	3011	O4	NAG	B	242	6.283	7.380	39.009	1.00	112.32
	3012	C5	NAG	B	242	5.757	8.728	40.956	1.00	82.98
	3013	O5	NAG	B	242	6.202	9.104	42.276	1.00	91.07
10	3014	C6	NAG	B	242	4.266	8.467	41.060	1.00	84.52
	3015	O6	NAG	B	242	3.514	9.640	40.779	1.00	85.63
	3016	C1	NAG	B	243	6.193	6.123	38.423	1.00	105.62
	3017	C2	NAG	B	243	5.464	6.267	37.081	1.00	107.32
	3018	N2	NAG	B	243	4.122	6.776	37.289	1.00	101.51
15	3019	C7	NAG	B	243	3.804	7.995	36.858	1.00	90.92
	3020	O7	NAG	B	243	4.599	8.719	36.255	1.00	78.67
	3021	C8	NAG	B	243	2.389	8.483	37.120	1.00	83.10
	3022	C3	NAG	B	243	5.435	4.929	36.344	1.00	112.30
	3023	O3	NAG	B	243	4.817	5.094	35.073	1.00	112.99
20	3024	C4	NAG	B	243	6.875	4.455	36.166	1.00	114.52
	3025	O4	NAG	B	243	6.914	3.184	35.480	1.00	130.57
	3026	C5	NAG	B	243	7.570	4.361	37.533	1.00	107.51
	3027	O5	NAG	B	243	7.529	5.646	38.195	1.00	110.47
	3028	C6	NAG	B	243	9.034	3.978	37.402	1.00	100.22
25	3029	O6	NAG	B	243	9.696	3.984	38.659	1.00	87.89
	3030	C1	MAN	B	244	7.657	3.203	34.307	1.00	139.64
	3031	C2	MAN	B	244	6.772	2.971	33.058	1.00	140.01
	3032	O2	MAN	B	244	7.304	3.675	31.948	1.00	144.21
	3033	C3	MAN	B	244	6.590	1.496	32.679	1.00	138.91
30	3034	O3	MAN	B	244	6.103	1.414	31.347	1.00	144.28
	3035	C4	MAN	B	244	7.910	0.735	32.788	1.00	139.81
	3036	O4	MAN	B	244	7.708	-0.643	32.517	1.00	144.34
	3037	C5	MAN	B	244	8.435	0.909	34.198	1.00	140.48
	3038	O5	MAN	B	244	8.779	2.294	34.406	1.00	147.09
35	3039	C6	MAN	B	244	9.676	0.070	34.479	1.00	136.69
	3040	O6	MAN	B	244	10.863	0.718	34.041	1.00	123.90
	3041	C1	NAG	B	335	10.916	24.720	18.959	1.00	65.94
	3042	C2	NAG	B	335	12.028	24.987	17.832	1.00	79.27
	3043	N2	NAG	B	335	11.848	24.183	16.736	1.00	91.33
40	3044	C7	NAG	B	335	11.340	24.727	15.629	1.00	98.55
	3045	O7	NAG	B	335	10.962	25.902	15.560	1.00	81.86
	3046	C8	NAG	B	335	11.212	23.824	14.411	1.00	99.41
	3047	C3	NAG	B	335	13.413	24.705	18.548	1.00	84.72
	3048	O3	NAG	B	335	14.442	25.019	17.611	1.00	91.27
45	3049	C4	NAG	B	335	13.604	25.515	19.838	1.00	80.89
	3050	O4	NAG	B	335	14.831	25.090	20.488	1.00	64.07
	3051	C5	NAG	B	335	12.419	25.265	20.794	1.00	64.08
	3052	O5	NAG	B	335	11.144	25.538	20.131	1.00	71.94
	3053	C6	NAG	B	335	12.531	26.144	22.030	1.00	64.49
50	3054	O6	NAG	B	335	11.291	26.809	22.362	1.00	45.77
	3055	C1	NAG	B	336	15.929	25.939	20.563	1.00	97.76
	3056	C2	NAG	B	336	16.577	25.748	21.946	1.00	97.78
	3057	N2	NAG	B	336	15.705	26.270	22.982	1.00	97.76
	3058	C7	NAG	B	336	15.077	25.437	23.810	1.00	97.93
55	3059	O7	NAG	B	336	15.179	24.203	23.741	1.00	97.68
	3060	C8	NAG	B	336	14.193	26.073	24.873	1.00	97.82
	3061	C3	NAG	B	336	17.943	26.425	22.064	1.00	97.90
	3062	O3	NAG	B	336	18.571	25.981	23.258	1.00	98.29
	3063	C4	NAG	B	336	18.847	26.092	20.880	1.00	98.00
60	3064	O4	NAG	B	336	20.012	26.915	20.922	1.00	97.87
	3065	C5	NAG	B	336	18.103	26.315	19.557	1.00	97.95
	3066	O5	NAG	B	336	16.862	25.561	19.525	1.00	97.83
	3067	C6	NAG	B	336	18.956	25.835	18.400	1.00	97.91
	3068	O6	NAG	B	336	18.216	25.798	17.193	1.00	97.89
65	3069	C1	FCA	B	337	11.537	27.883	23.223	1.00	97.62
	3070	C2	FCA	B	337	10.367	28.129	24.189	1.00	97.53
	3071	C3	FCA	B	337	9.202	28.823	23.571	1.00	97.82
	3072	C4	FCA	B	337	9.595	30.213	22.961	1.00	97.76
	3073	C5	FCA	B	337	10.713	29.895	21.926	1.00	97.77
70	3074	C6	FCA	B	337	11.421	31.110	21.306	1.00	97.74

3075	O2	FCA	B	337	9.934	26.823	24.727	1.00	97.69
3076	O3	FCA	B	337	8.162	29.022	24.541	1.00	97.99
3077	O4	FCA	B	337	10.062	31.100	24.005	1.00	97.77
3078	O5	FCA	B	337	11.775	29.137	22.508	1.00	97.61
3079	C1	NAG	B	340	-0.412	38.735	24.336	1.00	122.51
3080	C2	NAG	B	340	-1.134	39.580	25.381	1.00	120.32
3081	N2	NAG	B	340	-2.513	39.812	24.998	1.00	123.12
3082	C7	NAG	B	340	-3.481	39.652	25.892	1.00	119.35
3083	O7	NAG	B	340	-3.272	39.289	27.048	1.00	117.53
3084	C8	NAG	B	340	-4.900	39.928	25.422	1.00	119.54
3085	C3	NAG	B	340	-0.418	40.906	25.454	1.00	119.27
3086	O3	NAG	B	340	-1.096	41.797	26.326	1.00	109.33
3087	C4	NAG	B	340	1.035	40.774	25.885	1.00	127.45
3088	O4	NAG	B	340	1.546	42.148	25.882	1.00	140.24
3089	C5	NAG	B	340	1.739	39.801	24.880	1.00	128.90
3090	O5	NAG	B	340	0.965	38.548	24.746	1.00	126.48
3091	C6	NAG	B	340	3.135	39.394	25.344	1.00	127.49
3092	O6	NAG	B	340	3.474	38.081	24.908	1.00	123.34
3093	C1	NAG	B	341	2.837	42.676	25.784	1.00	149.17
3094	C2	NAG	B	341	3.740	42.731	27.002	1.00	145.12
3095	N2	NAG	B	341	2.968	42.757	28.228	1.00	146.42
3096	C7	NAG	B	341	2.704	41.612	28.847	1.00	145.07
3097	O7	NAG	B	341	3.106	40.526	28.416	1.00	132.12
3098	C8	NAG	B	341	1.890	41.672	30.122	1.00	142.75
3099	C3	NAG	B	341	4.552	44.017	26.806	1.00	143.92
3100	O3	NAG	B	341	5.474	44.200	27.872	1.00	142.89
3101	C4	NAG	B	341	5.304	43.958	25.449	1.00	148.66
3102	O4	NAG	B	341	5.954	45.201	25.210	1.00	144.18
3103	C5	NAG	B	341	4.351	43.643	24.269	1.00	155.68
3104	O5	NAG	B	341	3.515	42.481	24.540	1.00	161.36
3105	C6	NAG	B	341	5.092	43.354	22.983	1.00	161.88
3106	O6	NAG	B	341	4.581	44.135	21.915	1.00	165.58
3107	C1	NAG	B	366	-8.147	13.841	29.242	1.00	143.91
3108	C2	NAG	B	366	-8.310	12.851	30.401	1.00	148.60
3109	N2	NAG	B	366	-7.063	12.152	30.649	1.00	155.49
3110	C7	NAG	B	366	-6.400	12.345	31.787	1.00	156.20
3111	O7	NAG	B	366	-6.791	13.114	32.670	1.00	152.95
3112	C8	NAG	B	366	-5.103	11.570	31.975	1.00	155.57
3113	C3	NAG	B	366	-9.420	11.849	30.045	1.00	149.01
3114	O3	NAG	B	366	-9.658	10.967	31.133	1.00	143.79
3115	C4	NAG	B	366	-10.713	12.593	29.696	1.00	151.07
3116	O4	NAG	B	366	-11.684	11.663	29.237	1.00	149.83
3117	C5	NAG	B	366	-10.447	13.654	28.611	1.00	149.31
3118	O5	NAG	B	366	-9.380	14.536	29.019	1.00	146.79
3119	C6	NAG	B	366	-11.657	14.529	28.340	1.00	149.54
3120	O6	NAG	B	366	-11.370	15.902	28.578	1.00	136.69

Table 8. Atomic coordinates of PhFceRIα₁₋₁₇₂, Form H1

ATOM NUMBER	ATOM TYPE	RESIDUE	#	X	Y	Z	OCC	B
1	CB	VAL	1	53.051	36.792	77.715	1.00	118.55
2	CG1	VAL	1	52.370	35.571	77.956	1.00	118.55
3	CG2	VAL	1	53.204	37.651	79.132	1.00	118.55
4	C	VAL	1	54.467	36.682	75.485	1.00	75.78
5	O	VAL	1	53.770	37.511	74.950	1.00	75.78
6	N	VAL	1	55.482	37.216	77.849	1.00	75.78
7	CA	VAL	1	54.432	36.462	77.091	1.00	75.78
8	N	PRO	2	55.312	35.953	74.688	1.00	130.31
9	CD	PRO	2	56.277	34.989	75.182	1.00	94.32
10	CA	PRO	2	55.477	36.015	73.216	1.00	130.31
11	CB	PRO	2	56.190	34.719	72.910	1.00	94.32
12	CG	PRO	2	57.105	34.684	74.012	1.00	94.32
13	C	PRO	2	54.053	36.005	72.706	1.00	130.31
14	O	PRO	2	53.189	35.367	73.293	1.00	130.31
15	N	GLN	3	53.786	36.805	71.691	1.00	104.92
16	CA	GLN	3	52.463	36.918	71.130	1.00	104.92
17	CB	GLN	3	52.537	37.847	69.919	1.00	99.07
18	CG	GLN	3	51.192	38.291	69.421	1.00	99.07
19	CD	GLN	3	50.249	38.740	70.542	1.00	99.07
20	OE1	GLN	3	50.548	39.683	71.287	1.00	99.07
21	NE2	GLN	3	49.101	38.061	70.664	1.00	99.07
22	C	GLN	3	52.005	35.499	70.762	1.00	104.92
23	O	GLN	3	52.779	34.545	70.877	1.00	104.92
24	N	LYS	4	50.747	35.334	70.360	1.00	70.29
25	CA	LYS	4	50.255	33.998	69.981	1.00	70.29
26	CB	LYS	4	48.731	33.942	70.002	1.00	91.56
27	CG	LYS	4	47.997	34.836	69.020	1.00	91.56
28	CD	LYS	4	46.591	34.284	68.830	1.00	91.56
29	CE	LYS	4	45.661	35.309	68.214	1.00	91.56
30	NZ	LYS	4	45.296	36.401	69.165	1.00	91.56
31	C	LYS	4	50.735	33.524	68.613	1.00	70.29
32	O	LYS	4	50.793	34.314	67.654	1.00	70.29
33	N	PRO	5	51.056	32.216	68.503	1.00	78.97
34	CD	PRO	5	51.154	31.280	69.633	1.00	108.62
35	CA	PRO	5	51.541	31.566	67.284	1.00	78.97
36	CB	PRO	5	51.808	30.127	67.739	1.00	108.62
37	CG	PRO	5	52.211	30.315	69.151	1.00	108.62
38	C	PRO	5	50.601	31.638	66.091	1.00	78.97
39	O	PRO	5	49.439	32.036	66.221	1.00	78.97
40	N	LYS	6	51.124	31.294	64.916	1.00	88.04
41	CA	LYS	6	50.283	31.336	63.731	1.00	88.04
42	CB	LYS	6	50.440	32.681	63.010	1.00	139.11
43	CG	LYS	6	49.189	33.108	62.233	1.00	139.11
44	CD	LYS	6	49.300	34.555	61.830	1.00	139.11
45	CE	LYS	6	47.998	35.105	61.293	1.00	139.11
46	NZ	LYS	6	48.130	36.569	61.033	1.00	139.11
47	C	LYS	6	50.598	30.191	62.780	1.00	88.04
48	O	LYS	6	51.765	29.850	62.565	1.00	88.04
49	N	VAL	7	49.539	29.590	62.235	1.00	50.50
50	CA	VAL	7	49.660	28.476	61.307	1.00	50.50
51	CB	VAL	7	48.471	27.522	61.411	1.00	69.58
52	CG1	VAL	7	48.757	26.276	60.577	1.00	69.58
53	CG2	VAL	7	48.212	27.169	62.858	1.00	69.58
54	C	VAL	7	49.733	28.947	59.871	1.00	50.50
55	O	VAL	7	48.997	29.831	59.446	1.00	50.50
56	N	SER	8	50.597	28.301	59.112	1.00	106.26
57	CA	SER	8	50.788	28.646	57.723	1.00	106.26
58	CB	SER	8	52.121	29.344	57.568	1.00	69.57
59	OG	SER	8	53.155	28.427	57.902	1.00	69.57
60	C	SER	8	50.816	27.357	56.933	1.00	106.26
61	O	SER	8	51.370	26.353	57.380	1.00	106.26
62	N	LEU	9	50.221	27.381	55.754	1.00	69.51
63	CA	LEU	9	50.212	26.187	54.937	1.00	69.51
64	CB	LEU	9	48.809	25.862	54.432	1.00	46.80

	65	CG	LEU	9	47.549	26.374	55.111	1.00	46.80
	66	CD1	LEU	9	46.349	25.850	54.373	1.00	46.80
	67	CD2	LEU	9	47.523	25.926	56.559	1.00	46.80
	68	C	LEU	9	51.111	26.317	53.718	1.00	69.51
5	69	O	LEU	9	51.229	27.385	53.110	1.00	69.51
	70	N	ASN	10	51.725	25.199	53.358	1.00	65.02
	71	CA	ASN	10	52.576	25.120	52.197	1.00	65.02
	72	CB	ASN	10	54.050	25.035	52.622	1.00	82.93
	73	CG	ASN	10	54.979	24.700	51.475	1.00	82.93
10	74	OD1	ASN	10	54.991	25.378	50.451	1.00	82.93
	75	ND2	ASN	10	55.771	23.650	51.643	1.00	82.93
	76	C	ASN	10	52.130	23.839	51.492	1.00	65.02
	77	O	ASN	10	52.431	22.728	51.953	1.00	65.02
	78	N	PRO	11	51.306	23.967	50.430	1.00	60.91
15	79	CD	PRO	11	50.772	22.738	49.827	1.00	59.89
	80	CA	PRO	11	50.786	25.157	49.733	1.00	60.91
	81	CB	PRO	11	49.977	24.568	48.583	1.00	59.89
	82	CG	PRO	11	50.471	23.159	48.449	1.00	59.89
	83	C	PRO	11	49.881	26.032	50.613	1.00	60.91
20	84	O	PRO	11	49.435	25.‥8	51.675	1.00	60.91
	85	N	PRO	12	49.570	27.245	50.142	1.00	78.15
	86	CD	PRO	12	50.133	27.764	48.895	1.00	41.22
	87	CA	PRO	12	48.728	28.264	50.791	1.00	78.15
	88	CB	PRO	12	48.984	29.528	49.967	1.00	41.22
25	89	CG	PRO	12	50.225	29.226	49.207	1.00	41.22
	90	C	PRO	12	47.264	27.890	50.704	1.00	78.15
	91	O	PRO	12	46.420	28.401	51.437	1.00	78.15
	92	N	TRP	13	46.975	27.001	49.773	1.00	63.58
	93	CA	TRP	13	45.621	26.563	49.541	1.00	63.58
30	94	CB	TRP	13	45.619	25.679	48.308	1.00	43.81
	95	CG	TRP	13	46.483	26.211	47.211	1.00	43.81
	96	CD2	TRP	13	46.444	27.519	46.634	1.00	43.81
	97	CE2	TRP	13	47.339	27.524	45.549	1.00	43.81
	98	CE3	TRP	13	45.732	28.687	46.926	1.00	43.81
35	99	CD1	TRP	13	47.385	25.507	46.480	1.00	43.81
	100	NE1	TRP	13	47.903	26.281	45.477	1.00	43.81
	101	CZ2	TRP	13	47.543	28.650	44.746	1.00	43.81
	102	CZ3	TRP	13	45.935	29.812	46.128	1.00	43.81
	103	CH2	TRP	13	46.838	29.780	45.046	1.00	43.81
40	104	C	TRP	13	45.032	25.822	50.730	1.00	63.58
	105	O	TRP	13	45.556	24.777	51.137	1.00	63.58
	106	N	ASN	14	43.947	26.377	51.280	1.00	73.67
	107	CA	ASN	14	43.239	25.781	52.412	1.00	73.67
	108	CB	ASN	14	42.720	26.868	53.362	1.00	86.63
45	109	CG	ASN	14	41.638	27.726	52.745	1.00	86.63
	110	OD1	ASN	14	41.780	28.226	51.630	1.00	86.63
	111	ND2	ASN	14	40.548	27.912	53.477	1.00	86.63
	112	C	ASN	14	42.090	24.940	51.861	1.00	73.67
	113	O	ASN	14	41.276	24.409	52.609	1.00	73.67
50	114	N	ARG	15	42.045	24.837	50.534	1.00	50.70
	115	CA	ARG	15	41.058	24.054	49.800	1.00	50.70
	116	CB	ARG	15	40.174	24.947	48.943	1.00	57.52
	117	CG	ARG	15	39.558	26.093	49.674	1.00	57.52
	118	CD	ARG	15	38.636	26.850	48.745	1.00	57.52
55	119	NE	ARG	15	37.242	26.435	48.833	1.00	57.52
	120	CZ	ARG	15	36.364	26.620	47.853	1.00	57.52
	121	NH1	ARG	15	36.752	27.189	46.730	1.00	57.52
	122	NH2	ARG	15	35.093	26.286	47.999	1.00	57.52
	123	C	ARG	15	41.851	23.139	48.858	1.00	50.70
60	124	O	ARG	15	42.427	23.596	47.863	1.00	50.70
	125	N	ILE	16	41.902	21.849	49.150	1.00	58.15
	126	CA	ILE	16	42.633	20.980	48.254	1.00	58.15
	127	CB	ILE	16	43.956	20.548	48.866	1.00	51.72
	128	CG2	ILE	16	44.934	21.703	48.821	1.00	51.72
65	129	CG1	ILE	16	43.718	20.052	50.287	1.00	51.72
	130	CD1	ILE	16	44.968	19.557	50.978	1.00	51.72
	131	C	ILE	16	41.839	19.761	47.876	1.00	58.15
	132	O	ILE	16	40.875	19.403	48.540	1.00	58.15
	133	N	PHE	17	42.260	19.157	46.776	1.00	58.19
70	134	CA	PHE	17	41.660	17.957	46.241	1.00	58.19

	135	CB	PHE	17	42.213	17.669	44.860	1.00	25.51
	136	CG	PHE	17	41.536	18.414	43.776	1.00	25.51
	137	CD1	PHE	17	42.250	18.820	42.639	1.00	25.51
	138	CD2	PHE	17	40.171	18.682	43.857	1.00	25.51
5	139	CE1	PHE	17	41.608	19.487	41.592	1.00	25.51
	140	CE2	PHE	17	39.532	19.344	42.825	1.00	25.51
	141	CZ	PHE	17	40.253	19.752	41.673	1.00	25.51
	142	C	PHE	17	42.019	16.789	47.117	1.00	58.19
	143	O	PHE	17	43.030	16.815	47.836	1.00	58.19
10	144	N	LYS	18	41.202	15.749	47.024	1.00	64.21
	145	CA	LYS	18	41.421	14.528	47.770	1.00	64.21
	146	CB	LYS	18	40.266	13.572	47.476	1.00	120.30
	147	CG	LYS	18	40.180	12.351	48.352	1.00	120.30
	148	CD	LYS	18	38.856	11.639	48.078	1.00	120.30
15	149	CE	LYS	18	38.656	10.437	48.983	1.00	120.30
	150	NZ	LYS	18	39.547	9.324	48.594	1.00	120.30
	151	C	LYS	18	42.740	13.978	47.237	1.00	64.21
	152	O	LYS	18	42.970	13.995	46.027	1.00	64.21
	153	N	GLY	19	43.619	13.536	48.134	1.00	59.20
20	154	CA	GLY	19	44.893	12.963	47.706	1.00	59.20
	155	C	GLY	19	46.112	13.851	47.506	1.00	59.20
	156	O	GLY	19	47.199	13.352	47.174	1.00	59.20
	157	N	GLU	20	45.938	15.156	47.686	1.00	96.38
	158	CA	GLU	20	47.046	16.087	47.539	1.00	96.38
25	159	CB	GLU	20	46.547	17.429	46.993	1.00	62.66
	160	CG	GLU	20	45.820	17.303	45.661	1.00	62.66
	161	CD	GLU	20	45.468	18.648	45.025	1.00	62.66
	162	OE1	GLU	20	44.899	19.525	45.726	1.00	62.66
	163	OE2	GLU	20	45.754	18.811	43.815	1.00	62.66
30	164	C	GLU	20	47.666	16.261	48.917	1.00	96.38
	165	O	GLU	20	47.055	15.899	49.922	1.00	96.38
	166	N	ASN	21	48.886	16.783	48.966	1.00	82.14
	167	CA	ASN	21	49.550	16.992	50.245	1.00	82.14
35	168	CB	ASN	21	50.929	16.375	50.212	1.00	83.98
	169	CG	ASN	21	50.907	15.025	49.599	1.00	83.98
	170	OD1	ASN	21	50.088	14.203	49.969	1.00	83.98
	171	ND2	ASN	21	51.791	14.775	48.651	1.00	83.98
	172	C	ASN	21	49.661	18.458	50.598	1.00	82.14
	173	O	ASN	21	49.706	19.317	49.727	1.00	82.14
40	174	N	VAL	22	49.715	18.739	51.889	1.00	82.30
	175	CA	VAL	22	49.809	20.109	52.347	1.00	82.30
	176	CB	VAL	22	48.407	20.695	52.489	1.00	52.62
	177	CG1	VAL	22	47.687	19.993	53.637	1.00	52.62
	178	CG2	VAL	22	48.473	22.229	52.679	1.00	52.62
45	179	C	VAL	22	50.502	20.090	53.698	1.00	82.30
	180	O	VAL	22	50.248	19.192	54.503	1.00	82.30
	181	N	THR	23	51.376	21.063	53.954	1.00	73.57
	182	CA	THR	23	52.083	21.109	55.231	1.00	73.57
	183	CB	THR	23	53.598	21.205	55.035	1.00	78.82
50	184	OG1	THR	23	54.021	20.223	54.076	1.00	78.82
	185	CG2	THR	23	54.309	20.974	56.380	1.00	78.82
	186	C	THR	23	51.658	22.281	56.097	1.00	73.57
	187	O	THR	23	51.549	23.407	55.618	1.00	73.57
	188	N	LEU	24	51.417	22.007	57.374	1.00	80.82
55	189	CA	LEU	24	51.026	23.040	58.314	1.00	80.82
	190	CB	LEU	24	49.818	22.605	59.138	1.00	72.07
	191	CG	LEU	24	48.578	22.217	58.346	1.00	72.07
	192	CD1	LEU	24	47.353	22.285	59.242	1.00	72.07
	193	CD2	LEU	24	48.412	23.157	57.182	1.00	72.07
60	194	C	LEU	24	52.188	23.322	59.239	1.00	80.82
	195	O	LEU	24	52.771	22.420	59.825	1.00	80.82
	196	N	THR	25	52.527	24.591	59.367	1.00	57.44
	197	CA	THR	25	53.622	24.995	60.228	1.00	57.44
	198	CB	THR	25	54.748	25.593	59.431	1.00	58.08
65	199	OG1	THR	25	55.299	24.593	58.568	1.00	58.08
	200	CG2	THR	25	55.812	26.103	60.372	1.00	58.08
	201	C	THR	25	53.197	26.039	61.238	1.00	57.44
	202	O	THR	25	52.524	27.007	60.891	1.00	57.44
	203	N	CYS	26	53.589	25.833	62.489	1.00	94.33
70	204	CA	CYS	26	53.276	26.780	63.551	1.00	94.33

	205	C	CYS	26	54.464	27.725	63.557	1.00	94.33
	206	O	CYS	26	55.604	27.267	63.459	1.00	94.33
	207	CB	CYS	26	53.206	26.060	64.890	1.00	89.97
5	208	SG	CYS	26	52.191	26.860	66.176	1.00	89.97
	209	N	ASN	27	54.229	29.031	63.651	1.00	88.38
	210	CA	ASN	27	55.363	29.941	63.665	1.00	88.38
	211	CB	ASN	27	55.584	30.555	62.273	1.00	163.21
	212	CG	ASN	27	56.225	29.574	61.290	1.00	163.21
	213	OD1	ASN	27	57.082	28.768	61.667	1.00	163.21
10	214	ND2	ASN	27	55.825	29.654	60.020	1.00	163.21
	215	C	ASN	27	55.336	31.039	64.719	1.00	88.38
	216	O	ASN	27	54.563	31.989	64.641	1.00	88.38
	217	N	GLY	28	56.164	30.862	65.736	1.00	157.55
	218	CA	GLY	28	56.306	31.863	66.769	1.00	157.55
15	219	C	GLY	28	57.695	32.269	66.353	1.00	157.55
	220	O	GLY	28	58.644	31.591	66.702	1.00	157.55
	221	N	ASN	29	57.813	33.337	65.572	1.00	155.07
	222	CA	ASN	29	59.110	33.779	65.057	1.00	155.07
	223	CB	ASN	29	59.054	35.252	64.655	1.00	162.85
20	224	CG	ASN	29	57.897	35.564	63.723	1.00	162.85
	225	OD1	ASN	29	57.735	34.939	62.672	1.00	162.85
	226	ND2	ASN	29	57.088	36.545	64.103	1.00	162.85
	227	C	ASN	29	60.312	33.547	65.963	1.00	155.07
	228	O	ASN	29	61.386	33.183	65.471	1.00	155.07
25	229	N	ASN	30	60.152	33.787	67.269	1.00	156.06
	230	CA	ASN	30	61.241	33.545	68.220	1.00	156.06
	231	CB	ASN	30	60.696	33.490	69.653	1.00	177.59
	232	CG	ASN	30	60.720	34.850	70.334	1.00	177.59
	233	OD1	ASN	30	61.733	35.550	70.290	1.00	177.59
30	234	ND2	ASN	30	59.613	35.227	70.970	1.00	177.59
	235	C	ASN	30	61.697	32.182	67.729	1.00	156.06
	236	O	ASN	30	62.886	31.932	67.477	1.00	156.06
	237	N	PHE	31	60.702	31.316	67.577	1.00	152.23
	238	CA	PHE	31	60.896	30.010	66.990	1.00	152.23
35	239	CB	PHE	31	61.081	30.267	65.497	1.00	158.06
	240	CG	PHE	31	60.650	29.154	64.612	1.00	158.06
	241	CD1	PHE	31	59.315	28.746	64.550	1.00	158.06
	242	CD2	PHE	31	61.573	28.561	63.769	1.00	158.06
	243	CE1	PHE	31	58.924	27.755	63.653	1.00	158.06
40	244	CE2	PHE	31	61.197	27.579	62.877	1.00	158.06
	245	CZ	PHE	31	59.869	27.173	62.810	1.00	158.06
	246	C	PHE	31	62.099	29.281	67.576	1.00	152.23
	247	O	PHE	31	62.836	28.610	66.857	1.00	152.23
	248	N	PHE	32	62.304	29.414	68.880	1.00	166.63
45	249	CA	PHE	32	63.432	28.752	69.510	1.00	166.63
	250	CB	PHE	32	63.802	29.479	70.792	1.00	178.95
	251	CG	PHE	32	64.123	30.923	70.567	1.00	178.95
	252	CD1	PHE	32	63.361	31.922	71.164	1.00	178.95
	253	CD2	PHE	32	65.174	31.288	69.723	1.00	178.95
50	254	CE1	PHE	32	63.631	33.271	70.914	1.00	178.95
	255	CE2	PHE	32	65.452	32.634	69.466	1.00	178.95
	256	CZ	PHE	32	64.681	33.629	70.068	1.00	178.95
	257	C	PHE	32	63.116	27.288	69.760	1.00	166.63
	258	O	PHE	32	63.884	26.567	70.399	1.00	166.63
55	259	N	GLU	33	61.968	26.864	69.239	1.00	156.85
	260	CA	GLU	33	61.527	25.475	69.315	1.00	156.85
	261	CB	GLU	33	62.558	24.582	68.620	1.00	168.05
	262	CG	GLU	33	63.153	25.157	67.330	1.00	168.05
	263	CD	GLU	33	64.130	24.188	66.704	1.00	168.05
60	264	OE1	GLU	33	64.854	23.526	67.477	1.00	168.05
	265	OE2	GLU	33	64.175	24.084	65.461	1.00	168.05
	266	C	GLU	33	61.233	24.913	70.708	1.00	156.85
	267	O	GLU	33	60.369	24.046	70.851	1.00	156.85
	268	N	VAL	34	61.963	25.376	71.719	1.00	106.92
65	269	CA	VAL	34	61.748	24.926	73.095	1.00	106.92
	270	CB	VAL	34	60.953	25.998	73.882	1.00	129.93
	271	CG1	VAL	34	60.864	25.626	75.361	1.00	129.93
	272	CG2	VAL	34	61.607	27.359	73.695	1.00	129.93
	273	C	VAL	34	61.011	23.573	73.211	1.00	106.92
70	274	O	VAL	34	59.825	23.521	73.562	1.00	106.92

	275	N	SER	35	61.712	22.490	72.883	1.00	178.50
	276	CA	SER	35	61.170	21.135	72.978	1.00	178.50
	277	CB	SER	35	60.683	20.879	74.409	1.00	177.04
	278	OG	SER	35	61.781	20.767	75.302	1.00	177.04
5	279	C	SER	35	60.102	20.645	71.988	1.00	178.50
	280	O	SER	35	60.449	20.069	70.956	1.00	178.50
	281	N	SER	36	58.816	20.858	72.286	1.00	97.16
	282	CA	SER	36	57.742	20.347	71.411	1.00	97.16
	283	CB	SER	36	57.175	19.038	71.993	1.00	145.01
10	284	OG	SER	36	58.160	18.018	72.059	1.00	145.01
	285	C	SER	36	56.560	21.259	71.061	1.00	97.16
	286	O	SER	36	56.405	22.357	71.604	1.00	97.16
	287	N	THR	37	55.725	20.750	70.149	1.00	111.12
	288	CA	THR	37	54.530	21.433	69.638	1.00	111.12
15	289	CB	THR	37	54.686	21.780	68.144	1.00	142.34
	290	OG1	THR	37	55.863	22.572	67.954	1.00	142.34
	291	CG2	THR	37	53.465	22.536	67.638	1.00	142.34
	292	C	THR	37	53.273	20.565	69.746	1.00	111.12
	293	O	THR	37	53.323	19.357	69.509	1.00	111.12
20	294	N	LYS	38	52.147	21.193	70.075	1.00	89.74
	295	CA	LYS	38	50.879	20.480	70.195	1.00	89.74
	296	CB	LYS	38	50.253	20.739	71.559	1.00	101.72
	297	CG	LYS	38	50.833	19.880	72.648	1.00	101.72
	298	CD	LYS	38	50.223	20.211	73.991	1.00	101.72
25	299	CE	LYS	38	50.893	19.410	75.110	1.00	101.72
	300	NZ	LYS	38	50.571	19.965	76.465	1.00	101.72
	301	C	LYS	38	49.889	20.878	69.112	1.00	89.74
	302	O	LYS	38	49.478	22.036	69.039	1.00	89.74
	303	N	TRP	39	49.501	19.911	68.280	1.00	92.70
30	304	CA	TRP	39	48.549	20.162	67.196	1.00	92.70
	305	CB	TRP	39	48.948	19.417	65.833	1.00	89.95
	306	CG	TRP	39	50.148	19.958	65.279	1.00	89.95
	307	CD2	TRP	39	50.188	21.016	64.329	1.00	89.95
	308	CE2	TRP	39	51.536	21.192	63.941	1.00	89.95
35	309	CE3	TRP	39	49.211	21.846	63.759	1.00	89.95
	310	CD1	TRP	39	51.438	19.535	65.441	1.00	89.95
	311	NE1	TRP	39	52.282	20.269	64.639	1.00	89.95
	312	CZ2	TRP	39	51.938	22.145	63.017	1.00	89.95
	313	CZ3	TRP	39	49.603	22.799	62.839	1.00	89.95
40	314	CH2	TRP	39	50.958	22.943	62.475	1.00	89.95
	315	C	TRP	39	47.139	19.743	67.541	1.00	92.70
	316	O	TRP	39	46.926	18.717	68.177	1.00	92.70
	317	N	PHE	40	46.167	20.522	67.096	1.00	74.21
	318	CA	PHE	40	44.782	20.188	67.382	1.00	74.21
45	319	CB	PHE	40	44.177	21.186	68.365	1.00	91.61
	320	CG	PHE	40	44.868	21.229	69.698	1.00	91.61
	321	CD1	PHE	40	46.143	21.793	69.829	1.00	91.61
	322	CD2	PHE	40	44.231	20.730	70.833	1.00	91.61
	323	CE1	PHE	40	46.761	21.876	71.069	1.00	91.61
50	324	CE2	PHE	40	44.839	20.807	72.078	1.00	91.61
	325	CZ	PHE	40	46.110	21.379	72.196	1.00	91.61
	326	C	PHE	40	43.946	20.149	66.121	1.00	74.21
	327	O	PHE	40	43.709	21.176	65.474	1.00	74.21
	328	N	HIS	41	43.506	18.948	65.774	1.00	72.61
55	329	CA	HIS	41	42.691	18.750	64.593	1.00	72.61
	330	CB	HIS	41	43.15C	17.481	63.880	1.00	96.01
	331	CG	HIS	41	42.346	17.151	62.661	1.00	96.01
	332	CD2	HIS	41	42.300	16.023	61.911	1.00	96.01
	333	ND1	HIS	41	41.489	18.048	62.073	1.00	96.01
60	334	CE1	HIS	41	40.942	17.489	61.005	1.00	96.01
	335	NE2	HIS	41	41.419	16.264	60.887	1.00	96.01
	336	C	HIS	41	41.223	18.646	64.999	1.00	72.61
	337	O	HIS	41	40.831	17.703	65.696	1.00	72.61
	338	N	ASN	42	40.419	19.616	64.563	1.00	65.96
65	339	CA	ASN	42	38.998	19.638	64.896	1.00	65.96
	340	CB	ASN	42	38.304	18.373	64.347	1.00	107.42
	341	CG	ASN	42	37.832	18.533	62.897	1.00	107.42
	342	OD1	ASN	42	38.115	19.550	62.262	1.00	107.42
	343	ND2	ASN	42	37.110	17.532	62.380	1.00	107.42
70	344	C	ASN	42	38.869	19.713	66.422	1.00	65.96

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	345	O	ASN	42	37.863	19.297	67.008	1.00	65.96
	346	N	GLY	43	39.916	20.229	67.058	1.00	142.69
	347	CA	GLY	43	39.930	20.362	68.505	1.00	142.69
	348	C	GLY	43	40.418	19.152	69.292	1.00	142.69
5	349	O	GLY	43	40.304	19.125	70.508	1.00	142.69
	350	N	SER	44	40.972	18.149	68.621	1.00	82.57
	351	CA	SER	44	41.448	16.960	69.318	1.00	82.57
	352	CB	SER	44	40.876	15.716	68.658	1.00	65.56
	353	OG	SER	44	41.042	14.585	69.496	1.00	65.56
10	354	C	SER	44	42.966	16.877	69.294	1.00	82.57
	355	O	SER	44	43.558	16.765	68.218	1.00	82.57
	356	N	LEU	45	43.601	16.910	70.464	1.00	83.34
	357	CA	LEU	45	45.056	16.846	70.490	1.00	83.34
	358	CB	LEU	45	45.586	16.632	71.930	1.00	79.17
15	359	CG	LEU	45	47.121	16.657	72.177	1.00	79.17
	360	CD1	LEU	45	47.758	17.921	71.590	1.00	79.17
	361	CD2	LEU	45	47.403	16.581	73.681	1.00	79.17
	362	C	LEU	45	45.537	15.736	69.542	1.00	83.34
	363	O	LEU	45	45.074	14.588	69.585	1.00	83.34
20	364	N	SER	46	46.447	16.125	68.658	1.00	133.67
	365	CA	SER	46	47.037	15.236	67.671	1.00	133.67
	366	CB	SER	46	47.551	16.059	66.487	1.00	75.61
	367	OG	SER	46	48.435	15.315	65.662	1.00	75.61
	368	C	SER	46	48.196	14.486	68.299	1.00	133.67
25	369	O	SER	46	48.864	15.000	69.195	1.00	133.67
	370	N	GLU	47	48.431	13.268	67.827	1.00	113.73
	371	CA	GLU	47	49.545	12.470	68.329	1.00	113.73
	372	CB	GLU	47	49.354	10.985	67.982	1.00	165.00
	373	CG	GLU	47	48.217	10.318	68.775	1.00	165.00
30	374	CD	GLU	47	48.093	8.817	68.530	1.00	165.00
	375	OE1	GLU	47	47.813	8.412	67.380	1.00	165.00
	376	OE2	GLU	47	48.270	8.039	69.494	1.00	165.00
	377	C	GLU	47	50.821	13.023	67.695	1.00	113.73
	378	O	GLU	47	51.921	12.506	67.908	1.00	113.73
35	379	N	GLU	48	50.650	14.089	66.915	1.00	132.93
	380	CA	GLU	48	51.755	14.763	66.249	1.00	132.93
	381	CB	GLU	48	51.264	15.424	64.966	1.00	192.46
	382	CG	GLU	48	52.348	16.113	64.173	1.00	192.46
	383	CD	GLU	48	52.450	15.579	62.762	1.00	192.46
40	384	OE1	GLU	48	51.665	14.672	62.406	1.00	192.46
	385	OE2	GLU	48	53.316	16.062	62.005	1.00	192.46
	386	C	GLU	48	52.280	15.826	67.207	1.00	132.93
	387	O	GLU	48	51.506	16.635	67.730	1.00	132.93
	388	N	THR	49	53.591	15.827	67.436	1.00	120.56
45	389	CA	THR	49	54.193	16.789	68.350	1.00	120.56
	390	CB	THR	49	54.823	16.075	69.569	1.00	154.93
	391	OG1	THR	49	55.638	14.984	69.123	1.00	154.93
	392	CG2	THR	49	53.740	15.552	70.504	1.00	154.93
	393	C	THR	49	55.248	17.684	67.713	1.00	120.56
50	394	O	THR	49	55.697	18.652	68.323	1.00	120.56
	395	N	ASN	50	55.639	17.368	66.484	1.00	120.79
	396	CA	ASN	50	56.646	18.154	65.779	1.00	120.79
	397	CB	ASN	50	57.190	17.349	64.596	1.00	183.19
	398	CG	ASN	50	57.793	16.024	65.035	1.00	183.19
55	399	OD1	ASN	50	58.218	15.900	66.182	1.00	183.19
	400	ND2	ASN	50	57.865	15.054	64.124	1.00	183.19
	401	C	ASN	50	56.070	19.485	65.312	1.00	120.79
	402	O	ASN	50	54.854	19.616	65.160	1.00	120.79
	403	N	SER	51	56.944	20.466	65.084	1.00	104.18
60	404	CA	SER	51	56.522	21.811	64.657	1.00	104.18
	405	CB	SER	51	57.735	22.751	64.577	1.00	100.13
	406	OG	SER	51	58.559	22.431	63.468	1.00	100.13
	407	C	SER	51	55.753	21.880	63.329	1.00	104.18
	408	O	SER	51	55.086	22.879	63.053	1.00	104.18
65	409	N	SER	52	55.858	20.835	62.507	1.00	108.20
	410	CA	SER	52	55.154	20.803	61.223	1.00	108.20
	411	CB	SER	52	56.131	20.860	60.041	1.00	83.34
	412	OG	SER	52	56.705	22.151	59.913	1.00	83.34
	413	C	SER	52	54.291	19.566	61.083	1.00	108.20
70	414	O	SER	52	54.750	18.445	61.284	1.00	108.20

	415	N	LEU	53	53.038	19.790	60.720	1.00	62.72
	416	CA	LEU	53	52.057	18.730	60.536	1.00	62.72
	417	CB	LEU	53	50.730	19.214	61.130	1.00	43.93
	418	CG	LEU	53	49.456	18.379	61.050	1.00	43.93
5	419	CD1	LEU	53	49.665	17.079	61.786	1.00	43.93
	420	CD2	LEU	53	48.305	19.148	61.680	1.00	43.93
	421	C	LEU	53	51.912	18.398	59.035	1.00	62.72
	422	O	LEU	53	51.470	19.226	58.234	1.00	62.72
	423	N	ASN	54	52.294	17.192	58.642	1.00	92.98
10	424	CA	ASN	54	52.183	16.832	57.236	1.00	92.98
	425	CB	ASN	54	53.404	16.036	56.796	1.00	86.69
	426	CG	ASN	54	54.670	16.844	56.872	1.00	86.69
	427	OD1	ASN	54	54.805	17.866	56.186	1.00	86.69
	428	ND2	ASN	54	55.608	16.406	57.717	1.00	86.69
15	429	C	ASN	54	50.941	16.029	56.929	1.00	92.98
	430	O	ASN	54	50.701	14.991	57.529	1.00	92.98
	431	N	ILE	55	50.144	16.523	55.995	1.00	45.24
	432	CA	ILE	55	48.935	15.823	55.582	1.00	45.24
	433	CB	ILE	55	47.716	16.773	55.491	1.00	31.24
20	434	CG2	ILE	55	46.623	:5.157	54.647	1.00	31.24
	435	CG1	ILE	55	47.183	17.072	56.884	1.00	31.24
	436	CD1	ILE	55	45.969	17.961	56.867	1.00	31.24
	437	C	ILE	55	49.224	15.251	54.200	1.00	45.24
	438	O	ILE	55	49.262	15.977	53.201	1.00	45.24
25	439	N	VAL	56	49.437	13.942	54.160	1.00	82.87
	440	CA	VAL	56	49.730	13.244	52.923	1.00	82.87
	441	CB	VAL	56	50.831	12.192	53.155	1.00	72.67
	442	CG1	VAL	56	51.176	11.489	51.856	1.00	72.67
	443	CG2	VAL	56	52.057	12.862	53.731	1.00	72.67
30	444	C	VAL	56	48.467	12.569	52.398	1.00	82.87
	445	O	VAL	56	47.689	12.010	53.171	1.00	82.87
	446	N	ASN	57	48.268	12.636	51.085	1.00	59.63
	447	CA	ASN	57	47.099	12.059	50.438	1.00	59.63
	448	CB	ASN	57	47.302	10.562	50.308	1.00	98.65
35	449	CG	ASN	57	48.632	10.237	49.655	1.00	98.65
	450	OD1	ASN	57	48.980	10.808	48.609	1.00	98.65
	451	ND2	ASN	57	49.391	9.331	50.267	1.00	98.65
	452	C	ASN	57	45.864	12.412	51.249	1.00	59.63
	453	O	ASN	57	45.322	11.593	51.998	1.00	59.63
40	454	N	ALA	58	45.443	13.665	51.090	1.00	71.80
	455	CA	ALA	58	44.300	14.216	51.809	1.00	71.80
	456	CB	ALA	58	43.991	15.617	51.310	1.00	87.99
	457	C	ALA	58	43.073	13.358	51.690	1.00	71.80
	458	O	ALA	58	42.783	12.818	50.625	1.00	71.80
45	459	N	LYS	59	42.363	13.240	52.805	1.00	72.92
	460	CA	LYS	59	41.128	12.467	52.885	1.00	72.92
	461	CB	LYS	59	41.293	11.281	53.830	1.00	124.59
	462	CG	LYS	59	42.422	10.361	53.457	1.00	124.59
	463	CD	LYS	59	42.480	9.187	54.387	1.00	124.59
50	464	CE	LYS	59	43.356	8.128	53.783	1.00	124.59
	465	NZ	LYS	59	43.282	6.869	54.561	1.00	124.59
	466	C	LYS	59	40.082	13.397	53.457	1.00	72.92
	467	O	LYS	59	40.356	14.132	54.401	1.00	72.92
	468	N	PHE	60	38.887	13.381	52.897	1.00	56.87
55	469	CA	PHE	60	37.848	14.255	53.416	1.00	56.87
	470	CB	PHE	60	36.488	13.707	53.028	1.00	109.01
	471	CG	PHE	60	36.29?	13.613	51.562	1.00	109.01
	472	CD1	PHE	60	35.499	12.629	51.015	1.00	109.01
	473	CD2	PHE	60	36.957	14.485	50.714	1.00	109.01
60	474	CE1	PHE	60	35.336	12.536	49.634	1.00	109.01
	475	CE2	PHE	60	36.803	14.404	49.337	1.00	109.01
	476	CZ	PHE	60	36.006	13.414	48.793	1.00	109.01
	477	C	PHE	60	37.930	14.414	54.928	1.00	56.87
	478	O	PHE	60	37.628	15.478	55.475	1.00	56.87
65	479	N	GLU	61	38.352	13.350	55.598	1.00	64.50
	480	CA	GLU	61	38.460	13.336	57.054	1.00	64.50
	481	CB	GLU	61	38.892	11.953	57.542	1.00	154.96
	482	CG	GLU	61	37.855	10.870	57.334	1.00	154.96
	483	CD	GLU	61	37.517	10.655	55.871	1.00	154.96
70	484	OE1	GLU	61	38.443	10.355	55.087	1.00	154.96

	485	OE2	GLU	61	36.328	10.784	55.505	1.00	154.96
	486	C	GLU	61	39.436	14.356	57.576	1.00	64.50
	487	O	GLU	61	39.351	14.765	58.731	1.00	64.50
	488	N	ASP	62	40.371	14.745	56.713	1.00	71.49
5	489	CA	ASP	62	41.404	15.723	57.035	1.00	71.49
	490	CB	ASP	62	42.574	15.543	56.079	1.00	78.68
	491	CG	ASP	62	43.412	14.316	56.422	1.00	78.68
	492	OD1	ASP	62	43.641	14.093	57.639	1.00	78.68
	493	OD2	ASP	62	43.851	13.594	55.485	1.00	78.68
10	494	C	ASP	62	40.883	17.160	57.000	1.00	71.49
	495	O	ASP	62	41.574	18.102	57.400	1.00	71.49
	496	N	SER	63	39.654	17.326	56.523	1.00	52.56
	497	CA	SER	63	39.056	18.637	56.490	1.00	52.56
	498	CB	SER	63	37.722	18.586	55.773	1.00	54.10
15	499	OG	SER	63	37.914	18.110	54.456	1.00	54.10
	500	C	SER	63	38.850	19.020	57.936	1.00	52.56
	501	O	SER	63	39.035	18.202	58.826	1.00	52.56
	502	N	GLY	64	38.479	20.268	58.171	1.00	71.62
	503	CA	GLY	64	38.243	20.690	59.528	1.00	71.62
20	504	C	GLY	64	39.138	21.809	59.962	1.00	71.62
	505	O	GLY	64	39.954	22.299	59.196	1.00	71.62
	506	N	GLU	65	38.957	22.205	61.211	1.00	87.67
	507	CA	GLU	65	39.712	23.270	61.833	1.00	87.67
	508	CB	GLU	65	38.887	23.868	62.967	1.00	86.11
25	509	CG	GLU	65	39.602	24.889	63.834	1.00	86.11
	510	CD	GLU	65	38.934	25.056	65.194	1.00	86.11
	511	OE1	GLU	65	39.124	24.172	66.068	1.00	86.11
	512	OE2	GLU	65	38.210	26.059	65.386	1.00	86.11
	513	C	GLU	65	40.988	22.684	62.395	1.00	87.67
30	514	O	GLU	65	41.072	21.485	62.640	1.00	87.67
	515	N	TYR	66	41.980	23.539	62.598	1.00	99.15
	516	CA	TYR	66	43.258	23.129	63.151	1.00	99.15
	517	CB	TYR	66	44.246	22.786	62.044	1.00	44.24
	518	CG	TYR	66	44.017	21.547	61.224	1.00	44.24
35	519	CD1	TYR	66	43.042	21.512	60.225	1.00	44.24
	520	CE1	TYR	66	42.884	20.381	59.401	1.00	44.24
	521	CD2	TYR	66	44.838	20.429	61.399	1.00	44.24
	522	CE2	TYR	66	44.700	19.299	60.600	1.00	44.24
	523	CZ	TYR	66	43.719	19.270	59.596	1.00	44.24
40	524	OH	TYR	66	43.560	18.121	58.822	1.00	44.24
	525	C	TYR	66	43.848	24.303	63.935	1.00	99.15
	526	O	TYR	66	43.714	25.462	63.526	1.00	99.15
	527	N	LYS	67	44.502	23.996	65.052	1.00	76.23
	528	CA	LYS	67	45.158	25.008	65.883	1.00	76.23
45	529	CB	LYS	67	44.357	25.311	67.152	1.00	84.41
	530	CG	LYS	67	42.934	25.780	66.944	1.00	84.41
	531	CD	LYS	67	42.212	25.802	68.294	1.00	84.41
	532	CE	LYS	67	40.725	26.104	68.164	1.00	84.41
	533	NZ	LYS	67	40.042	25.844	69.456	1.00	84.41
50	534	C	LYS	67	46.477	24.393	66.303	1.00	76.23
	535	O	LYS	67	46.621	23.170	66.300	1.00	76.23
	536	N	CYS	68	47.449	25.235	66.625	1.00	101.62
	537	CA	CYS	68	48.729	24.757	67.110	1.00	101.62
	538	C	CYS	68	49.018	25.644	68.2‹3	1.00	101.62
55	539	O	CYS	68	48.586	26.797	68.3‹5	1.00	101.62
	540	CB	CYS	68	49.836	24.883	66.058	1.00	149.58
	541	SG	CYS	68	50.287	26.560	65.501	1.00	149.58
	542	N	GLN	69	49.716	25.099	69.281	1.00	93.84
	543	CA	GLN	69	50.045	25.874	70.458	1.00	93.84
60	544	CB	GLN	69	48.935	25.756	71.497	1.00	108.47
	545	CG	GLN	69	49.325	26.336	72.838	1.00	108.47
	546	CD	GLN	69	48.228	26.198	73.866	1.00	108.47
	547	OE1	GLN	69	47.421	25.266	73.801	1.00	108.47
	548	NE2	GLN	69	48.197	27.116	74.835	1.00	108.47
65	549	C	GLN	69	51.362	25.450	71.087	1.00	93.84
	550	O	GLN	69	51.813	24.310	70.919	1.00	93.84
	551	N	HIS	70	51.986	26.399	71.778	1.00	149.64
	552	CA	HIS	70	53.221	26.162	72.504	1.00	149.64
	553	CB	HIS	70	54.272	27.216	72.161	1.00	188.52
70	554	CG	HIS	70	54.952	26.965	70.857	1.00	1‹9.52

	555	CD2	HIS	70	54.804	25.981	69.944	1.00	188.52
	556	ND1	HIS	70	55.951	27.788	70.358	1.00	188.52
	557	CE1	HIS	70	56.375	27.316	69.210	1.00	188.52
	558	NE2	HIS	70	55.693	26.212	68.928	1.00	188.52
5	559	C	HIS	70	52.788	26.284	73.952	1.00	149.64
	560	O	HIS	70	52.566	27.385	74.454	1.00	149.64
	561	N	GLN	71	52.642	25.132	74.599	1.00	126.80
	562	CA	GLN	71	52.191	25.045	75.981	1.00	126.80
	563	CB	GLN	71	52.974	23.964	76.726	1.00	175.94
10	564	CG	GLN	71	52.367	23.589	78.072	1.00	175.94
	565	CD	GLN	71	53.119	22.461	78.752	1.00	175.94
	566	OE1	GLN	71	54.130	21.984	78.241	1.00	175.94
	567	NE2	GLN	71	52.631	22.031	79.909	1.00	175.94
	568	C	GLN	71	52.267	26.359	76.745	1.00	126.80
15	569	O	GLN	71	53.343	26.934	76.927	1.00	126.80
	570	N	GLN	72	51.096	26.825	77.169	1.00	138.09
	571	CA	GLN	72	50.936	28.060	77.933	1.00	138.09
	572	CB	GLN	72	51.762	28.017	79.214	1.00	197.82
	573	CG	GLN	72	51.264	27.031	80.242	1.00	197.82
20	574	CD	GLN	72	49.767	27.138	80.538	1.00	197.82
	575	OE1	GLN	72	49.158	28.202	80.397	1.00	197.82
	576	NE2	GLN	72	49.175	26.028	80.973	1.00	197.82
	577	C	GLN	72	51.252	29.347	77.196	1.00	138.09
	578	O	GLN	72	51.503	30.377	77.821	1.00	138.09
25	579	N	VAL	73	51.243	29.291	75.871	1.00	127.03
	580	CA	VAL	73	51.505	30.477	75.070	1.00	127.03
	581	CB	VAL	73	52.817	30.340	74.250	1.00	90.79
	582	CG1	VAL	73	53.197	31.683	73.626	1.00	90.79
	583	CG2	VAL	73	53.943	29.826	75.148	1.00	90.79
30	584	C	VAL	73	50.314	30.625	74.134	1.00	127.03
	585	O	VAL	73	50.467	30.866	72.936	1.00	127.03
	586	N	ASN	74	49.119	30.457	74.693	1.00	129.72
	587	CA	ASN	74	47.890	30.577	73.920	1.00	129.72
	588	CB	ASN	74	47.721	31.993	73.390	1.00	137.31
35	589	CG	ASN	74	47.576	33.011	74.476	1.00	137.31
	590	OD1	ASN	74	48.512	33.785	74.713	1.00	137.31
	591	ND2	ASN	74	46.400	33.015	75.123	1.00	137.31
	592	C	ASN	74	47.820	29.655	72.709	1.00	129.72
	593	O	ASN	74	48.836	29.209	72.176	1.00	129.72
40	594	N	GLU	75	46.600	29.404	72.254	1.00	128.29
	595	CA	GLU	75	46.377	28.580	71.080	1.00	128.29
	596	CB	GLU	75	44.998	27.934	71.175	1.00	132.07
	597	CG	GLU	75	44.672	27.459	72.584	1.00	132.07
	598	CD	GLU	75	43.266	26.922	72.700	1.00	132.07
45	599	OE1	GLU	75	42.439	27.252	71.821	1.00	132.07
	600	OE2	GLU	75	42.989	26.185	73.673	1.00	132.07
	601	C	GLU	75	46.446	29.547	69.897	1.00	128.29
	602	O	GLU	75	46.432	30.757	70.089	1.00	128.29
	603	N	SER	76	46.545	29.033	68.681	1.00	77.19
50	604	CA	SER	76	46.595	29.901	67.506	1.00	77.19
	605	CB	SER	76	47.321	29.207	66.363	1.00	54.46
	606	OG	SER	76	46.418	28.351	65.649	1.00	54.46
	607	C	SER	76	45.175	30.169	67.033	1.00	77.19
	608	O	SER	76	44.208	29.659	67.603	1.00	77.19
55	609	N	GLU	77	45.038	30.966	65.983	1.00	74.40
	610	CA	GLU	77	43.711	31.198	65.444	1.00	74.40
	611	CB	GLU	77	43.652	32.492	64.632	1.00	153.94
	612	CG	GLU	77	43.693	33.746	65.491	1.00	153.94
	613	CD	GLU	77	42.624	33.749	66.578	1.00	153.94
60	614	OE1	GLU	77	41.418	33.712	66.237	1.00	153.94
	615	OE2	GLU	77	42.992	33.787	67.775	1.00	153.94
	616	C	GLU	77	43.460	29.998	64.558	1.00	74.40
	617	O	GLU	77	44.375	29.495	63.913	1.00	74.40
	618	N	PRO	78	42.215	29.512	64.527	1.00	88.95
65	619	CD	PRO	78	41.068	29.938	65.344	1.00	122.79
	620	CA	PRO	78	41.857	28.352	63.712	1.00	88.95
	621	CB	PRO	78	40.385	28.138	64.046	1.00	122.79
	622	CG	PRO	78	40.268	28.670	65.428	1.00	122.79
	623	C	PRO	78	42.061	28.542	62.221	1.00	88.95
70	624	O	PRO	78	41.901	29.640	61.688	1.00	88.95

	625	N	VAL	79	42.415	27.447	61.560	1.00	101.27
	626	CA	VAL	79	42.604	27.427	60.119	1.00	101.27
	627	CB	VAL	79	44.042	27.114	59.735	1.00	79.48
	628	CG1	VAL	79	44.177	27.097	58.226	1.00	79.48
5	629	CG2	VAL	79	44.962	28.130	60.341	1.00	79.48
	630	C	VAL	79	41.727	26.304	59.592	1.00	101.27
	631	O	VAL	79	41.846	25.155	60.025	1.00	101.27
	632	N	TYR	80	40.851	26.629	58.655	1.00	55.37
	633	CA	TYR	80	39.973	25.618	58.115	1.00	55.37
10	634	CB	TYR	80	38.551	26.145	58.016	1.00	122.28
	635	CG	TYR	80	38.004	26.497	59.364	1.00	122.28
	636	CD1	TYR	80	38.278	27.733	59.942	1.00	122.28
	637	CE1	TYR	80	37.817	28.049	61.208	1.00	122.28
	638	CD2	TYR	80	37.250	25.577	60.088	1.00	122.28
15	639	CE2	TYR	80	36.782	25.877	61.357	1.00	122.28
	640	CZ	TYR	80	37.069	27.117	61.915	1.00	122.28
	641	OH	TYR	80	36.615	27.424	63.180	1.00	122.28
	642	C	TYR	80	40.390	25.066	56.779	1.00	55.37
	643	O	TYR	80	40.474	25.780	55.795	1.00	55.37
20	644	N	LEU	81	40.627	23.768	56.765	1.00	67.93
	645	CA	LEU	81	41.026	23.065	55.578	1.00	67.93
	646	CB	LEU	81	42.016	22.014	55.982	1.00	70.09
	647	CG	LEU	81	42.558	21.223	54.819	1.00	70.09
	648	CD1	LEU	81	43.387	22.150	53.967	1.00	70.09
25	649	CD2	LEU	81	43.411	20.066	55.338	1.00	70.09
	650	C	LEU	81	39.731	22.405	55.006	1.00	67.93
	651	O	LEU	81	38.856	22.098	55.763	1.00	67.93
	652	N	GLU	82	39.732	22.188	53.691	1.00	70.25
	653	CA	GLU	82	38.569	21.530	53.079	1.00	70.25
30	654	CB	GLU	82	37.486	22.562	52.737	1.00	131.12
	655	CG	GLU	82	36.199	21.935	52.234	1.00	131.12
	656	CD	GLU	82	34.994	22.847	52.359	1.00	131.12
	657	OE1	GLU	82	35.091	24.023	51.958	1.00	131.12
	658	OE2	GLU	82	33.940	22.384	52.847	1.00	131.12
35	659	C	GLU	82	38.957	20.709	51.843	1.00	70.25
	660	O	GLU	82	39.425	21.261	50.850	1.00	70.25
	661	N	VAL	83	38.769	19.386	51.918	1.00	52.36
	662	CA	VAL	83	39.106	18.469	50.815	1.00	52.36
	663	CB	VAL	83	39.452	17.094	51.350	1.00	43.44
40	664	CG1	VAL	83	40.082	16.245	50.244	1.00	43.44
	665	CG2	VAL	83	40.359	17.241	52.544	1.00	43.44
	666	C	VAL	83	37.995	18.302	49.768	1.00	52.36
	667	O	VAL	83	36.852	18.022	50.105	1.00	52.36
	668	N	PHE	84	38.342	18.479	48.498	1.00	63.83
45	669	CA	PHE	84	37.368	18.369	47.426	1.00	63.83
	670	CB	PHE	84	37.359	19.633	46.562	1.00	62.38
	671	CG	PHE	84	36.918	20.841	47.294	1.00	62.38
	672	CD1	PHE	84	37.692	21.345	48.329	1.00	62.38
	673	CD2	PHE	84	35.680	21.429	47.020	1.00	62.38
50	674	CE1	PHE	84	37.244	22.418	49.092	1.00	62.38
	675	CE2	PHE	84	35.223	22.506	47.780	1.00	62.38
	676	CZ	PHE	84	36.007	22.998	48.823	1.00	62.38
	677	C	PHE	84	37.606	17.175	46.527	1.00	63.83
	678	O	PHE	84	38.619	16.477	46.630	1.00	63.83
55	679	N	SER	85	36.635	16.952	45.650	1.00	70.22
	680	CA	SER	85	36.663	15.891	44.671	1.00	70.22
	681	CB	SER	85	36.006	14.615	45.197	1.00	107.42
	682	OG	SER	85	36.099	13.567	44.235	1.00	107.42
	683	C	SER	85	35.833	16.465	43.552	1.00	70.22
60	684	O	SER	85	34.608	16.501	43.625	1.00	70.22
	685	N	ASP	86	36.513	16.953	42.528	1.00	30.45
	686	CA	ASP	86	35.835	17.517	41.391	1.00	30.45
	687	CB	ASP	86	35.151	18.796	41.799	1.00	66.75
	688	CG	ASP	86	34.005	19.121	40.908	1.00	66.75
65	689	OD1	ASP	86	34.186	19.182	39.664	1.00	66.75
	690	OD2	ASP	86	32.909	19.311	41.455	1.00	66.75
	691	C	ASP	86	36.876	17.768	40.303	1.00	30.45
	692	O	ASP	86	38.074	17.603	40.551	1.00	30.45
	693	N	TRP	87	36.427	18.122	39.101	1.00	54.88
70	694	CA	TRP	87	37.329	18.392	37.986	1.00	54.88

	695	CB	TRP	87	36.541	18.398	36.686	1.00	120.63
	696	CG	TRP	87	36.228	17.051	36.187	1.00	120.63
	697	CD2	TRP	87	35.123	16.242	36.559	1.00	120.63
	698	CE2	TRP	87	35.205	15.040	35.822	1.00	120.63
5	699	CE3	TRP	87	34.043	16.411	37.446	1.00	120.63
	700	CD1	TRP	87	36.936	16.335	35.269	1.00	120.63
	701	NE1	TRP	87	36.336	15.125	35.036	1.00	120.63
	702	CZ2	TRP	87	34.277	14.011	35.939	1.00	120.63
	703	CZ3	TRP	87	33.109	15.387	37.568	1.00	120.63
10	704	CH2	TRP	87	33.231	14.202	36.813	1.00	120.63
	705	C	TRP	87	38.051	19.726	38.150	1.00	54.88
	706	O	TRP	87	39.248	19.818	37.884	1.00	54.88
	707	N	LEU	88	37.307	20.751	38.578	1.00	42.94
	708	CA	LEU	88	37.831	22.113	38.806	1.00	42.94
15	709	CB	LEU	88	37.131	23.157	37.946	1.00	57.40
	710	CG	LEU	88	37.526	23.193	36.485	1.00	57.40
	711	CD1	LEU	88	36.761	24.330	35.822	1.00	57.40
	712	CD2	LEU	88	39.030	23.370	36.354	1.00	57.40
	713	C	LEU	88	37.671	22.549	40.235	1.00	42.94
20	714	O	LEU	88	36.666	22.301	40.870	1.00	42.94
	715	N	LEU	89	38.681	23.225	40.733	1.00	58.27
	716	CA	LEU	89	38.667	23.700	42.085	1.00	58.27
	717	CB	LEU	89	39.556	22.835	42.951	1.00	5.00
	718	CG	LEU	89	39.739	23.331	44.403	1.00	5.00
25	719	CD1	LEU	89	38.371	23.632	45.112	1.00	5.00
	720	CD2	LEU	89	40.628	22.281	45.195	1.00	5.00
	721	C	LEU	89	39.237	25.082	42.056	1.00	58.27
	722	O	LEU	89	40.346	25.279	41.555	1.00	58.27
	723	N	LEU	90	38.486	26.043	42.582	1.00	24.40
30	724	CA	LEU	90	38.995	27.407	42.636	1.00	24.40
	725	CB	LEU	90	37.861	28.425	42.585	1.00	63.96
	726	CG	LEU	90	38.331	29.867	42.711	1.00	63.96
	727	CD1	LEU	90	39.284	30.173	41.570	1.00	63.96
	728	CD2	LEU	90	37.134	30.803	42.692	1.00	63.96
35	729	C	LEU	90	39.702	27.535	43.969	1.00	24.40
	730	O	LEU	90	39.057	27.496	45.000	1.00	24.40
	731	N	GLN	91	41.017	27.690	43.970	1.00	52.44
	732	CA	GLN	91	41.721	27.825	45.234	1.00	52.44
	733	CB	GLN	91	43.018	27.058	45.151	1.00	32.27
40	734	CG	GLN	91	42.820	25.718	44.534	1.00	32.27
	735	CD	GLN	91	44.020	24.841	44.727	1.00	32.27
	736	OE1	GLN	91	45.010	24.901	43.957	1.00	32.27
	737	NE2	GLN	91	43.962	24.016	45.788	1.00	32.27
	738	C	GLN	91	41.981	29.299	45.554	1.00	52.44
45	739	O	GLN	91	42.060	30.142	44.657	1.00	52.44
	740	N	ALA	92	42.075	29.633	46.831	1.00	55.47
	741	CA	ALA	92	42.345	31.018	47.175	1.00	55.47
	742	CB	ALA	92	41.076	31.735	47.638	1.00	37.36
	743	C	ALA	92	43.381	31.100	48.246	1.00	55.47
50	744	O	ALA	92	43.384	30.316	49.183	1.00	55.47
	745	N	SER	93	44.263	32.064	48.077	1.00	51.36
	746	CA	SER	93	45.329	32.345	49.008	1.00	51.36
	747	CB	SER	93	45.997	33.647	48.583	1.00	54.66
	748	OG	SER	93	45.009	34.650	48.346	1.00	54.66
55	749	C	SER	93	44.690	32.509	50.378	1.00	51.36
	750	O	SER	93	45.238	32.104	51.395	1.00	51.36
	751	N	ALA	94	43.521	33.124	50.397	1.00	46.22
	752	CA	ALA	94	42.822	33.313	51.645	1.00	46.22
	753	CB	ALA	94	43.522	34.352	52.496	1.00	74.92
60	754	C	ALA	94	41.393	33.723	51.340	1.00	46.22
	755	O	ALA	94	41.111	34.357	50.317	1.00	46.22
	756	N	GLU	95	40.489	33.326	52.231	1.00	89.58
	757	CA	GLU	95	39.074	33.605	52.065	1.00	89.58
	758	CB	GLU	95	38.283	32.448	52.662	1.00	145.77
65	759	CG	GLU	95	38.549	31.139	51.938	1.00	145.77
	760	CD	GLU	95	37.950	29.953	52.650	1.00	145.77
	761	OE1	GLU	95	38.060	28.826	52.118	1.00	145.77
	762	OE2	GLU	95	37.373	30.145	53.742	1.00	145.77
	763	C	GLU	95	38.662	34.938	52.678	1.00	89.58
70	764	O	GLU	95	37.681	35.546	52.289	1.00	89.58

	765	N	VAL	96	39.453	35.379	53.644	1.00	75.49
	766	CA	VAL	96	39.233	36.643	54.322	1.00	75.49
	767	CB	VAL	96	38.995	36.436	55.819	1.00	87.57
	768	CG1	VAL	96	38.710	37.771	56.480	1.00	87.57
5	769	CG2	VAL	96	37.847	35.467	56.032	1.00	87.57
	770	C	VAL	96	40.537	37.402	54.128	1.00	75.49
	771	O	VAL	96	41.578	37.016	54.665	1.00	75.49
	772	N	VAL	97	40.482	38.471	53.345	1.00	96.50
	773	CA	VAL	97	41.670	39.254	53.066	1.00	96.50
10	774	CB	VAL	97	41.929	39.335	51.553	1.00	66.57
	775	CG1	VAL	97	42.920	40.443	51.259	1.00	66.57
	776	CG2	VAL	97	42.472	38.004	51.049	1.00	66.57
	777	C	VAL	97	41.598	40.665	53.613	1.00	96.50
	778	O	VAL	97	40.583	41.352	53.473	1.00	96.50
15	779	N	MET	98	42.693	41.088	54.237	1.00	97.55
	780	CA	MET	98	42.784	42.425	54.799	1.00	97.55
	781	CB	MET	98	43.870	42.482	55.887	1.00	148.78
	782	CG	MET	98	43.567	41.601	57.108	1.00	148.78
	783	SD	MET	98	44.803	41.635	58.454	1.00	148.78
20	784	CE	MET	98	45.665	40.108	58.182	1.00	148.78
	785	C	MET	98	43.098	43.411	53.682	1.00	97.55
	786	O	MET	98	44.143	43.318	53.034	1.00	97.55
	787	N	GLU	99	42.161	44.329	53.455	1.00	85.18
	788	CA	GLU	99	42.265	45.380	52.450	1.00	85.18
25	789	CB	GLU	99	41.565	46.635	52.988	1.00	186.55
	790	CG	GLU	99	41.620	47.868	52.109	1.00	186.55
	791	CD	GLU	99	40.716	48.978	52.629	1.00	186.55
	792	OE1	GLU	99	40.827	49.337	53.823	1.00	186.55
	793	OE2	GLU	99	39.894	49.490	51.839	1.00	186.55
30	794	C	GLU	99	43.724	45.677	52.137	1.00	85.18
	795	O	GLU	99	44.605	45.506	52.990	1.00	85.18
	796	N	GLY	100	43.991	46.106	50.909	1.00	64.51
	797	CA	GLY	100	45.362	46.432	50.549	1.00	64.51
	798	C	GLY	100	46.371	45.293	50.459	1.00	64.51
35	799	O	GLY	100	47.508	45.528	50.054	1.00	64.51
	800	N	GLN	101	45.987	44.075	50.839	1.00	91.02
	801	CA	GLN	101	46.896	42.930	50.742	1.00	91.02
	802	CB	GLN	101	46.631	41.933	51.875	1.00	93.41
	803	CG	GLN	101	47.181	42.383	53.207	1.00	93.41
40	804	CD	GLN	101	48.671	42.663	53.133	1.00	93.41
	805	OE1	GLN	101	49.117	43.530	52.384	1.00	93.41
	806	NE2	GLN	101	49.448	41.926	53.906	1.00	93.41
	807	C	GLN	101	46.716	42.260	49.373	1.00	91.02
	808	O	GLN	101	45.909	42.712	48.567	1.00	91.02
45	809	N	PRO	102	47.484	41.195	49.078	1.00	67.73
	810	CD	PRO	102	48.769	40.802	49.675	1.00	29.55
	811	CA	PRO	102	47.324	40.547	47.778	1.00	67.73
	812	CB	PRO	102	48.730	40.145	47.432	1.00	29.55
	813	CG	PRO	102	49.248	39.718	48.721	1.00	29.55
50	814	C	PRO	102	46.398	39.353	47.784	1.00	67.73
	815	O	PRO	102	46.385	38.564	48.719	1.00	67.73
	816	N	LEU	103	45.636	39.227	46.707	1.00	40.45
	817	CA	LEU	103	44.688	38.154	46.552	1.00	40.45
	818	CB	LEU	103	43.308	38.743	46.277	1.00	52.62
55	819	CG	LEU	103	42.141	37.774	46.464	1.00	52.62
	820	CD1	LEU	103	42.345	36.942	47.721	1.00	52.62
	821	CD2	LEU	103	40.852	38.574	46.533	1.00	52.62
	822	C	LEU	103	45.115	37.227	45.415	1.00	40.45
	823	O	LEU	103	45.314	37.665	44.280	1.00	40.45
60	824	N	PHE	104	45.274	35.945	45.739	1.00	56.34
	825	CA	PHE	104	45.680	34.942	44.762	1.00	56.34
	826	CB	PHE	104	46.898	34.159	45.251	1.00	133.82
	827	CG	PHE	104	48.053	35.016	45.592	1.00	133.82
	828	CD1	PHE	104	48.298	35.367	46.905	1.00	133.82
65	829	CD2	PHE	104	48.870	35.528	44.594	1.00	133.82
	830	CE1	PHE	104	49.344	36.223	47.229	1.00	133.82
	831	CE2	PHE	104	49.924	36.389	44.906	1.00	133.82
	832	CZ	PHE	104	50.161	36.738	46.224	1.00	133.82
	833	C	PHE	104	44.570	33.958	44.477	1.00	56.34
70	834	O	PHE	104	43.923	33.468	45.388	1.00	56.34

	835	N	LEU	105	44.363	33.668	43.202	1.00	51.84
	836	CA	LEU	105	43.341	32.730	42.792	1.00	51.84
	837	CB	LEU	105	42.199	33.440	42.086	1.00	27.36
	838	CG	LEU	105	41.385	34.348	42.989	1.00	27.36
5	839	CD1	LEU	105	40.132	34.710	42.214	1.00	27.36
	840	CD2	LEU	105	40.988	33.638	44.293	1.00	27.36
	841	C	LEU	105	43.897	31.690	41.857	1.00	51.84
	842	O	LEU	105	44.802	31.948	41.068	1.00	51.84
	843	N	ARG	106	43.337	30.499	41.929	1.00	60.02
10	844	CA	ARG	106	43.820	29.474	41.063	1.00	60.02
	845	CB	ARG	106	44.949	28.740	41.722	1.00	28.53
	846	CG	ARG	106	45.476	27.618	40.886	1.00	28.53
	847	CD	ARG	106	46.314	26.830	41.814	1.00	28.53
	848	NE	ARG	106	47.260	25.934	41.174	1.00	28.53
15	849	CZ	ARG	106	47.904	25.010	41.864	1.00	28.53
	850	NH1	ARG	106	47.633	24.925	43.173	1.00	28.53
	851	NH2	ARG	106	48.819	24.231	41.267	1.00	28.53
	852	C	ARG	106	42.775	28.496	40.663	1.00	60.02
	853	O	ARG	106	42.121	27.884	41.498	1.00	60.02
20	854	N	CYS	107	42.625	28.378	39.353	1.00	30.47
	855	CA	CYS	107	41.692	27.449	38.763	1.00	30.47
	856	C	CYS	107	42.484	26.168	38.645	1.00	30.47
	857	O	CYS	107	43.098	25.892	37.607	1.00	30.47
	858	CB	CYS	107	41.261	27.937	37.398	1.00	52.55
25	859	SG	CYS	107	39.630	27.258	36.984	1.00	52.55
	860	N	HIS	108	42.476	25.399	39.733	1.00	44.34
	861	CA	HIS	108	43.224	24.162	39.808	1.00	44.34
	862	CB	HIS	108	43.644	23.916	41.229	1.00	41.81
	863	CG	HIS	108	44.610	22.800	41.351	1.00	41.81
30	864	CD2	HIS	108	44.648	21.734	42.178	1.00	41.81
	865	ND1	HIS	108	45.701	22.686	40.519	1.00	41.81
	866	CE1	HIS	108	46.370	21.595	40.832	1.00	41.81
	867	NE2	HIS	108	45.753	20.999	41.835	1.00	41.81
	868	C	HIS	108	42.526	22.934	39.310	1.00	44.34
35	869	O	HIS	108	41.515	22.530	39.838	1.00	44.34
	870	N	GLY	109	43.084	22.315	38.293	1.00	45.07
	871	CA	GLY	109	42.461	21.121	37.772	1.00	45.07
	872	C	GLY	109	42.909	19.890	38.534	1.00	45.07
	873	O	GLY	109	44.015	19.831	39.097	1.00	45.07
40	874	N	TRP	110	42.026	18.902	38.565	1.00	46.18
	875	CA	TRP	110	42.293	17.641	39.239	1.00	46.18
	876	CB	TRP	110	41.156	16.653	38.932	1.00	36.88
	877	CG	TRP	110	41.347	15.329	39.576	1.00	36.88
	878	CD2	TRP	110	41.040	15.001	40.923	1.00	36.88
45	879	CE2	TRP	110	41.526	13.697	41.176	1.00	36.88
	880	CE3	TRP	110	40.388	15.690	41.973	1.00	36.88
	881	CD1	TRP	110	41.989	14.231	39.047	1.00	36.88
	882	NE1	TRP	110	42.110	13.251	39.999	1.00	36.88
	883	CZ2	TRP	110	41.408	13.055	42.401	1.00	36.88
50	884	CZ3	TRP	110	40.264	15.061	43.204	1.00	36.88
	885	CH2	TRP	110	40.773	13.748	43.408	1.00	36.88
	886	C	TRP	110	43.615	17.100	38.726	1.00	46.18
	887	O	TRP	110	43.910	17.235	37.539	1.00	46.18
	888	N	ARG	111	44.416	16.510	39.609	1.00	63.08
55	889	CA	ARG	111	45.704	15.952	39.200	1.00	63.08
	890	CB	ARG	111	45.488	14.690	38.373	1.00	97.86
	891	CG	ARG	111	44.790	13.594	39.132	1.00	97.86
	892	CD	ARG	111	45.652	13.108	40.265	1.00	97.86
	893	NE	ARG	111	46.850	12.447	39.758	1.00	97.96
60	894	CZ	ARG	111	47.845	12.019	40.528	1.00	97.96
	895	NH1	ARG	111	47.785	12.190	41.846	1.00	97.96
	896	NH2	ARG	111	48.894	11.413	39.982	1.00	97.96
	897	C	ARG	111	46.465	16.961	38.358	1.00	63.08
	898	O	ARG	111	47.152	16.596	37.406	1.00	63.08
65	899	N	ASN	112	46.324	18.237	38.685	1.00	111.35
	900	CA	ASN	112	47.011	19.247	37.914	1.00	111.35
	901	CB	ASN	112	48.500	19.213	38.245	1.00	81.63
	902	CG	ASN	112	48.814	19.880	39.568	1.00	81.63
	903	OD1	ASN	112	48.719	21.101	39.701	1.00	81.63
70	904	ND2	ASN	112	49.182	19.082	40.556	1.00	81.63

	905	C	ASN	112	46.791	18.987	36.424	1.00	111.35
	906	O	ASN	112	47.744	18.946	35.648	1.00	111.35
	907	N	TRP	113	45.540	18.783	36.027	1.00	91.49
	908	CA	TRP	113	45.258	18.560	34.623	1.00	91.49
5	909	CB	TRP	113	43.894	17.929	34.393	1.00	88.74
	910	CG	TRP	113	43.813	16.506	34.706	1.00	88.74
	911	CD2	TRP	113	42.611	15.767	34.927	1.00	88.74
	912	CE2	TRP	113	42.998	14.439	35.200	1.00	88.74
	913	CE3	TRP	113	41.258	16.105	34.927	1.00	88.74
10	914	CD1	TRP	113	44.845	15.625	34.837	1.00	88.74
	915	NE1	TRP	113	44.354	14.376	35.137	1.00	88.74
	916	CZ2	TRP	113	42.063	13.451	35.465	1.00	88.74
	917	CZ3	TRP	113	40.338	15.124	35.188	1.00	88.74
	918	CH2	TRP	113	40.742	13.810	35.459	1.00	88.74
15	919	C	TRP	113	45.255	19.871	33.895	1.00	91.49
	920	O	TRP	113	44.941	20.922	34.463	1.00	91.49
	921	N	ASP	114	45.567	19.780	32.611	1.00	60.02
	922	CA	ASP	114	45.599	20.940	31.755	1.00	60.02
	923	CB	ASP	114	46.201	20.569	30.390	1.00	89.00
20	924	CG	ASP	114	47.637	20.066	30.498	1.00	89.00
	925	OD1	ASP	114	48.360	20.492	31.430	1.00	89.00
	926	OD2	ASP	114	48.053	19.254	29.643	1.00	89.00
	927	C	ASP	114	44.210	21.555	31.585	1.00	60.02
	928	O	ASP	114	43.248	20.897	31.224	1.00	60.02
25	929	N	VAL	115	44.104	22.832	31.879	1.00	103.64
	930	CA	VAL	115	42.836	23.482	31.712	1.00	103.64
	931	CB	VAL	115	42.283	23.916	33.063	1.00	73.31
	932	CG1	VAL	115	40.951	24.620	32.902	1.00	73.31
	933	CG2	VAL	115	42.153	22.682	33.943	1.00	73.31
30	934	C	VAL	115	43.127	24.647	30.805	1.00	103.64
	935	O	VAL	115	44.162	25.304	30.904	1.00	103.64
	936	N	TYR	116	42.232	24.861	29.868	1.00	59.95
	937	CA	TYR	116	42.415	25.932	28.943	1.00	59.95
35	938	CB	TYR	116	42.503	25.377	27.529	1.00	98.72
	939	CG	TYR	116	43.712	24.492	27.362	1.00	98.72
	940	CD1	TYR	116	43.675	23.152	27.726	1.00	98.72
	941	CE1	TYR	116	44.815	22.360	27.650	1.00	98.72
	942	CD2	TYR	116	44.922	25.017	26.914	1.00	98.72
40	943	CE2	TYR	116	46.067	24.233	26.839	1.00	98.72
	944	CZ	TYR	116	46.008	22.908	27.207	1.00	98.72
	945	OH	TYR	116	47.147	22.132	27.144	1.00	98.72
	946	C	TYR	116	41.271	26.898	29.083	1.00	59.95
	947	O	TYR	116	40.499	26.821	30.047	1.00	59.95
45	948	N	LYS	117	41.176	27.814	28.127	1.00	66.79
	949	CA	LYS	117	40.132	28.813	28.132	1.00	66.79
	950	CB	LYS	117	38.946	28.332	27.295	1.00	151.68
	951	CG	LYS	117	37.902	29.406	27.008	1.00	151.68
	952	CD	LYS	117	38.475	30.515	26.129	1.00	151.68
50	953	CE	LYS	117	37.451	31.604	25.848	1.00	151.68
	954	NZ	LYS	117	38.062	32.685	25.034	1.00	151.68
	955	C	LYS	117	39.676	29.122	29.559	1.00	66.79
	956	O	LYS	117	38.472	29.233	29.810	1.00	66.79
	957	N	VAL	118	40.622	29.256	30.495	1.00	43.61
55	958	CA	VAL	118	40.243	29.564	31.879	1.00	43.61
	959	CB	VAL	118	41.429	29.461	32.852	1.00	34.30
	960	CG1	VAL	118	40.912	29.485	34.289	1.00	34.30
	961	CG2	VAL	118	42.246	28.215	32.562	1.00	34.30
	962	C	VAL	118	39.657	30.977	31.998	1.00	43.61
60	963	O	VAL	118	40.002	31.881	31.235	1.00	43.61
	964	N	ILE	119	38.772	31.168	32.963	1.00	47.57
	965	CA	ILE	119	38.135	32.458	33.140	1.00	47.57
	966	CB	ILE	119	36.895	32.621	32.203	1.00	48.87
	967	CG2	ILE	119	36.185	33.914	32.512	1.00	48.87
65	968	CG1	ILE	119	37.317	32.657	30.730	1.00	48.87
	969	CD1	ILE	119	36.187	33.009	29.752	1.00	48.87
	970	C	ILE	119	37.651	32.620	34.567	1.00	47.57
	971	O	ILE	119	36.846	31.827	35.052	1.00	47.57
	972	N	TYR	120	38.125	33.645	35.256	1.00	51.27
70	973	CA	TYR	120	37.647	33.835	36.608	1.00	51.27
	974	CB	TYR	120	38.727	34.342	37.510	1.00	24.86

	975	CG	TYR	120	39.921	33.471	37.546	1.00	24.86
	976	CD1	TYR	120	40.623	33.174	36.393	1.00	24.86
	977	CE1	TYR	120	41.794	32.429	36.448	1.00	24.86
	978	CD2	TYR	120	40.397	33.004	38.754	1.00	24.86
5	979	CE2	TYR	120	41.562	32.258	38.832	1.00	24.86
	980	CZ	TYR	120	42.260	31.972	37.681	1.00	24.86
	981	OH	TYR	120	43.423	31.233	37.816	1.00	24.86
	982	C	TYR	120	36.531	34.832	36.621	1.00	51.27
	983	O	TYR	120	36.486	35.751	35.802	1.00	51.27
10	984	N	TYR	121	35.645	34.659	37.584	1.00	57.39
	985	CA	TYR	121	34.506	35.530	37.701	1.00	57.39
	986	CB	TYR	121	33.215	34.815	37.266	1.00	81.52
	987	CG	TYR	121	33.180	34.361	35.836	1.00	81.52
	988	CD1	TYR	121	33.923	33.263	35.423	1.00	81.52
15	989	CE1	TYR	121	33.918	32.846	34.105	1.00	81.52
	990	CD2	TYR	121	32.419	35.042	34.889	1.00	81.52
	991	CE2	TYR	121	32.407	34.642	33.554	1.00	81.52
	992	CZ	TYR	121	33.163	33.537	33.171	1.00	81.52
	993	OH	TYR	121	33.195	33.117	31.859	1.00	81.52
20	994	C	TYR	121	34.315	35.966	39.124	1.00	57.39
	995	O	TYR	121	34.522	35.184	40.054	1.00	57.39
	996	N	LYS	122	33.907	37.218	39.282	1.00	81.15
	997	CA	LYS	122	33.595	37.748	40.589	1.00	81.15
	998	CB	LYS	122	34.433	38.961	40.948	1.00	110.18
25	999	CG	LYS	122	34.253	39.334	42.403	1.00	110.18
	1000	CD	LYS	122	34.827	40.684	42.722	1.00	110.18
	1001	CE	LYS	122	33.834	41.772	42.392	1.00	110.18
	1002	NZ	LYS	122	34.358	43.095	42.796	1.00	110.18
	1003	C	LYS	122	32.159	38.177	40.444	1.00	81.15
30	1004	O	LYS	122	31.834	39.050	39.642	1.00	81.15
	1005	N	ASP	123	31.289	37.539	41.209	1.00	100.05
	1006	CA	ASP	123	29.875	37.861	41.159	1.00	100.05
	1007	CB	ASP	123	29.640	39.238	41.781	1.00	124.27
	1008	CG	ASP	123	30.336	39.380	43.124	1.00	124.27
35	1009	OD1	ASP	123	30.145	38.499	43.991	1.00	124.27
	1010	OD2	ASP	123	31.075	40.370	43.309	1.00	124.27
	1011	C	ASP	123	29.401	37.816	39.720	1.00	100.05
	1012	O	ASP	123	29.086	38.844	39.125	1.00	100.05
	1013	N	GLY	124	29.407	36.612	39.157	1.00	103.70
40	1014	CA	GLY	124	28.929	36.423	37.803	1.00	103.70
	1015	C	GLY	124	29.750	37.084	36.729	1.00	103.70
	1016	O	GLY	124	29.983	36.517	35.684	1.00	103.70
	1017	N	GLU	125	30.231	38.285	37.011	1.00	86.80
	1018	CA	GLU	125	31.033	39.025	36.046	1.00	86.80
45	1019	CB	GLU	125	30.929	40.506	36.309	1.00	167.98
	1020	CG	GLU	125	29.523	41.030	36.184	1.00	167.98
	1021	CD	GLU	125	29.407	42.485	36.603	1.00	167.98
	1022	OE1	GLU	125	30.209	43.326	36.133	1.00	167.98
	1023	OE2	GLU	125	28.505	42.791	37.413	1.00	167.98
50	1024	C	GLU	125	32.515	38.651	35.940	1.00	86.80
	1025	O	GLU	125	33.206	38.440	36.952	1.00	86.80
	1026	N	ALA	126	33.003	38.614	34.700	1.00	117.82
	1027	CA	ALA	126	34.395	38.279	34.411	1.00	117.82
	1028	CB	ALA	126	34.627	38.310	32.891	1.00	16.51
55	1029	C	ALA	126	35.399	39.201	35.101	1.00	117.82
	1030	O	ALA	126	35.141	40.384	35.284	1.00	117.82
	1031	N	LEU	127	36.556	38.665	35.467	1.00	95.95
	1032	CA	LEU	127	37.572	39.490	36.104	1.00	95.95
	1033	CB	LEU	127	38.604	38.639	36.840	1.00	46.01
60	1034	CG	LEU	127	38.205	37.916	38.119	1.00	46.01
	1035	CD1	LEU	127	39.484	37.355	38.754	1.00	46.01
	1036	CD2	LEU	127	37.491	38.848	39.082	1.00	46.01
	1037	C	LEU	127	38.281	40.327	35.050	1.00	95.95
	1038	O	LEU	127	38.475	39.885	33.911	1.00	95.95
65	1039	N	LYS	128	38.664	41.538	35.450	1.00	158.42
	1040	CA	LYS	128	39.342	42.486	34.573	1.00	158.42
	1041	CB	LYS	128	39.220	43.899	35.142	1.00	155.76
	1042	CG	LYS	128	37.787	44.386	35.312	1.00	155.76
	1043	CD	LYS	128	37.114	44.590	33.960	1.00	155.76
70	1044	CE	LYS	128	35.689	45.116	34.097	1.00	155.76

	1045	NZ	LYS	128	35.067	45.392	32.766	1.00	155.76
	1046	C	LYS	128	40.813	42.148	34.369	1.00	158.42
	1047	O	LYS	128	41.144	41.178	33.693	1.00	158.42
	1048	N	TYR	129	41.698	42.949	34.954	1.00	117.79
5	1049	CA	TYR	129	43.132	42.714	34.800	1.00	117.79
	1050	CB	TYR	129	43.851	43.967	34.297	1.00	165.79
	1051	CG	TYR	129	43.199	44.664	33.137	1.00	165.79
	1052	CD1	TYR	129	42.151	45.563	33.344	1.00	165.79
	1053	CE1	TYR	129	41.561	46.234	32.280	1.00	165.79
10	1054	CD2	TYR	129	43.643	44.447	31.832	1.00	165.79
	1055	CE2	TYR	129	43.060	45.112	30.759	1.00	165.79
	1056	CZ	TYR	129	42.022	46.005	30.991	1.00	165.79
	1057	OH	TYR	129	41.451	46.671	29.932	1.00	165.79
	1058	C	TYR	129	43.834	42.279	36.077	1.00	117.79
15	1059	O	TYR	129	44.261	43.117	36.875	1.00	117.79
	1060	N	TRP	130	43.956	40.972	36.267	1.00	50.95
	1061	CA	TRP	130	44.647	40.433	37.422	1.00	50.95
	1062	CB	TRP	130	43.933	39.172	37.899	1.00	147.57
	1063	CG	TRP	130	42.728	39.505	38.701	1.00	147.57
20	1064	CD2	TRP	130	42.410	39.002	39.993	1.00	147.57
	1065	CE2	TRP	130	41.230	39.650	40.406	1.00	147.57
	1066	CE3	TRP	130	43.023	38.088	40.853	1.00	147.57
	1067	CD1	TRP	130	41.744	40.394	38.378	1.00	147.57
	1068	NE1	TRP	130	40.841	40.486	39.400	1.00	147.57
25	1069	CZ2	TRP	130	40.636	39.388	41.632	1.00	147.57
	1070	CZ3	TRP	130	42.436	37.831	42.068	1.00	147.57
	1071	CH2	TRP	130	41.257	38.488	42.454	1.00	147.57
	1072	C	TRP	130	46.011	40.129	36.846	1.00	50.95
	1073	O	TRP	130	46.184	40.232	35.628	1.00	50.95
30	1074	N	TYR	131	46.980	39.759	37.670	1.00	143.97
	1075	CA	TYR	131	48.287	39.493	37.101	1.00	143.97
	1076	CB	TYR	131	49.320	39.136	38.170	1.00	125.03
	1077	CG	TYR	131	50.636	38.736	37.544	1.00	125.03
	1078	CD1	TYR	131	51.129	39.426	36.443	1.00	125.03
35	1079	CE1	TYR	131	52.276	39.026	35.794	1.00	125.03
	1080	CD2	TYR	131	51.347	37.634	37.995	1.00	125.03
	1081	CE2	TYR	131	52.511	37.230	37.352	1.00	125.03
	1082	CZ	TYR	131	52.964	37.927	36.249	1.00	125.03
	1083	OH	TYR	131	54.078	37.504	35.573	1.00	125.03
40	1084	C	TYR	131	48.285	38.404	36.033	1.00	143.97
	1085	O	TYR	131	48.818	38.608	34.943	1.00	143.97
	1086	N	GLU	132	47.700	37.254	36.351	1.00	105.73
	1087	CA	GLU	132	47.628	36.119	35.427	1.00	105.73
	1088	CB	GLU	132	47.113	36.560	34.053	1.00	172.31
45	1089	CG	GLU	132	46.992	35.425	33.034	1.00	172.31
	1090	CD	GLU	132	46.449	35.896	31.695	1.00	172.31
	1091	OE1	GLU	132	45.321	36.436	31.670	1.00	172.31
	1092	OE2	GLU	132	47.148	35.724	30.670	1.00	172.31
	1093	C	GLU	132	48.962	35.397	35.256	1.00	105.73
50	1094	O	GLU	132	50.022	35.935	35.552	1.00	105.73
	1095	N	ASN	133	48.887	34.172	34.758	1.00	117.87
	1096	CA	ASN	133	50.061	33.336	34.554	1.00	117.87
	1097	CB	ASN	133	50.894	33.311	35.844	1.00	184.60
	1098	CG	ASN	133	52.234	32.621	35.675	1.00	184.60
55	1099	OD1	ASN	133	52.612	32.227	34.573	1.00	184.60
	1100	ND2	ASN	133	52.966	32.479	36.775	1.00	184.60
	1101	C	ASN	133	49.470	31.961	34.285	1.00	117.87
	1102	O	ASN	133	48.297	31.741	34.563	1.00	117.87
	1103	N	HIS	134	50.248	31.038	33.732	1.00	156.61
60	1104	CA	HIS	134	49.714	29.700	33.509	1.00	156.61
	1105	CB	HIS	134	50.697	28.835	32.710	1.00	161.49
	1106	CG	HIS	134	50.137	27.491	32.325	1.00	161.49
	1107	CD2	HIS	134	50.423	26.249	32.787	1.00	161.49
	1108	ND1	HIS	134	49.130	27.348	31.409	1.00	161.49
65	1109	CE1	HIS	134	48.802	26.061	31.313	1.00	161.49
	1110	NE2	HIS	134	49.569	25.382	32.136	1.00	161.49
	1111	C	HIS	134	49.547	29.124	34.915	1.00	156.61
	1112	O	HIS	134	49.172	27.967	35.093	1.00	156.61
	1113	N	ASN	135	49.821	29.965	35.910	1.00	97.51
70	1114	CA	ASN	135	49.755	29.570	37.304	1.00	97.51

	1115	CB	ASN	135	51.160	29.704	37.934	1.00	110.39
	1116	CG	ASN	135	52.230	28.875	37.217	1.00	110.39
	1117	OD1	ASN	135	51.990	27.742	36.801	1.00	110.39
	1118	ND2	ASN	135	53.438	29.433	37.117	1.00	110.39
5	1119	C	ASN	135	48.729	30.282	38.193	1.00	97.51
	1120	O	ASN	135	48.097	29.646	39.031	1.00	97.51
	1121	N	ILE	136	48.542	31.589	38.037	1.00	101.73
	1122	CA	ILE	136	47.60.	32.267	38.943	1.00	101.73
	1123	CB	ILE	136	48.307	32.728	40.212	1.00	31.25
10	1124	CG2	ILE	136	47.296	33.031	41.311	1.00	31.25
	1125	CG1	ILE	136	49.240	31.649	40.728	1.00	31.25
	1126	CD1	ILE	136	49.753	31.893	42.146	1.00	31.25
	1127	C	ILE	136	46.867	33.476	38.424	1.00	101.73
	1128	O	ILE	136	46.274	33.477	37.354	1.00	101.73
15	1129	N	SER	137	46.901	34.498	39.257	1.00	57.41
	1130	CA	SER	137	46.286	35.780	39.011	1.00	57.41
	1131	CB	SER	137	44.901	35.617	38.380	1.00	67.48
	1132	OG	SER	137	44.052	35.011	39.328	1.00	67.48
	1133	C	SER	137	46.183	36.488	40.392	1.00	57.41
20	1134	O	SER	137	45.619	35.936	41.348	1.00	57.41
	1135	N	ILE	138	46.730	37.708	40.476	1.00	65.35
	1136	CA	ILE	138	46.751	38.515	41.708	1.00	65.35
	1137	CB	ILE	138	48.186	38.693	42.184	1.00	90.30
	1138	CG2	ILE	138	48.232	39.050	43.659	1.00	90.30
25	1139	CG1	ILE	138	48.941	37.407	41.930	1.00	90.30
	1140	CD1	ILE	138	50.416	37.583	41.970	1.00	90.30
	1141	C	ILE	138	46.148	39.928	41.561	1.00	65.35
	1142	O	ILE	138	46.060	40.471	40.456	1.00	65.35
	1143	N	THR	139	45.745	40.515	42.683	1.00	86.56
30	1144	CA	THR	139	45.164	41.843	42.672	1.00	86.56
	1145	CB	THR	139	43.649	41.817	42.377	1.00	127.73
	1146	OG1	THR	139	43.399	41.192	41.115	1.00	127.73
	1147	CG2	THR	139	43.093	43.253	42.386	1.00	127.73
	1148	C	THR	139	45.331	42.466	44.043	1.00	86.56
35	1149	O	THR	139	45.198	41.779	45.051	1.00	86.56
	1150	N	ASN	140	45.624	43.763	44.089	1.00	96.52
	1151	CA	ASN	140	45.753	44.415	45.370	1.00	96.52
	1152	CB	ASN	140	46.301	45.834	45.214	1.00	124.36
	1153	CG	ASN	140	46.721	46.427	46.534	1.00	124.36
40	1154	OD1	ASN	140	46.321	45.925	47.576	1.00	124.36
	1155	ND2	ASN	140	47.512	47.492	46.515	1.00	124.36
	1156	C	ASN	140	44.325	44.432	45.916	1.00	96.52
	1157	O	ASN	140	43.390	44.861	45.244	1.00	96.52
	1158	N	ALA	141	44.168	43.921	47.126	1.00	84.53
45	1159	CA	ALA	141	42.876	43.846	47.769	1.00	84.53
	1160	CB	ALA	141	43.022	43.170	49.104	1.00	49.12
	1161	C	ALA	141	42.197	45.188	47.942	1.00	84.53
	1162	O	ALA	141	42.778	46.143	48.459	1.00	84.53
	1163	N	THR	142	40.942	45.223	47.514	1.00	86.11
50	1164	CA	THR	142	40.094	46.401	47.593	1.00	86.11
	1165	CB	THR	142	39.660	46.860	46.184	1.00	85.26
	1166	OG1	THR	142	40.816	47.143	45.386	1.00	85.26
	1167	CG2	THR	142	38.793	48.102	46.268	1.00	85.26
	1168	C	THR	142	38.847	45.955	48.337	1.00	86.11
55	1169	O	THR	142	38.577	44.766	48.411	1.00	86.11
	1170	N	VAL	143	38.089	46.889	48.897	1.00	105.48
	1171	CA	VAL	143	36.863	46.494	49.566	1.00	105.48
	1172	CB	VAL	143	36.240	47.653	50.360	1.00	154.19
	1173	CG1	VAL	143	35.816	48.766	49.413	1.00	154.19
60	1174	CG2	VAL	143	35.055	47.144	51.159	1.00	154.19
	1175	C	VAL	143	35.917	46.092	48.428	1.00	105.48
	1176	O	VAL	143	34.937	45.371	48.635	1.00	105.48
	1177	N	GLU	144	36.238	46.560	47.223	1.00	97.40
	1178	CA	GLU	144	35.454	46.269	46.022	1.00	97.40
65	1179	CB	GLU	144	35.815	47.241	44.905	1.00	151.67
	1180	CG	GLU	144	35.304	48.645	45.100	1.00	151.67
	1181	CD	GLU	144	35.772	49.574	44.000	1.00	151.67
	1182	OE1	GLU	144	35.580	49.236	42.811	1.00	151.67
	1183	OE2	GLU	144	36.330	50.643	44.324	1.00	151.67
70	1184	C	GLU	144	35.682	44.857	45.517	1.00	97.40

	1185	O	GLU	144	34.784	44.232	44.963	1.00	97.40
	1186	N	ASP	145	36.905	44.376	45.690	1.00	99.27
	1187	CA	ASP	145	37.266	43.040	45.268	1.00	99.27
	1188	CB	ASP	145	38.759	42.808	45.491	1.00	103.93
5	1189	CG	ASP	145	39.616	43.652	44.576	1.00	103.93
	1190	OD1	ASP	145	39.333	43.649	43.359	1.00	103.93
	1191	OD2	ASP	145	40.568	44.306	45.064	1.00	103.93
	1192	C	ASP	145	36.461	42.016	46.042	1.00	99.27
	1193	O	ASP	145	36.442	40.847	45.687	1.00	99.27
10	1194	N	SER	146	35.793	42.455	47.104	1.00	71.52
	1195	CA	SER	146	34.985	41.545	47.900	1.00	71.52
	1196	CB	SER	146	34.386	42.266	49.105	1.00	85.74
	1197	OG	SER	146	35.371	42.424	50.111	1.00	85.74
	1198	C	SER	146	33.900	40.948	47.012	1.00	71.52
15	1199	O	SER	146	33.469	41.569	46.036	1.00	71.52
	1200	N	GLY	147	33.493	39.724	47.333	1.00	96.87
	1201	CA	GLY	147	32.481	39.051	46.546	1.00	96.87
	1202	C	GLY	147	32.739	37.567	46.394	1.00	96.87
	1203	O	GLY	147	33.695	37.032	46.955	1.00	96.87
20	1204	N	THR	148	31.883	36.908	45.617	1.00	103.30
	1205	CA	THR	148	31.975	35.469	45.377	1.00	103.30
	1206	CB	THR	148	30.596	34.819	45.355	1.00	64.66
	1207	OG1	THR	148	30.231	34.568	43.990	1.00	64.66
	1208	CG2	THR	148	29.559	35.746	45.982	1.00	64.66
25	1209	C	THR	148	32.629	35.167	44.035	1.00	103.30
	1210	O	THR	148	32.261	35.726	42.998	1.00	103.30
	1211	N	TYR	149	33.586	34.253	44.059	1.00	77.50
	1212	CA	TYR	149	34.294	33.888	42.853	1.00	77.50
	1213	CB	TYR	149	35.798	34.053	43.059	1.00	78.57
30	1214	CG	TYR	149	36.237	35.491	43.209	1.00	78.57
	1215	CD1	TYR	149	35.965	36.210	44.372	1.00	78.57
	1216	CE1	TYR	149	36.349	37.540	44.492	1.00	78.57
	1217	CD2	TYR	149	36.907	36.141	42.169	1.00	78.57
	1218	CE2	TYR	149	37.291	37.463	42.277	1.00	78.57
35	1219	CZ	TYR	149	37.012	38.161	43.437	1.00	78.57
	1220	OH	TYR	149	37.388	39.485	43.527	1.00	78.57
	1221	C	TYR	149	34.018	32.469	42.439	1.00	77.50
	1222	O	TYR	149	33.424	31.694	43.185	1.00	77.50
	1223	N	TYR	150	34.473	32.150	41.232	1.00	44.44
40	1224	CA	TYR	150	34.335	30.823	40.648	1.00	44.44
	1225	CB	TYR	150	32.851	30.446	40.588	1.00	66.36
	1226	CG	TYR	150	32.132	30.968	39.376	1.00	66.36
	1227	CD1	TYR	150	32.205	30.288	38.157	1.00	66.36
	1228	CE1	TYR	150	31.585	30.776	37.034	1.00	66.36
45	1229	CD2	TYR	150	31.411	32.156	39.433	1.00	66.36
	1230	CE2	TYR	150	30.788	32.655	38.315	1.00	66.36
	1231	CZ	TYR	150	30.878	31.959	37.120	1.00	66.36
	1232	OH	TYR	150	30.243	32.436	36.007	1.00	66.36
	1233	C	TYR	150	34.957	30.881	39.240	1.00	44.44
50	1234	O	TYR	150	34.796	31.872	38.536	1.00	44.44
	1235	N	CYS	151	35.677	29.842	38.833	1.00	64.10
	1236	CA	CYS	151	36.290	29.853	37.513	1.00	64.10
	1237	C	CYS	151	35.713	28.792	36.616	1.00	64.10
	1238	O	CYS	151	35.015	27.897	37.067	1.00	64.10
55	1239	CB	CYS	151	37.813	29.668	37.612	1.00	75.24
	1240	SG	CYS	151	38.407	28.123	38.380	1.00	75.24
	1241	N	THR	152	36.021	28.904	35.334	1.00	63.66
	1242	CA	THR	152	35.553	27.971	34.330	1.00	63.66
	1243	CB	THR	152	34.453	28.599	33.459	1.00	48.15
60	1244	OG1	THR	152	35.025	29.615	32.619	1.00	48.15
	1245	CG2	THR	152	33.360	29.204	34.341	1.00	48.15
	1246	C	THR	152	36.779	27.708	33.479	1.00	63.66
	1247	O	THR	152	37.709	28.512	33.473	1.00	63.66
	1248	N	GLY	153	36.786	26.586	32.770	1.00	68.75
65	1249	CA	GLY	153	37.917	26.256	31.929	1.00	68.75
	1250	C	GLY	153	37.588	24.988	31.180	1.00	68.75
	1251	O	GLY	153	36.783	24.186	31.649	1.00	68.75
	1252	N	LYS	154	38.192	24.800	30.016	1.00	56.66
	1253	CA	LYS	154	37.936	23.603	29.248	1.00	56.66
70	1254	CB	LYS	154	37.984	23.917	27.751	1.00	131.33

	1255	CG	LYS	154	37.756	22.699	26.874	1.00	131.33
	1256	CD	LYS	154	38.014	22.985	25.401	1.00	131.33
	1257	CE	LYS	154	37.989	21.684	24.596	1.00	131.33
	1258	NZ	LYS	154	38.322	21.823	23.146	1.00	131.33
5	1259	C	LYS	154	38.932	22.501	29.582	1.00	56.66
	1260	O	LYS	154	40.141	22.713	29.562	1.00	56.66
	1261	N	VAL	155	38.412	21.321	29.913	1.00	93.07
	1262	CA	VAL	155	39.260	20.162	30.203	1.00	93.07
	1263	CB	VAL	155	38.924	19.490	31.544	1.00	78.48
10	1264	CG1	VAL	155	40.072	18.590	31.955	1.00	78.48
	1265	CG2	VAL	155	38.659	20.536	32.606	1.00	78.48
	1266	C	VAL	155	38.956	19.179	29.095	1.00	93.07
	1267	O	VAL	155	37.802	19.005	28.719	1.00	93.07
	1268	N	TRP	156	39.992	18.547	28.566	1.00	110.90
15	1269	CA	TRP	156	39.826	17.597	27.476	1.00	110.90
	1270	CB	TRP	156	39.093	16.344	27.963	1.00	64.42
	1271	CG	TRP	156	39.889	15.530	28.952	1.00	64.42
	1272	CD2	TRP	156	41.144	14.909	28.711	1.00	64.42
	1273	CE2	TRP	156	41.538	14.254	29.912	1.00	64.42
20	1274	CE3	TRP	156	41.989	14.836	27.593	1.00	64.42
	1275	CD1	TRP	156	39.562	15.241	30.265	1.00	64.42
	1276	NE1	TRP	156	40.550	14.478	30.845	1.00	64.42
	1277	CZ2	TRP	156	42.732	13.535	30.029	1.00	64.42
	1278	CZ3	TRP	156	43.178	14.125	27.705	1.00	64.42
25	1279	CH2	TRP	156	43.539	13.482	28.919	1.00	64.42
	1280	C	TRP	156	39.063	18.269	26.335	1.00	110.90
	1281	O	TRP	156	39.674	18.848	25.432	1.00	110.90
	1282	N	GLN	157	37.738	18.225	26.366	1.00	82.18
	1283	CA	GLN	157	36.980	18.857	25.298	1.00	82.18
30	1284	CB	GLN	157	36.566	17.802	24.260	1.00	143.76
	1285	CG	GLN	157	37.656	16.778	23.860	1.00	143.76
	1286	CD	GLN	157	37.147	15.761	22.835	1.00	143.76
	1287	OE1	GLN	157	35.954	15.470	22.790	1.00	143.76
	1288	NE2	GLN	157	38.050	15.211	22.025	1.00	143.76
35	1289	C	GLN	157	35.737	19.520	25.889	1.00	82.18
	1290	O	GLN	157	34.910	20.068	25.166	1.00	82.18
	1291	N	LEU	158	35.620	19.488	27.213	1.00	73.39
	1292	CA	LEU	158	34.443	20.030	27.881	1.00	73.39
	1293	CB	LEU	158	33.835	18.977	28.773	1.00	92.19
40	1294	CG	LEU	158	34.030	17.598	28.187	1.00	92.19
	1295	CD1	LEU	158	33.153	16.628	28.944	1.00	92.19
	1296	CD2	LEU	158	33.664	17.618	26.702	1.00	92.19
	1297	C	LEU	158	34.658	21.254	28.724	1.00	73.39
	1298	O	LEU	158	35.763	21.525	29.180	1.00	73.39
45	1299	N	ASP	159	33.564	21.955	28.992	1.00	43.69
	1300	CA	ASP	159	33.615	23.183	29.761	1.00	43.69
	1301	CB	ASP	159	32.773	24.249	29.074	1.00	86.10
	1302	CG	ASP	159	33.085	24.373	27.594	1.00	86.10
	1303	OD1	ASP	159	34.289	24.477	27.249	1.00	86.10
50	1304	OD2	ASP	159	32.128	24.374	26.778	1.00	86.10
	1305	C	ASP	159	33.103	23.041	31.167	1.00	43.69
	1306	O	ASP	159	31.900	22.907	31.357	1.00	43.69
	1307	N	TYR	160	33.976	23.093	32.170	1.00	43.37
	1308	CA	TYR	160	33.462	22.999	33.539	1.00	43.37
55	1309	CB	TYR	160	34.282	22.024	34.398	1.00	105.78
	1310	CG	TYR	160	34.323	20.649	33.808	1.00	105.78
	1311	CD1	TYR	160	35.087	20.415	32.671	1.00	105.78
	1312	CE1	TYR	160	35.035	19.211	32.001	1.00	105.78
	1313	CD2	TYR	160	33.500	19.617	34.286	1.00	105.78
60	1314	CE2	TYR	160	33.436	18.387	33.612	1.00	105.78
	1315	CZ	TYR	160	34.209	18.205	32.458	1.00	105.78
	1316	OH	TYR	160	34.143	17.068	31.692	1.00	105.78
	1317	C	TYR	160	33.340	24.331	34.265	1.00	43.37
	1318	O	TYR	160	33.620	25.407	33.736	1.00	43.37
65	1319	N	GLU	161	32.893	24.230	35.498	1.00	53.88
	1320	CA	GLU	161	32.709	25.388	36.333	1.00	53.88
	1321	CB	GLU	161	31.270	25.866	36.228	1.00	72.58
	1322	CG	GLU	161	30.834	26.756	37.346	1.00	72.58
	1323	CD	GLU	161	29.490	27.372	37.067	1.00	72.58
70	1324	OE1	GLU	161	28.930	28.016	37.992	1.00	72.58

	1325	OE2	GLU	161	29.002	27.212	35.918	1.00	72.58
	1326	C	GLU	161	33.002	24.902	37.725	1.00	53.88
	1327	O	GLU	161	32.658	23.765	38.063	1.00	53.88
	1328	N	SER	162	33.651	25.737	38.523	1.00	54.33
5	1329	CA	SER	162	33.967	25.330	39.868	1.00	54.33
	1330	CB	SER	162	35.289	25.931	40.327	1.00	58.04
	1331	OG	SER	162	35.183	27.339	40.452	1.00	58.04
	1332	C	SER	162	32.868	25.781	40.794	1.00	54.33
	1333	O	SER	162	31.975	26.508	40.391	1.00	54.33
10	1334	N	GLU	163	32.923	25.298	42.028	1.00	45.72
	1335	CA	GLU	163	31.959	25.656	43.045	1.00	45.72
	1336	CB	GLU	163	32.210	24.853	44.313	1.00	129.00
	1337	CG	GLU	163	31.766	23.437	44.264	1.00	129.00
	1338	CD	GLU	163	30.264	23.378	44.300	1.00	129.00
15	1339	OE1	GLU	163	29.702	24.206	45.051	1.00	129.00
	1340	OE2	GLU	163	29.657	22.531	43.595	1.00	129.00
	1341	C	GLU	163	32.259	27.102	43.356	1.00	45.72
	1342	O	GLU	163	33.425	27.501	43.399	1.00	45.72
	1343	N	PRO	164	31.219	27.914	43.576	1.00	67.32
20	1344	CD	PRO	164	29.759	27.742	43.567	1.00	86.92
	1345	CA	PRO	164	31.578	29.289	43.884	1.00	67.32
	1346	CB	PRO	164	30.227	29.992	43.934	1.00	86.92
	1347	CG	PRO	164	29.312	28.921	44.383	1.00	86.92
	1348	C	PRO	164	32.342	29.348	45.213	1.00	67.32
25	1349	O	PRO	164	32.402	28.372	45.973	1.00	67.32
	1350	N	LEU	165	32.943	30.507	45.461	1.00	65.83
	1351	CA	LEU	165	33.699	30.751	46.675	1.00	65.83
	1352	CB	LEU	165	35.183	30.549	46.392	1.00	49.81
	1353	CG	LEU	165	36.123	30.662	47.579	1.00	49.81
30	1354	CD1	LEU	165	35.645	29.788	48.747	1.00	49.81
	1355	CD2	LEU	165	37.495	30.247	47.100	1.00	49.81
	1356	C	LEU	165	33.424	32.177	47.156	1.00	65.83
	1357	O	LEU	165	33.235	33.094	46.344	1.00	65.83
	1358	N	ASN	166	33.376	32.358	48.473	1.00	106.87
35	1359	CA	ASN	166	33.117	33.676	49.033	1.00	106.87
	1360	CB	ASN	166	31.975	33.597	50.055	1.00	138.19
	1361	CG	ASN	166	30.601	33.541	49.380	1.00	138.19
	1362	OD1	ASN	166	30.053	32.448	49.150	1.00	138.19
	1363	ND2	ASN	166	30.075	34.724	49.034	1.00	138.19
40	1364	C	ASN	166	34.356	34.348	49.629	1.00	106.87
	1365	O	ASN	166	34.960	33.853	50.578	1.00	106.87
	1366	N	ILE	167	34.719	35.487	49.041	1.00	79.40
	1367	CA	ILE	167	35.882	36.278	49.444	1.00	79.40
	1368	CB	ILE	167	36.849	36.419	48.260	1.00	72.10
45	1369	CG2	ILE	167	37.796	37.571	48.491	1.00	72.10
	1370	CG1	ILE	167	37.558	35.074	48.042	1.00	72.10
	1371	CD1	ILE	167	38.444	35.007	46.826	1.00	72.10
	1372	C	ILE	167	35.502	37.662	49.951	1.00	79.40
	1373	O	ILE	167	34.768	38.397	49.295	1.00	79.40
50	1374	N	THR	168	36.013	38.003	51.126	1.00	78.85
	1375	CA	THR	168	35.727	39.284	51.750	1.00	78.85
	1376	CB	THR	168	34.988	39.074	53.096	1.00	110.41
	1377	OG1	THR	168	33.724	38.444	52.850	1.00	110.41
	1378	CG2	THR	168	34.753	40.400	53.805	1.00	110.41
55	1379	C	THR	168	37.012	40.064	52.000	1.00	78.85
	1380	O	THR	168	37.999	39.523	52.508	1.00	78.85
	1381	N	VAL	169	36.997	41.338	51.634	1.00	91.78
	1382	CA	VAL	169	38.163	42.177	51.829	1.00	91.78
	1383	CB	VAL	169	38.475	42.968	50.576	1.00	74.43
60	1384	CG1	VAL	169	39.886	43.524	50.663	1.00	74.43
	1385	CG2	VAL	169	38.303	42.079	49.361	1.00	74.43
	1386	C	VAL	169	37.898	43.146	52.965	1.00	91.78
	1387	O	VAL	169	37.524	44.297	52.738	1.00	91.78
	1388	N	ILE	170	38.085	42.676	54.192	1.00	138.54
65	1389	CA	ILE	170	37.838	43.522	55.342	1.00	138.54
	1390	CB	ILE	170	38.201	42.815	56.649	1.00	99.90
	1391	CG2	ILE	170	38.104	43.798	57.810	1.00	99.90
	1392	CG1	ILE	170	37.253	41.628	56.869	1.00	99.90
	1393	CD1	ILE	170	37.436	40.914	58.193	1.00	99.90
70	1394	C	ILE	170	38.598	44.837	55.255	1.00	138.54

	1395	O	ILE	170	39.816	44.880	55.419	1.00	138.54
	1396	N	LYS	171	37.856	45.912	55.002	1.00	166.26
	1397	CA	LYS	171	38.420	47.254	54.878	1.00	166.26
	1398	CB	LYS	171	37.322	48.228	54.430	1.00	153.43
5	1399	CG	LYS	171	37.806	49.608	53.987	1.00	153.43
	1400	CD	LYS	171	36.637	50.449	53.489	1.00	153.43
	1401	CE	LYS	171	37.084	51.765	52.885	1.00	153.43
	1402	NZ	LYS	171	35.907	52.541	52.405	1.00	153.43
	1403	C	LYS	171	39.042	47.737	56.189	1.00	166.26
10	1404	O	LYS	171	39.710	46.977	56.894	1.00	166.26
	1405	C1	NAG	221	52.176	13.407	48.424	1.00	124.69
	1406	C2	NAG	221	52.353	13.121	46.936	1.00	124.69
	1407	N2	NAG	221	51.119	13.440	46.226	1.00	124.69
	1408	C7	NAG	221	51.096	14.392	45.292	1.00	124.69
15	1409	O7	NAG	221	52.111	14.981	44.911	1.00	124.69
	1410	C8	NAG	221	49.744	14.746	44.682	1.00	124.69
	1411	C3	NAG	221	52.712	11.631	46.753	1.00	124.69
	1412	O3	NAG	221	53.109	11.400	45.409	1.00	124.69
	1413	C4	NAG	221	53.847	11.168	47.703	1.00	124.69
20	1414	O4	NAG	221	53.876	9.724	47.741	1.00	124.69
	1415	C5	NAG	221	53.635	11.683	49.139	1.00	124.69
	1416	O5	NAG	221	53.371	13.099	49.133	1.00	124.69
	1417	C6	NAG	221	54.853	11.458	50.023	1.00	124.69
	1418	O6	NAG	221	54.616	11.876	51.361	1.00	124.69
25	1419	C1	NAG	222	55.008	9.074	47.260	1.00	186.41
	1420	C2	NAG	222	55.394	7.926	48.219	1.00	186.41
	1421	N2	NAG	222	55.812	8.470	49.500	1.00	186.41
	1422	C7	NAG	222	55.243	8.053	50.628	1.00	186.41
	1423	O7	NAG	222	54.288	7.270	50.654	1.00	186.41
30	1424	C8	NAG	222	55.823	8.589	51.930	1.00	186.41
	1425	C3	NAG	222	56.531	7.079	47.623	1.00	186.41
	1426	O3	NAG	222	56.764	5.942	48.445	1.00	186.41
	1427	C4	NAG	222	56.174	6.622	46.205	1.00	186.41
	1428	O4	NAG	222	57.286	5.958	45.616	1.00	186.41
35	1429	C5	NAG	222	55.775	7.830	45.345	1.00	186.41
	1430	O5	NAG	222	54.681	8.548	45.963	1.00	186.41
	1431	C6	NAG	222	55.302	7.412	43.963	1.00	186.41
	1432	O6	NAG	222	54.550	8.444	43.340	1.00	186.41
	1433	C1	NAG	242	36.605	17.603	61.014	1.00	57.79
40	1434	C2	NAG	242	36.383	16.211	60.400	1.00	57.79
	1435	N2	NAG	242	37.564	15.387	60.550	1.00	57.79
	1436	C7	NAG	242	37.706	14.678	61.665	1.00	57.79
	1437	O7	NAG	242	36.949	14.833	62.624	1.00	57.79
	1438	C8	NAG	242	38.838	13.642	61.747	1.00	57.79
45	1439	C3	NAG	242	36.035	16.395	58.924	1.00	57.79
	1440	O3	NAG	242	35.897	15.142	58.256	1.00	57.79
	1441	C4	NAG	242	34.754	17.226	58.828	1.00	57.79
	1442	O4	NAG	242	34.498	17.491	57.446	1.00	57.79
	1443	C5	NAG	242	34.988	18.570	59.547	1.00	57.79
50	1444	O5	NAG	242	35.393	18.365	60.921	1.00	57.79
	1445	C6	NAG	242	33.781	19.492	59.556	1.00	57.79
	1446	O6	NAG	242	34.170	20.863	59.403	1.00	57.79
	1447	C1	NAG	243	33.499	16.811	56.792	1.00	110.47
	1448	C2	NAG	243	33.279	17.515	55.463	1.00	110.47
55	1449	N2	NAG	243	32.859	18.887	55.667	1.00	110.47
	1450	C7	NAG	243	33.584	19.876	55.149	1.00	110.47
	1451	O7	NAG	243	34.659	19.682	54.574	1.00	110.47
	1452	C8	NAG	243	33.036	21.294	55.277	1.00	110.47
	1453	C3	NAG	243	32.273	16.758	54.610	1.00	110.47
60	1454	O3	NAG	243	32.168	17.391	53.345	1.00	110.47
	1455	C4	NAG	243	32.746	15.314	54.413	1.00	110.47
	1456	O4	NAG	243	31.718	14.574	53.705	1.00	110.47
	1457	C5	NAG	243	33.038	14.665	55.789	1.00	110.47
	1458	O5	NAG	243	33.967	15.474	56.555	1.00	110.47
65	1459	C6	NAG	243	33.671	13.290	55.655	1.00	110.47
	1460	O6	NAG	243	34.005	12.749	56.924	1.00	110.47
	1461	C1	MAN	244	32.107	13.609	52.777	1.00	99.82
	1462	C2	MAN	244	31.311	12.313	53.039	1.00	99.82
	1463	O2	MAN	244	29.925	12.615	53.134	1.00	99.82
70	1464	C3	MAN	244	31.545	11.278	51.921	1.00	99.82

	1465	O3	MAN	244	30.713	10.135	52.110	1.00	99.82
	1466	C4	MAN	244	31.266	11.903	50.555	1.00	99.82
	1467	O4	MAN	244	31.547	10.959	49.527	1.00	99.82
5	1468	C5	MAN	244	32.168	13.132	50.412	1.00	99.82
	1469	O5	MAN	244	31.840	14.107	51.442	1.00	99.82
	1470	C6	MAN	244	32.132	13.816	49.038	1.00	99.82
	1471	O6	MAN	244	30.954	14.583	48.837	1.00	99.82
	1472	C1	NAG	250	57.134	13.804	64.271	1.00	196.94
	1473	C2	NAG	250	57.130	13.286	65.723	1.00	196.94
10	1474	N2	NAG	250	58.492	13.078	66.175	1.00	196.94
	1475	C7	NAG	250	58.871	13.481	67.385	1.00	196.94
	1476	O7	NAG	250	58.184	14.217	68.096	1.00	196.94
	1477	C8	NAG	250	60.225	12.994	67.883	1.00	196.94
	1478	C3	NAG	250	56.359	11.960	65.803	1.00	196.94
15	1479	O3	NAG	250	56.224	11.547	67.156	1.00	196.94
	1480	C4	NAG	250	54.974	12.098	65.176	1.00	196.94
	1481	O4	NAG	250	54.343	10.826	65.136	1.00	196.94
	1482	C5	NAG	250	55.102	12.658	63.758	1.00	196.94
	1483	O5	NAG	250	55.794	13.927	63.783	1.00	196.94
20	1484	C6	NAG	250	53.754	12.893	63.115	1.00	196.94
	1485	O6	NAG	250	53.895	13.367	61.783	1.00	196.94
	1486	C1	NAG	274	45.966	34.168	75.904	1.00	202.51
	1487	C2	NAG	274	44.449	34.481	75.778	1.00	202.51
	1488	N2	NAG	274	44.020	34.633	74.386	1.00	202.51
25	1489	C7	NAG	274	42.782	34.284	74.009	1.00	202.51
	1490	O7	NAG	274	42.000	33.685	74.755	1.00	202.51
	1491	C8	NAG	274	42.322	34.648	72.599	1.00	202.51
	1492	C3	NAG	274	44.167	35.773	76.602	1.00	202.51
	1493	O3	NAG	274	42.768	35.996	76.692	1.00	202.51
30	1494	C4	NAG	274	44.757	35.723	78.040	1.00	202.51
	1495	O4	NAG	274	44.775	37.037	78.589	1.00	202.51
	1496	C5	NAG	274	46.191	35.157	78.058	1.00	202.51
	1497	O5	NAG	274	46.265	33.950	77.282	1.00	202.51
	1498	C6	NAG	274	46.690	34.798	79.448	1.00	202.51
35	1499	O6	NAG	274	47.729	33.828	79.381	1.00	202.51
	1500	C1	NAG	340	47.734	48.240	47.742	1.00	87.46
	1501	C2	NAG	340	49.212	48.677	47.819	1.00	87.46
	1502	N2	NAG	340	50.123	47.546	47.707	1.00	87.46
	1503	C7	NAG	340	50.634	47.210	46.522	1.00	87.46
40	1504	O7	NAG	340	50.025	47.375	45.468	1.00	87.46
	1505	C8	NAG	340	52.024	46.596	46.490	1.00	87.46
	1506	C3	NAG	340	49.416	49.457	49.129	1.00	87.46
	1507	O3	NAG	340	50.779	49.830	49.261	1.00	87.46
	1508	C4	NAG	340	48.512	50.694	49.007	1.00	87.46
45	1509	O4	NAG	340	48.730	51.749	49.989	1.00	87.46
	1510	C5	NAG	340	47.044	50.277	48.965	1.00	87.46
	1511	O5	NAG	340	46.834	49.391	47.812	1.00	87.46
	1512	C6	NAG	340	46.182	51.556	48.793	1.00	87.46
	1513	O6	NAG	340	44.848	51.307	48.368	1.00	87.46
50	1514	C1	NAG	341	49.306	51.566	51.238	1.00	143.93
	1515	C2	NAG	341	50.167	52.801	51.506	1.00	143.93
	1516	N2	NAG	341	51.241	52.873	50.540	1.00	143.93
	1517	C7	NAG	341	51.195	53.774	49.564	1.00	143.93
	1518	O7	NAG	341	50.313	54.630	49.471	1.00	143.93
55	1519	C8	NAG	341	52.303	53.716	48.535	1.00	143.93
	1520	C3	NAG	341	50.722	52.777	52.923	1.00	143.93
	1521	O3	NAG	341	51.522	53.931	53.148	1.00	143.93
	1522	C4	NAG	341	49.548	52.753	53.891	1.00	143.93
	1523	O4	NAG	341	50.031	52.717	55.229	1.00	143.93
60	1524	C5	NAG	341	48.686	51.510	53.587	1.00	143.93
	1525	O5	NAG	341	48.239	51.510	52.203	1.00	143.93
	1526	C6	NAG	341	47.428	51.437	54.427	1.00	143.93
	1527	O6	NAG	341	46.455	50.627	53.780	1.00	143.93
	1528	C1	NAG	366	28.633	34.916	48.881	1.00	149.17
65	1529	C2	NAG	366	27.879	34.326	50.081	1.00	149.17
	1530	N2	NAG	366	28.118	32.897	50.186	1.00	149.17
	1531	C7	NAG	366	28.345	32.346	51.378	1.00	149.17
	1532	O7	NAG	366	28.482	33.013	52.407	1.00	149.17
	1533	C8	NAG	366	28.441	30.828	51.448	1.00	149.17
70	1534	C3	NAG	366	26.372	34.552	49.849	1.00	149.17

	1535	O3	NAG	366	25.761	34.256	51.198	1.00	149.17
	1536	C4	NAG	366	25.976	35.987	49.514	1.00	149.17
	1537	O4	NAG	366	24.660	35.921	48.921	1.00	149.17
5	1538	C5	NAG	366	26.928	36.592	48.459	1.00	149.17
	1539	O5	NAG	366	28.320	36.323	48.766	1.00	149.17
	1540	C6	NAG	366	26.769	38.111	48.368	1.00	149.17
	1541	O6	NAG	366	27.829	38.807	49.016	1.00	149.17
	1542	C1	NAG	367	23.729	36.910	49.196	1.00	173.80
10	1543	C2	NAG	367	22.797	37.075	47.975	1.00	173.80
	1544	N2	NAG	367	23.536	37.637	46.860	1.00	173.80
	1545	C7	NAG	367	23.834	36.896	45.796	1.00	173.80
	1546	O7	NAG	367	23.531	35.706	45.691	1.00	173.80
	1547	C8	NAG	367	24.586	37.593	44.674	1.00	173.80
15	1548	C3	NAG	367	21.617	37.991	48.311	1.00	173.80
	1549	O3	NAG	367	20.711	38.025	47.218	1.00	173.80
	1550	C4	NAG	367	20.897	37.499	49.566	1.00	173.80
	1551	O4	NAG	367	19.890	38.438	49.924	1.00	173.80
	1552	C5	NAG	367	21.917	37.360	50.705	1.00	173.80
20	1553	O5	NAG	367	22.977	36.460	50.326	1.00	173.80
	1554	C6	NAG	367	21.347	36.810	51.995	1.00	173.80
	1555	O6	NAG	367	22.385	36.606	52.948	1.00	173.80

Table 9. PhFcɛRIα₁.₁₇₂, Form T1; residue exposure

>>>>　coordinate set= pent63_8c1.pdb

	segid	resid	resname	access	access-main	access-side
	CCCC	4	LYS	22.3151	10.9559	31.4026
5	CCCC	5	PRO	1.1153	1.4307	0.6949
	CCCC	6	LYS	16.7221	1.1596	29.1721
	CCCC	7	VAL	1.5573	2.7252	0.0000
	CCCC	8	SER	8.9731	1.8795	23.1603
	CCCC	9	LEU	3.7370	4.7824	2.6917
10	CCCC	10	ASN	12.6673	0.9406	24.3940
	CCC͡	11	PRO	8.2815	0.5829	18.5464
	CCCC	12	PRO	9.7742	2.0935	20.0152
	CCCC	13	TRP	1.5926	0.1230	2.1805
	CCCC	14	ASN	3.3766	0.2934	6.4597
15	CCCC	15	ARG	1.6352	0.0000	2.5696
	CCCC	16	ILE	1.1737	0.0003	2.3470
	CCCC	17	PHE	0.2696	0.0000	0.4237
	CCCC	18	LYS	8.1283	3.2126	12.0608
	CCCC	19	GLY	5.5800	5.5800	0.0000
20	CCCC	20	GLU	3.3428	0.0000	6.0170
	CCCC	21	ASN	5.3342	3.9503 ·	6.7182
	CCCC	22	VAL	0.3267	0.4564	0.1538
	CCCC	23	THR	5.3278	0.0157	12.4107
	CCCC	24	LEU	0.2562	0.0002	0.5121
25	CCCC	25	THR	4.7853	0.0000	11.1657
	CCCC	26	CYS	0.2343	0.3249	0.0530
	CCCC	27	ASN	7.7637	1.8546	13.6728
	CCCC	28	GLY	7.9103	7.9103	0.0000
	CCCC	29	ASN	16.6538	7.7758	25.5318
30	CCCC	30	ASN	14.2106	9.9392	18.4821
	CCCC	31	PHE	18.4293	8.6833	23.9984
	CCCC	32	PHE	6.9543	6.9847	6.9370
	CCCC	33	GLU	17.3275	4.6057	27.5049
	CCCC	34	VAL	9.7070	3.0781	18.5455
35	CCCC	35	SER	14.3512	2.1631	38.7274
	CCCC	36	SER	7.0113	1.9003	17.2334
	CCCC	37	THR	0.7139	1.2493	0.0000
	CCCC	38	LYS	8.3149	0.3194	14.7113
	CCCC	39	TRP	0.0064	0.0013	0.0084
40	CCCC	40	PHE	3.0089	0.0000	4.7283
	CCCC	41	HIS	3.3635	0.3462	5.3750
	CCCC	42	ASN	5.9924	6.1741	5.8107
	CCCC	43	GLY	8.7956	8.7956	0.0000
	CCCC	44	SER	10.0868	2.4356	25.3890
45	CCCC	45	LEU	14.4496	6.7421	22.1571
	CCCC	46	SER	4.8664	3.2655	8.0682
	CCCC	47	GLU	13.8158	4.4486	21.3095
	CCCC	48	GLU	3.7957	0.7742	6.2129
	CCCC	49	THR	11.0308	0.0826	25.6285
50	CCCC	50	ASN	3.7680	0.9608	6.5753
	CCCC	51	SER	0.9943	0.0001	2.9826

CCCC	52	SER	2.8849	0.0003	8.6541
CCCC	53	LEU	2.6956	0.0208	5.3704
CCCC	54	ASN	7.0487	3.7820	10.3153
CCCC	55	ILE	2.0484	1.5241	2.5727
CCCC	56	VAL	8.3718	1.8780	17.0302
CCCC	57	ASN	6.8809	0.9872	12.7747
CCCC	58	ALA	0.3689	0.4454	0.0628
CCCC	59	LYS	8.8541	0.0311	15.9126
CCCC	60	PHE	3.1986	0.2109	4.9058
CCCC	61	GLU	8.5928	0.1580	15.3407
CCCC	62	ASP	4.2001	0.0802	8.3200
CCCC	63	SER	0.1586	0.0000	0.4759
CCCC	64	GLY	0.0205	0.0205	0.0000
CCCC	65	GLU	3.1362	0.1046	5.5614
CCCC	66	TYR	0.7765	0.0000	1.1648
CCCC	67	LYS	3.3029	0.0005	5.9449
CCCC	68	CYS	0.0000	0.0000	0.0000
CCCC	69	GLN	3.8782	0.0000	6.9808
CCCC	70	HIS	2.2973	0.2891	3.6361
CCCC	71	GLN	15.5567	6.4047	22.8783
CCCC	72	GLN	18.9536	6.5187	28.9015
CCCC	73	VAL	6.3773	2.6597	11.3340
CCCC	74	ASN	7.2490	0.8511	13.6469
CCCC	75	GLU	9.5776	4.4490	13.6806
CCCC	76	SER	0.7222	1.0831	0.0006
CCCC	77	GLU	13.3681	1.0686	23.2077
CCCC	78	PRO	2.7891	1.9776	3.8710
CCCC	79	VAL	5.1775	0.7766	11.0455
CCCC	80	TYR	3.7512	1.4544	4.8996
CCCC	81	LEU	0.2610	0.0000	0.5221
CCCC	82	GLU	5.7107	0.0011	10.2784
CCCC	83	VAL	1.5280	2.6739	0.0000
CCCC	84	PHE	2.6808	0.7184	3.8022
CCCC	85	SER	5.8787	5.8008	6.0345
CCCC	86	ASP	6.0903	2.6973	9.4832
CCCC	37	TRP	3.0930	0.2603	4.2261
CCCC	88	LEU	0.0403	0.0675	0.0131
CCCC	89	LEU	0.1021	0.0000	0.2041
CCCC	90	LEU	0.0000	0.0000	0.0000
CCCC	91	GLN	0.2597	0.0000	0.4674
CCCC	92	ALA	0.0596	0.0563	0.0730
CCCC	93	SER	4.6788	3.0077	8.0211
CCCC	94	ALA	8.5911	1.3052	37.7350
CCCC	95	GLU	4.4767	1.5831	6.7916
CCCC	96	VAL	4.3906	4.6557	4.0371
CCCC	97	VAL	1.4394	1.1406	1.8378
CCCC	98	MET	13.6889	0.2044	27.1734
CCCC	99	GLU	7.4797	4.8677	9.5692
CCCC	100	GLY	5.3567	5.3567	0.0000
CCCC	101	GLN	9.7722	0.0006	17.5894
CCCC	102	PRO	9.4569	1.5764	19.9642
CCCC	103	LEU	0.0179	0.0357	0.0000
CCCC	104	PHE	6.2358	0.0000	9.7991
CCCC	105	LEU	0.0474	0.0488	0.0461
CCCC	106	ARG	2.3314	0.0000	3.6636
CCCC	107	CYS	0.7781	1.1549	0.0246

	CCCC	108	HIS	1.2171	0.3012	1.8277
	CCCC	109	GLY	1.2651	1.2651	0.0000
	CCCC	110	TRP	1.9508	0.3094	2.6074
	CCCC	111	ARG	7.1821	6.7612	7.4226
5	CCCC	112	ASN	12.7243	3.8235	21.6251
	CCCC	113	TRP	2.9331	3.2961	2.7878
	CCCC	114	ASP	11.7314	2.0501	21.4128
	CCCC	115	VAL	0.8918	0.6165	1.2589
	CCCC	116	TYR	5.7191	0.0000	8.5787
10	CCCC	117	LYS	10.9908	0.9471	19.0258
	CCCC	118	VAL	0.0001	0.0000	0.0002
	CCCC	119	ILE	4.7127	0.0007	9.4248
	CCCC	120	TYR	0.0060	0.0000	0.0091
	CCCC	121	TYR	3.6424	0.0150	5.4562
15	CCCC	122	LYS	3.9385	0.8428	6.4150
	CCCC	123	ASP	11.0597	7.2355	14.8840
	CCCC	124	GLY	13.5829	13.5829	0.0000
	CCCC	125	GLU	13.1544	0.5211	23.2611
	CCCC	126	ALA	15.0490	5.4493	53.4477
20	CCCC	127	LEU	9.4150	6.1124	12.7176
	CCCC	128	LYS	11.5717	1.7494	19.4295
	CCCC	129	TYR	10.5011	5.5905	12.9565
	CCCC	130	TRP	8.0873	0.9625	10.9373
	CCCC	131	TYR	11.7870	1.0734	17.1438
25	CCCC	132	GLU	12.6705	2.2279	21.0247
	CCCC	133	ASN	5.3027	5.3599	5.2454
	CCCC	134	HIS	8.2476	1.2608	12.9055
	CCCC	135	ASN	1.2965	0.3213	2.2717
	CCCC	136	ILE	2.0165	1.3778	2.6552
30	CCCC	137	SER	9.9968	7.2656	15.4593
	CCCC	138	ILE	3.6077	0.9873	6.2280
	CCCC	139	THR	15.8360	2.4317	33.7085
	CCCC	140	ASN	6.0823	3.6720	8.4926
	CCCC	141	ALA	0.0000	0.0000	0.0000
35	CCCC	142	THR	6.7820	0.1381	15.6405
	CCCC	143	VAL	5.0630	1.4175	9.9237
	CCCC	144	GLU	14.1160	4.3532	21.9263
	CCCC	145	ASP	4.3317	0.0259	8.6374
	CCCC	146	SER	5.1283	3.0010	9.3829
40	CCCC	147	GLY	3.4210	3.4210	0.0000
	CCCC	148	THR	5.2803	0.0914	12.1988
	CCCC	149	TYR	0.2014	0.0000	0.3021
	CCCC	150	TYR	3.7574	0.0000	5.6362
	CCCC	151	CYS	0.0001	0.0001	0.0000
45	CCCC	152	THR	3.8919	0.0107	9.0668
	CCCC	153	GLY	1.0188	1.0188	0.0000
	CCCC	154	LYS	6.4238	0.0528	11.5207
	CCCC	155	VAL	0.4180	0.0000	0.9754
	CCCC	156	TRP	3.3279	3.7718	3.1504
50	CCCC	157	GLN	13.1268	3.2479	21.0299
	CCCC	158	LEU	8.7018	0.1257	17.2778
	CCCC	159	ASP	14.2676	4.9595	23.5758
	CCCC	160	TYR	2.2687	2.5573	2.1243
	CCCC	161	GLU	12.1767	4.4230	18.3798
55	CCCC	162	SER	1.1841	1.7762	0.0000
	CCCC	163	GLU	9.4913	0.1747	16.9445

	CCCC	164	PRO	9.7765	1.5124	20.7953
	CCCC	165	LEU	1.6495	0.1289	3.1701
	CCCC	166	ASN	3.4007	0.7824	6.0190
	CCCC	167	ILE	0.5293	1.0585	0.0000
5	CCCC	168	THR	3.2321	0.0380	7.4909
	CCCC	169	VAL	0.0723	0.1266	0.0000
	CCCC	170	ILE	2.2951	0.0689	4.5213
	CCCC	171	LYS	14.3432	12.9256	15.4773
	CCCC	221	NAG	11.7001	0.0000	11.7001
10	CCCC	222	NAG	14.4010	0.0000	14.4010
	CCCC	242	NAG	7.1046	0.0000	7.1046
	CCCC	243	NAG	8.0078	0.0000	8.0078
	CCCC	244	MAN	16.5438	0.0000	16.5438
	CCCC	250	NAG	16.2147	0.0000	16.2147
15	CCCC	274	NAG	21.7742	0.0000	21.7742
	CCCC	335	NAG	15.0979	0.0000	15.0979
	CCCC	340	NAG	17.6065	0.0000	17.6065
	CCCC	366	NAG	11.8776	0.0000	11.8776
	CCCC	367	NAG	19.0810	0.0000	19.0810
20	AAAA	4	LYS	15.9363	6.7194	23.3099
	AAAA	5	PRO	1.1488	1.4481	0.7498
	AAAA	6	LYS	13.8574	1.1896	23.9916
	AAAA	7	VAL	1.5646	2.7375	0.0007
	AAAA	8	SER	9.0558	1.9390	23.2893
25	AAAA	9	LEU	3.8393	4.9388	2.7398
	AAAA	10	ASN	12.5152	0.9543	24.0762
	AAAA	11	PRO	8.3710	0.5349	18.8192
	AAAA	12	PRO	9.8889	2.0781	20.3033
	AAAA	13	TRP	1.5673	0.1143	2.1485
30	AAAA	14	ASN	3.1275	0.2808	5.9741
	AAAA	15	ARG	1.6130	0.0057	2.5315
	AAAA	16	ILE	1.1993	0.0000	2.3986
	AAAA	17	PHE	0.2501	0.0000	0.3929
	AAAA	18	LYS	10.8021	3.4649	16.6720
35	AAAA	19	GLY	5.6939	5.6939	0.0000
	AAAA	20	GLU	3.4960	0.0003	6.2926
	AAAA	21	ASN	5.3970	4.0391	6.7548
	AAAA	22	VAL	0.2660	0.3430	0.1633
	AAAA	23	THR	5.2134	0.0418	12.1090
40	AAAA	24	LEU	0.2554	0.0007	0.5101
	AAAA	25	THR	4.8655	0.0005	11.3521
	AAAA	26	CYS	0.2307	0.3194	0.0532
	AAAA	27	ASN	0.4259	0.2949	0.5569
	AAAA	28	GLY	4.4162	4.4162	0.0000
45	AAAA	29	ASN	7.6150	7.1438	8.0862
	AAAA	30	ASN	11.3939	10.0050	12.7829
	AAAA	31	PHE	14.7556	4.8219	20.4320
	AAAA	32	PHE	2.7147	4.5718	1.6536
	AAAA	33	GLU	7.5248	4.4574	9.9787
50	AAAA	34	VAL	4.0858	3.0519	5.4642
	AAAA	35	SER	14.4683	2.1629	39.0790
	AAAA	36	SER	6.9471	1.9207	16.9999
	AAAA	37	THR	0.7130	1.2478	0.0000
	AAAA	38	LYS	8.2623	0.2915	14.6390
55	AAAA	39	TRP	0.0071	0.0080	0.0067
	AAAA	40	PHE	2.9948	0.0014	4.7054

	AAAA	41	HIS	3.3204	0.4762	5.2166
	AAAA	42	ASN	6.4516	7.1677	5.7356
	AAAA	43	GLY	9.6929	9.6929	0.0000
	AAAA	44	SER	12.5467	3.0596	31.5209
5	AAAA	45	LEU	14.0597	6.3669	21.7524
	AAAA	46	SER	5.9554	3.7890	10.2883
	AAAA	47	GLU	19.8848	8.0231	29.3741
	AAAA	48	GLU	6.1436	2.1551	9.3344
	AAAA	49	THR	10.8974	0.0037	25.4223
10	AAAA	50	ASN	3.7283	0.9830	6.4736
	AAAA	51	SER	1.0424	0.0007	3.1257
	AAAA	52	SER	2.9027	0.0000	8.7080
	AAAA	53	LEU	2.6315	0.0203	5.2426
	AAAA	54	ASN	7.1111	3.9443	10.2778
15	AAAA	55	ILE	2.0993	1.5522	2.6464
	AAAA	56	VAL	11.4229	1.8784	24.1489
	AAAA	57	ASN	9.2772	0.9862	17.5682
	AAAA	58	ALA	0.3197	0.3981	0.0062
	AAAA	59	LYS	13.5164	0.0175	24.3155
20	AAAA	60	PHE	3.5563	0.1394	5.5088
	AAAA	61	GLU	8.5716	0.1791	15.2857
	AAAA	62	ASP	4.2001	0.0591	8.3412
	AAAA	63	SER	0.1501	0.0000	0.4504
	AAAA	64	GLY	0.0335	0.0335	0.0000
25	AAAA	65	GLU	8.1768	0.0971	14.6406
	AAAA	66	TYR	0.7839	0.0002	1.1758
	AAAA	67	LYS	3.2196	0.0004	5.7951
	AAAA	68	CYS	0.0000	0.0000	0.0000
	AAAA	69	GLN	3.8577	0.0000	6.9439
30	AAAA	70	HIS	0.2845	0.2473	0.3093
	AAAA	71	GLN	14.8691	6.1965	21.8072
	AAAA	72	GLN	18.3340	6.2079	28.0348
	AAAA	73	VAL	3.2302	2.5357	4.1564
	AAAA	74	ASN	7.3440	0.8492	13.8389
35	AAAA	75	GLU	9.5554	4.4097	13.6718
	AAAA	76	SER	0.5321	0.7981	0.0000
	AAAA	77	GLU	16.0334	0.9282	28.1176
	AAAA	78	PRO	8.2987	5.2204	12.4031
	AAAA	79	VAL	5.9326	1.3229	12.0789
40	AAAA	80	TYR	6.7460	1.9053	9.1664
	AAAA	81	LEU	0.2734	0.0000	0.5469
	AAAA	82	GLU	5.7587	0.0007	10.3651
	AAAA	83	VAL	1.5339	2.6843	0.0000
	AAAA	84	PHE	2.7544	0.6865	3.9361
45	AAAA	85	SER	11.1143	5.9578	21.4274
	AAAA	86	ASP	6.1024	2.2574	9.9474
	AAAA	87	TRP	9.2004	0.2983	12.7613
	AAAA	88	LEU	0.0297	0.0543	0.0051
	AAAA	89	LEU	0.0927	0.0000	0.1854
50	AAAA	90	LEU	0.0001	0.0000	0.0002
	AAAA	91	GLN	0.2535	0.0000	0.4563
	AAAA	92	ALA	0.0453	0.0480	0.0344
	AAAA	93	SER	4.6084	2.9327	7.9597
	AAAA	94	ALA	8.7098	1.2990	38.3529
55	AAAA	95	GLU	7.3017	1.5643	11.8916
	AAAA	96	VAL	12.9692	4.7889	23.8762

	AAAA	97	VAL	1.4036	1.0908	1.8207
	AAAA	98	MET	7.3760	0.2425	14.5094
	AAAA	99	GLU	7.1208	4.6443	9.1019
	AAAA	100	GLY	5.2380	5.2380	0.0000
5	AAAA	101	GLN	3.2910	0.0195	5.9082
	AAAA	102	PRO	5.1174	1.6052	9.8002
	AAAA	103	LEU	0.0323	0.0600	0.0045
	AAAA	104	PHE	6.3337	0.0009	9.9525
	AAAA	105	LEU	0.0742	0.0597	0.0887
10	AAAA	106	ARG	2.3217	0.0000	3.6484
	AAAA	107	CYS	0.7916	1.1873	0.0000
	AAAA	108	HIS	1.2205	0.3014	1.8333
	AAAA	109	GLY	1.3688	1.3688	0.0000
	AAAA	110	TRP	4.3961	0.3129	6.0293
15	AAAA	111	ARG	14.1659	6.8259	18.3603
	AAAA	112	ASN	12.3349	3.8047	20.8651
	AAAA	113	TRP	7.3124	3.4188	8.8699
	AAAA	114	ASP	11.5788	1.5704	21.5873
	AAAA	115	VAL	0.8933	0.6941	1.1589
20	AAAA	116	TYR	5.1843	0.0006	7.7761
	AAAA	117	LYS	7.1256	0.9679	12.0517
	AAAA	118	VAL	0.0000	0.0000	0.0000
	AAAA	119	ILE	1.4302	0.0000	2.8604
	AAAA	120	TYR	0.0104	0.0005	0.0153
25	AAAA	121	TYR	2.8600	0.0167	4.2816
	AAAA	122	LYS	3.8739	0.7828	6.3468
	AAAA	123	ASP	11.0893	7.0588	15.1198
	AAAA	124	GLY	13.7649	13.7649	0.0000
	AAAA	125	GLU	8.1492	0.5254	14.2483
30	AAAA	126	ALA	1.3596	0.7744	3.7005
	AAAA	127	LEU	5.0008	0.9822	9.0194
	AAAA	128	LYS	10.8601	0.1501	19.4280
	AAAA	129	TYR	5.7014	3.8333	6.6354
	AAAA	130	TRP	7.7631	0.9621	10.4835
35	AAAA	131	TYR	3.0458	1.1141	4.0116
	AAAA	132	GLU	11.1091	2.1808	18.2518
	AAAA	133	ASN	5.2028	5.3196	5.0859
	AAAA	134	HIS	8.3482	1.2156	13.1032
	AAAA	135	ASN	1.2934	0.3190	2.2679
40	AAAA	136	ILE	2.1274	1.3695	2.8853
	AAAA	137	SER	10.0348	7.2335	15.6375
	AAAA	138	ILE	3.6211	1.0099	6.2322
	AAAA	139	THR	16.0640	2.580͡	34.0420
	AAAA	140	ASN	5.4194	3.6273	7.2114
45	AAAA	141	ALA	0.0000	0.0000	0.0000
	AAAA	142	THR	7.2278	0.4616	16.2495
	AAAA	143	VAL	7.6811	1.4982	15.9250
	AAAA	144	GLU	14.2939	4.1689	22.3939
	AAAA	145	ASP	4.3509	0.0318	8.6701
50	AAAA	146	SER	5.2566	3.1044	9.5609
	AAAA	147	GLY	3.2376	3.2376	0.0000
	AAAA	148	THR	5.2658	0.0995	12.1542
	AAAA	149	TYR	0.2165	0.0000	0.3248
	AAAA	150	TYR	3.8830	0.0000	5.8245
55	AAAA	151	CYS	0.0000	0.0000	0.0000
	AAAA	152	THR	3.7398	0.0010	8.7248

	AAAA	153	GLY	1.0201	1.0201	0.0000
	AAAA	154	LYS	4.0119	0.0425	7.1873
	AAAA	155	VAL	0.4567	0.0000	1.0656
	AAAA	156	TRP	11.1226	3.7204	14.0834
5	AAAA	157	GLN	8.2831	3.3029	12.2673
	AAAA	158	LEU	13.8927	0.1434	27.6420
	AAAA	159	ASP	9.7733	4.0346	15.5120
	AAAA	160	TYR	3.4354	2.0054	4.1504
	AAAA	161	GLU	8.2007	5.4400	10.4093
10	AAAA	162	SER	1.2173	1.8259	0.0002
	AAAA	163	GLU	9.4751	0.3080	16.8088
	AAAA	164	PRO	9.8187	1.5247	20.8774
	AAAA	165	LEU	1.6583	0.0972	3.2194
	AAAA	166	ASN	4.2239	1.2362	7.2117
15	AAAA	167·	ILE	0.5672	1.1307	0.0038
	AAAA	168	THR	9.3576	0.0604	21.7538
	AAAA	169	VAL	0.5466	0.9510	0.0074
	AAAA	170	ILE	10.6664	1.5666	19.7663
	AAAA	171	LYS	20.0709	14.6286	24.4247
20	AAAA	221	NAG	13.0731	0.0000	13.0731
	AAAA	222	NAG	19.9260	0.0000	19.9260
	AAAA	242	NAG	10.0968	0.0000	10.0968
	AAAA	243	NAG	9.7429	0.0000	9.7429
	AAAA	244	MAN	16.5025	0.0000	16.5025
25	AAAA	250	NAG	16.0048	0.0000 ·	16.0048
	AAAA	274	NAG	21.9758	0.0000	21.9758
	AAAA	335	NAG	15.0266	0.0000	15.0266
	AAAA	340	NAG	10.2058	0.0000	10.2058
	AAAA	366	NAG	14.2003	0.0000	14.2003
30	AAAA	367	NAG	21.1043	0.0000	21.1043
	BBBB	4	LYS	21.2711	8.1950	31.7320
	BBBB	5	PRO	0.9327	1.4134	0.2918
	BBBB	6	LYS	13.5721	0.9858	23.6411
	BBBB	7	VAL	1.5696	2.7468	0.0000
35	BBBB	8	SER	9.0540	1.8158	23.5305
	BBBB	9	LEU	3.7548	4.6164	2.8932
	BBBB	10	ASN	12.3838	0.9742	23.7933
	BBBB	11	PRO	8.3839	0.5771	18.7929
	BBBB	12	PRO	10.2255	2.2114	20.9110
40	BBBB	13	TRP	1.5767	0.1420	2.1505
	BBBB	14	ASN	3.6856	0.2734	7.0977
	BBBB	15	ARG	1.6517	0.0084	2.5908
	BBBB	16	ILE	1.1539	0.0000	2.3079
	BBBB	17	PHE	0.2627	0.0000	0.4128
45	BBBB	18	LYS	10.5872	3.1464	16.5399
	BBBB	19	GLY	5.2452	5.2452	0.0000
	BBBB	20	GLU	3.4004	0.0000	6.1208
	BBBB	21	ASN	5.3165	3.8893	6.7437
	BBBB	22	VAL	0.3290	0.4639	0.1492
50	BBBB	23	THR	5.3376	0.0419	12.3986
	BBBB	24	LEU	0.2556	0.0000	0.5112
	BBBB	25	THR	4.8687	0.0000	11.3603
	BBBB	26	CYS	0.2112	0.2986	0.0364
	BBBB	27	ASN	0.5141	0.1099	0.9184
55	BBBB	28	GLY	2.2181	2.2181	0.0000
	BBBB	29	ASN	10.0991	5.9026	14.2956

	BBBB	30	ASN	8.2629	8.5326	7.9932
	BBBB	31	PHE	13.1098	3.1872	18.7798
	BBBB	32	PHE	3.2118	5.7094	1.7846
	BBBB	33	GLU	9.8599	4.6157	14.0553
5	BBBB	34	VAL	4.2409	3.1111	5.7472
	BBBB	35	SER	14.4622	2.1340	39.1186
	BBBB	36	SER	7.0903	1.9980	17.2748
	BBBB	37	THR	0.7246	1.2681	0.0000
	BBBB	38	LYS	8.3435	0.2936	14.7834
10	BBBB	39	TRP	0.0045	0.0000	0.0063
	BBBB	40	PHE	3.0307	0.0013	4.7618
	BBBB	41	HIS	3.2985	0.2952	5.3007
	BBBB	42	ASN	3.9446	4.4215	3.4677
	BBBB	43	GLY	6.4448	6.4448	0.0000
15	BBBB	44	SER	7.9300	1.5277	20.7347
	BBBB	45	LEU	14.0360	6.3402	21.7318
	BBBB	46	SER	5.3085	3.4386	9.0482
	BBBB	47	GLU	19.8137	7.9994	29.2651
	BBBB	48	GLU	6.1811	2.3816	9.2207
20	BBBB	49	THR	10.8045	0.0111	25.1957
	BBBB	50	ASN	3.7967	1.0050	6.5885
	BBBB	51	SER	1.0119	0.0000	3.0357
	BBBB	52	SER	2.8985	0.0010	8.6934
	BBBB	53	LEU	2.8664	0.0001	5.7327
25	BBBB	54	ASN	7.0968	3.9693	10.2244
	BBBB	55	ILE	2.0503	1.4906	2.6099
	BBBB	56	VAL	11.3539	1.8189	24.0671
	BBBB	57	ASN	9.2620	1.0325	17.4916
	BBBB	58	ALA	0.3961	0.4951	0.0000
30	BBBB	59	LYS	13.4689	0.0284	24.2213
	BBBB	60	PHE	3.3978	0.2767	5.1813
	BBBB	61	GLU	8.8117	0.1782	15.7185
	BBBB	62	ASP	4.1350	0.0756	8.1943
	BBBB	63	SER	0.1730	0.0000	0.5191
35	BBBB	64	GLY	0.0000	0.0000	0.0000
	BBBB	65	GLU	6.5484	0.0001	11.7871
	BBBB	66	TYR	0.7915	0.0000	1.1872
	BBBB	67	LYS	3.2805	0.0000	5.9049
	BBBB	68	CYS	0.0000	0.0000	0.0000
40	BBBB	69	GLN	3.8141	0.0000	6.8654
	BBBB	70	HIS	0.1609	0.2608	0.0943
	BBBB	71	GLN	10.6127	5.2959	14.8662
	BBBB	72	GLN	8.4010	6.0152	10.3096
	BBBB	73	VAL	2.9562	2.5768	3.4619
45	BBBB	74	ASN	7.3147	0.9982	13.6312
	BBBB	75	GLU	9.4113	4.1701	13.6043
	BBBB	76	SER	0.5684	0.8526	0.0000
	BBBB	77	GLU	15.8600	1.0254	27.7278
	BBBB	78	PRO	8.2998	5.0247	12.6666
50	BBBB	79	VAL	5.5759	1.3782	11.1729
	BBBB	80	TYR	6.2317	1.9484	8.3734
	BBBB	81	LEU	0.2490	0.0005	0.4975
	BBBB	82	GLU	5.8300	0.0000	10.4940
	BBBB	83	VAL	1.5904	2.7832	0.0000
55	BBBB	84	PHE	2.7220	0.7033	3.8756
	BBBB	85	SER	10.7069	5.7965	20.5277

BBBB	86	ASP	5.9874	2.1888	9.7860
BBBB	87	TRP	9.1171	0.3262	12.6335
BBBB	88	LEU	0.0289	0.0578	0.0000
BBBB	89	LEU	0.0888	0.0000	0.1776
BBBB	90	LEU	0.0000	0.0000	0.0000
BBBB	91	GLN	0.2626	0.0000	0.4726
BBBB	92	ALA	0.0481	0.0399	0.0813
BBBB	93	SER	4.6672	2.9572	8.0872
BBBB	94	ALA	8.7256	1.3164	38.3623
BBBB	95	GLU	7.1764	1.5358	11.6889
BBBB	96	VAL	12.6418	4.7054	23.2237
BBBB	97	VAL	1.4061	1.1339	1.7691
BBBB	98	MET	11.9430	0.2070	23.6789
BBBB	99	GLU	7.2607	4.6466	9.3520
BBBB	100	GLY	5.1244	5.1244	0.0000
BBBB	101	GLN	4.0221	0.0000	7.2398
BBBB	102	PRO	7.3498	1.5529	15.0790
BBBB	103	LEU	0.0071	0.0138	0.0004
BBBB	104	PHE	6.2937	0.0007	9.8898
BBBB	105	LEU	0.0567	0.0603	0.0531
BBBB	106	ARG	2.3037	0.0000	3.6201
BBBB	107	CYS	0.8127	1.2098	0.0186
BBBB	108	HIS	1.1982	0.2627	1.8218
BBBB	109	GLY	1.2842	1.2842	0.0000
BBBB	110	TRP	4.4804	0.3255	6.1423
BBBB	111	ARG	14.4479	6.9241	18.7472
BBBB	112	ASN	12.2860	3.9115	20.6605
BBBB	113	TRP	7.0297	3.4023	8.4806
BBBB	114	ASP	11.5554	1.8648	21.2461
BBBB	115	VAL	0.8700	0.6238	1.1983
BBBB	116	TYR	5.8899	0.0000	8.8349
BBBB	117	LYS	11.0072	0.9540	19.0498
BBBB	118	VAL	0.0000	0.0000	0.0000
BBBB	119	ILE	4.7824	0.0000	9.5649
BBBB	120	TYR	0.0292	0.0003	0.0436
BBBB	121	TYR	3.6258	0.0127	5.4323
BBBB	122	LYS	3.8173	0.8234	6.2125
BBBB	123	ASP	11.1350	7.1239	15.1460
BBBB	124	GLY	13.9353	13.9353	0.0000
BBBB	125	GLU	13.4298	0.5494	23.7341
BBBB	126	ALA	15.0233	5.4413	53.3510
BBBB	127	LEU	9.2699	5.9635	12.5762
BBBB	128	LYS	11.66_3	1.8096	19.5508
BBBB	129	TYR	10.3608	5.2815	12.9005
BBBB	130	TRP	8.0170	1.0064	10.8213
BBBB	131	TYR	11.7311	1.0656	17.0638
BBBB	132	GLU	12.8760	2.2402	21.3846
BBBB	133	ASN	5.2983	5.3131	5.2835
BBBB	134	HIS	7.9203	1.2177	12.3886
BBBB	135	ASN	1.3098	0.3200	2.2995
BBBB	136	ILE	2.0145	1.4037	2.6254
BBBB	137	SER	9.9370	7.1329	15.5453
BBBB	138	ILE	3.5989	0.9814	6.2165
BBBB	139	THR	16.3957	2.4548	34.9836
BBBB	140	ASN	6.1076	3.6820	8.5333
BBBB	141	ALA	0.0000	0.0000	0.0000

	BBBB	142	THR	6.9409	0.3571	15.7193
	BBBB	143	VAL	8.0179	1.4651	16.7550
	BBBB	144	GLU	13.9749	4.2931	21.7203
	BBBB	145	ASP	4.2546	0.0236	8.4857
5	BBBB	146	SER	5.2200	3.1447	9.3705
	BBBB	147	GLY	3.2638	3.2638	0.0000
	BBBB	148	THR	5.2033	0.0855	12.0270
	BBBB	149	TYR	0.2349	0.0000	0.3523
	BBBB	150	TYR	3.8297	0.0006	5.7443
10	BBBB	151	CYS	0.0001	0.0002	0.0000
	BBBB	152	THR	3.8729	0.0115	9.0216
	BBBB	153	GLY	1.0080	1.0080	0.0000
	BBBB	154	LYS	6.2899	0.0456	11.2854
	BBBB	155	VAL	0.4338	0.0000	1.0121
15	BBBB	156	TRP	10.7302	3.5331	13.6790
	BBBB	157	GLN	13.5388	3.3217	21.7125
	BBBB	158	LEU	13.7581	0.1277	27.3885
	BBBB	159	ASP	13.8236	4.9295	22.7177
	BBBB	160	TYR	3.3842	2.5049	3.8239
20	BBBB	161	GLU	12.8172	5.3317	18.8056
	BBBB	162	SER	1.1166	1.6744	0.0011
	BBBB	163	GLU	9.2415	0.1789	16.4915
	BBBB	164	PRO	9.7119	1.5204	20.6339
	BBBB	165	LEU	1.6353	0.0985	3.1722
25	BBBB	166	ASN	4.1241	1.1171	7.1311
	BBBB	167	ILE	0.5678	1.1351	0.0006
	BBBB	168	THR	9.4957	0.0238	22.1247
	BBBB	169	VAL	0.5214	0.9124	0.0000
	BBBB	170	ILE	10.7674	1.5460	19.9889
30	BBBB	171	LYS	19.3575	14.1022	23.5617
	BBBB	221	NAG	13.1653	0.0000	13.1653
	BBBB	222	NAG	20.0638	0.0000	20.0638
	BBBB	242	NAG	5.8770	0.0000	5.8770
	BBBB	243	NAG	6.5918	0.0000	6.5918
35	BBBB	244	MAN	16.4886	0.0000	16.4886
	BBBB	250	NAG	16.1285	0.0000	16.1285
	BBBB	274	NAG	20.2170	0.0000	20.2170
	BBBB	335	NAG	14.9859	0.0000	14.9859
	BBBB	340	NAG	17.5037	0.0000	17.5037
40	BBBB	366	NAG	14.5337	0.0000	14.5337
	BBBB	367	NAG	21.0686	0.0000	21.0686
	DDDD	4	LYS	22.4057	10.8330	31.6640
	DDDD	5	PRO	1.1546	1.4746	0.7280
	DDDD	6	LYS	17.0122	1.1737	29.6830
45	DDDD	7	VAL	1.5813	2.7670	0.0004
	DDDD	8	SER	9.0050	1.8942	23.2265
	DDDD	9	LEU	3.6933	4.6049	2.7818
	DDDD	10	ASN	12.3091	1.0020	23.6161
	DDDD	11	PRO	8.3171	0.5504	18.6727
50	DDDD	12	PRO	9.9864	2.1032	20.4973
	DDDD	13	TRP	1.5517	0.0931	2.1352
	DDDD	14	ASN	3.3780	0.3110	6.4451
	DDDD	15	ARG	1.6343	0.0116	2.5615
	DDDD	16	ILE	1.1547	0.0005	2.3088
55	DDDD	17	PHE	0.2492	0.0000	0.3916
	DDDD	18	LYS	4.6732	2.0544	6.7683

	DDDD	19	GLY	3.1162	3.1162	0.0000
	DDDD	20	GLU	3.5200	0.0000	6.3359
	DDDD	21	ASN	5.4287	3.8849	6.9725
	DDDD	22	VAL	0.3155	0.4412	0.1479
5	DDDD	23	THR	5.1394	0.0324	11.9489
	DDDD	24	LEU	0.2366	0.0000	0.4733
	DDDD	25	THR	4.8738	0.0000	11.3721
	DDDD	26	CYS	0.2520	0.3402	0.0757
	DDDD	27	ASN	7.6624	1.9816	13.3432
10	DDDD	28	GLY	7.7316	7.7316	0.0000
	DDDD	29	ASN	17.3095	8.4320	26.1871
	DDDD	30	ASN	14.6001	10.1471	19.0532
	DDDD	31	PHE	18.5570	8.7657	24.1521
	DDDD	32	PHE	7.0815	6.8006	7.2420
15	DDDD	33	GLU	17.2171	4.7180	27.2164
	DDDD	34	VAL	10.0324	3.1007	19.2746
	DDDD	35	SER	14.2871	2.1039	38.6536
	DDDD	36	SER	6.9328	1.7803	17.2376
	DDDD	37	THR	0.7026	1.2295	0.0000
20	DDDD	38	LYS	8.3451	0.3160	14.7683
	DDDD	39	TRP	0.0041	0.0023	0.0049
	DDDD	40	PHE	2.9900	0.0009	4.6980
	DDDD	41	HIS	3.3768	0.3997	5.3616
	DDDD	42	ASN	6.4948	7.0880	5.9016
25	DDDD	43	GLY	9.5817	9.5817	0.0000
	DDDD	44	SER	12.6350	2.9429	32.0194
	DDDD	45	LEU	14.2578	6.4935	22.0220
	DDDD	46	SER	5.6757	3.8029	9.4212
	DDDD	47	GLU	19.9087	7.8667	29.5423
30	DDDD	48	GLU	6.0890	2.3899	9.0482
	DDDD	49	THR	10.8314	0.0116	25.2577
	DDDD	50	ASN	3.8373	0.9946	6.6800
	DDDD	51	SER	0.9841	0.0000	2.9524
	DDDD	52	SER	2.8765	0.0001	8.6293
35	DDDD	53	LEU	2.8376	0.0187	5.6565
	DDDD	54	ASN	7.0382	3.8726	10.2037
	DDDD	55	ILE	2.0467	1.4442	2.6492
	DDDD	56	VAL	11.5050	1.8629	24.3611
	DDDD	57	ASN	8.8180	1.0298	16.6062
40	DDDD	58	ALA	0.2350	0.2934	0.0018
	DDDD	59	LYS	13.6844	0.0264	24.6108
	DDDD	60	PHE	2.6066	0.0006	4.0957
	DDDD	61	GLU	8.6110	0.1659	15.3671
	DDDD	62	ASP	4.2057	0.0884	8.3230
45	DDDD	63	SER	0.1340	0.0000	0.4019
	DDDD	64	GLY	0.0349	0.0349	0.0000
	DDDD	65	GLU	8.1888	0.0852	14.6716
	DDDD	66	TYR	0.7677	0.0000	1.1516
	DDDD	67	LYS	3.2893	0.0000	5.9208
50	DDDD	68	CYS	0.0005	0.0000	0.0014
	DDDD	69	GLN	3.8578	0.0000	6.9441
	DDDD	70	HIS	2.2626	0.2237	3.6218
	DDDD	71	GLN	15.3304	6.1240	22.6955
	DDDD	72	GLN	18.9257	6.3446	28.9906
55	DDDD	73	VAL	6.4935	2.6517	11.6159
	DDDD	74	ASN	7.2861	0.8315	13.7407

DDDD	75	GLU	9.5469	4.3906	13.6720
DDDD	76	SER	0.4742	0.7107	0.0011
DDDD	77	GLU	16.0719	0.9787	28.1465
DDDD	78	PRO	8.1673	5.2859	12.0091
DDDD	79	VAL	5.7531	1.2596	11.7443
DDDD	80	TYR	6.8446	2.1690	9.1823
DDDD	81	LEU	0.2183	0.0000	0.4367
DDDD	82	GLU	5.8647	0.0374	10.5265
DDDD	83	VAL	1.5404	2.6954	0.0005
DDDD	84	PHE	2.7805	0.6706	3.9861
DDDD	85	SER	6.8439	5.9428	8.6459
DDDD	86	ASP	6.0109	2.1275	9.8943
DDDD	87	TRP	4.6976	0.2328	6.4835
DDDD	88	LEU	0.0296	0.0530	0.0062
DDDD	89	LEU	0.0803	0.0002	0.1605
DDDD	90	LEU	0.0000	0.0000	0.0000
DDDD	91	GLN	0.2460	0.0003	0.4426
DDDD	92	ALA	0.0626	0.0754	0.0113
DDDD	93	SER	4.5712	2.8665	7.9807
DDDD	94	ALA	8.7178	1.3188	38.3138
DDDD	95	GLU	7.2886	1.5976	11.8415
DDDD	96	VAL	12.8114	4.6767	23.6578
DDDD	97	VAL	1.4641	1.1764	1.8477
DDDD	98	MET	13.4393	0.1457	26.7329
DDDD	99	GLU	7.1147	4.7251.	9.0264
DDDD	100	GLY	5.3684	5.3684	0.0000
DDDD	101	GLN	9.8859	0.0000	17.7946
DDDD	102	PRO	9.5952	1.6262	20.2206
DDDD	103	LEU	0.0075	0.0150	0.0000
DDDD	104	PHE	6.3221	0.0000	9.9347
DDDD	105	LEU	0.0690	0.0712	0.0667
DDDD	106	ARG	2.3233	0.0001	3.6509
DDDD	107	CYS	0.8061	1.2091	0.0000
DDDD	108	HIS	1.1851	0.2808	1.7880
DDDD	109	GLY	1.2333	1.2333	0.0000
DDDD	110	TRP	0.7404	0.3219	0.9078
DDDD	111	ARG	7.9699	6.6124	8.7456
DDDD	112	ASN	12.5024	3.9088	21.0960
DDDD	113	TRP	2.0923	3.4514	1.5487
DDDD	114	ASP	11.6891	1.9841	21.3940
DDDD	115	VAL	0.8907	0.6666	1.1894
DDDD	116	TYR	3.5406	0.0000	5.3109
DDDD	117	LYS	7.4915	0.9137	12.7537
DDDD	118	VAL	0.0000	0.0000	0.0000
DDDD	119	ILE	1.5354	0.0000	3.0708
DDDD	120	TYR	0.0227	0.0000	0.0341
DDDD	121	TYR	3.0000	0.0000	4.5000
DDDD	122	LYS	3.8497	0.8215	6.2723
DDDD	123	ASP	11.0185	7.2080	14.8291
DDDD	124	GLY	13.8186	13.8186	0.0000
DDDD	125	GLU	7.1969	0.5597	12.5066
DDDD	126	ALA	1.6231	0.9637	4.2606
DDDD	127	LEU	5.5580	1.1317	9.9843
DDDD	128	LYS	11.0326	0.1803	19.7145
DDDD	129	TYR	6.0662	4.5993	6.7997
DDDD	130	TRP ·	6.9751 .	0.9821	9.3722

	DDDD	131	TYR	3.2844	1.1357	4.3587
	DDDD	132	GLU	10.5294	2.1545	17.2294
	DDDD	133	ASN	5.3145	5.3786	5.2503
	DDDD	134	HIS	8.2621	1.1783	12.9846
5	DDDD	135	ASN	1.2924	0.3403	2.2445
	DDDD	136	ILE	2.0846	1.3968	2.7725
	DDDD	137	SER	10.0460	7.2958	15.5465
	DDDD	138	ILE	3.5719	0.9619	6.1819
	DDDD	139	THR	16.0437	2.5113	34.0868
10	DDDD	140	ASN	6.1043	3.6342	8.5744
	DDDD	141	ALA	0.0006	0.0000	0.0028
	DDDD	142	THR	7.0414	0.4613	15.8150
	DDDD	143	VAL	7.7914	1.5021	16.1770
	DDDD	144	GLU	13.9850	4.2384	21.7824
15	DDDD	145	ASP	4.1793	0.0265	8.3322
	DDDD	146	SER	5.2665	3.1409	9.5178
	DDDD	147	GLY	3.2916	3.2916	0.0000
	DDDD	148	THR	5.1835	0.0792	11.9891
	DDDD	149	TYR	0.2058	0.0000	0.3087
20	DDDD	150	TYR	3.8607	0.0000	5.7910
	DDDD	151	CYS	0.0000	0.0000	0.0000
	DDDD	152	THR	3.9195	0.0065	9.1368
	DDDD	153	GLY	1.0864	1.0864	0.0000
	DDDD	154	LYS	5.0786	0.0302	9.1174
25	DDDD	155	VAL	0.4195	0.0000	0.9789
	DDDD	156	TRP	1.3921	2.1135	1.1036
	DDDD	157	GLN	5.1050	3.3675	6.4950
	DDDD	158	LEU	13.2526	0.1201	26.3851
	DDDD	159	ASP	7.9559	2.3964	13.5153
30	DDDD	160	TYR	2.2863	2.2919	2.2835
	DDDD	161	GLU	10.7234	4.9235	15.3634
	DDDD	162	SER	1.2506	1.8759	0.0000
	DDDD	163	GLU	9.3458	0.2040	16.6593
	DDDD	164	PRO	9.8122	1.5651	20.8083
35	DDDD	165	LEU	1.6668	0.0989	3.2347
	DDDD	166	ASN	4.0892	1.1470	7.0314
	DDDD	167	ILE	0.5690	1.1374	0.0006
	DDDD	168	THR	9.4203	0.0533	21.9098
	DDDD	169	VAL	0.5492	0.9611	0.0000
40	DDDD	170	ILE	10.5373	1.6298	19.4449
	DDDD	171	LYS	19.4334	14.2443	23.5846
	DDDD	221	NAG	12.4351	0.0000	12.4351
	DDDD	222	NAG	14.2041	0.0000	14.2041
	DDDD	242	NAG	9.7024	0.0000	9.7024
45	DDDD	243	NAG	9.7925	0.0000	9.7925
	DDDD	244	MAN	16.4248	0.0000	16.4248
	DDDD	250	NAG	15.9655	0.0000	15.9655
	DDDD	274	NAG	21.7485	0.0000	21.7485
	DDDD	335	NAG	15.0635	0.0000	15.0635
50	DDDD	340	NAG	17.6569	0.0000	17.6569
	DDDD	366	NAG	14.5792	0.0000	14.5792
	DDDD	367	NAG	20.8687	0.0000	20.8687
	EEEE	4	LYS	22.3558	10.9740	31.4612
	EEEE	5	PRO	1.1163	1.4301	0.6978
55	EEEE	6	LYS	16.9326	1.2182	29.5041
	EEEE	7	VAL	1.5370	2.6897	0.0000

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	EEEE	8	SER	9.0470	1.8198	23.5014
	EEEE	9	LEU	3.7362	4.7200	2.7524
	EEEE	10	ASN	12.0492	0.9478	23.1505
	EEEE	11	PRO	8.3799	0.5532	18.8156
5	EEEE	12	PRO	9.8266	2.0198	20.2356
	EEEE	13	TRP	1.5826	0.0955	2.1775
	EEEE	14	ASN	3.6101	0.2979	6.9223
	EEEE	15	ARG	1.6218	0.0098	2.5429
	EEEE	16	ILE	1.1456	0.0000	2.2912
10	EEEE	17	PHE	0.2563	0.0000	0.4027
	EEEE	18	LYS	10.9294	3.6992	16.7135
	EEEE	19	GLY	5.6751	5.6751	0.0000
	EEEE	20	GLU	3.4651	0.0024	6.2352
	EEEE	21	ASN	5.3587	3.9397	6.7777
15	EEEE	22	VAL	0.3206	0.4678	0.1243
	EEEE	23	THR	5.2106	0.0240	12.1261
	EEEE	24	LEU	0.2668	0.0000	0.5335
	EEEE	25	THR	4.8755	0.0000	11.3763
	EEEE	26	CYS	0.2422	0.3394	0.0477
20	EEEE	27	ASN	7.5792	1.5782	13.5803
	EEEE	28	GLY	7.7171	7.7171	0.0000
	EEEE	29	ASN	17.1451	8.1440	26.1463
	EEEE	30	ASN	14.2079	9.6254	18.7903
	EEEE	31	PHE	18.7547	8.6665	24.5194
25	EEEE	32	PHE	7.2539	7.0102	7.3931
	EEEE	33	GLU	17.0855	4.7908	26.9213
	EEEE	34	VAL	10.0735	3.1424	19.3149
	EEEE	35	SER	13.8902	2.0792	37.5120
	EEEE	36	SER	6.8523	1.7904	16.9760
30	EEEE	37	THR	0.6763	1.1836	0.0000
	EEEE	38	LYS	8.3619	0.3108	14.8028
	EEEE	39	TRP	0.0083	0.0020	0.0108
	EEEE	40	PHE	3.0042	0.0000	4.7209
	EEEE	41	HIS	3.3299	0.3808	5.2960
35	EEEE	42	ASN	6.3452	7.0674	5.6231
	EEEE	43	GLY	9.6662	9.6662	0.0000
	EEEE	44	SER	12.6323	3.0497	31.7975
	EEEE	45	LEU	14.2883	6.9452	21.6315
	EEEE	46	SER	5.9546	3.8685	10.1268
40	EEEE	47	GLU	19.8778	7.9851	29.3920
	EEEE	48	GLU	6.2775	2.2956	9.4630
	EEEE	49	THR	11.1492	0.0819	25.9055
	EEEE	50	ASN	3.8263	0.9910	6.6616
	EEEE	51	SER	0.9846	0.0000	2.9539
45	EEEE	52	SER	2.8049	0.0006	8.4134
	EEEE	53	LEU	2.6766	0.0083	5.3450
	EEEE	54	ASN	7.1063	3.8883	10.3243
	EEEE	55	ILE	2.1074	1.5164	2.6984
	EEEE	56	VAL	11.4388	1.7734	24.3260
50	EEEE	57	ASN	8.9664	1.0480	16.8848
	EEEE	58	ALA	0.3426	0.4045	0.0949
	EEEE	59	LYS	13.5640	0.0175	24.4012
	EEEE	60	PHE	3.4104	0.0051	5.3562
	EEEE	61	GLU	8.6064	0.1863	15.3424
55	EEEE	62	ASP	4.2246	0.0962	8.3531
	EEEE	63	SER	0.1134	0.0000	0.3402

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	EEEE	64	GLY	0.0266	0.0266	0.0000
	EEEE	65	GLU	4.0549	0.0880	7.2284
	EEEE	66	TYR	0.7832	0.0000	1.1748
	EEEE	67	LYS	3.2565	0.0000	5.8617
5	EEEE	68	CYS	0.0003	0.0005	0.0000
	EEEE	69	GLN	3.8454	0.0000	6.9217
	EEEE	70	HIS	2.2450	0.2224	3.5934
	EEEE	71	GLN	5.9169	3.6396	7.7387
	EEEE	72	GLN	7.4965	6.0264	8.6726
10	EEEE	73	VAL	6.4019	2.4812	11.6294
	EEEE	74	ASN	7.3226	0.8649	13.7804
	EEEE	75	GLU	9.5795	4.4019	13.7216
	EEEE	76	SER	0.7013	1.0519	0.0000
	EEEE	77	GLU	13.4227	1.1013	23.2799
15	EEEE	78	PRO	2.4705	1.5274	3.7280
	EEEE	79	VAL	5.5768	0.7997	11.9463
	EEEE	80	TYR	3.6523	1.2328	4.8621
	EEEE	81	LEU	0.2451	0.0000	0.4902
	EEEE	82	GLU	5.5763	0.0256	10.0168
20	EEEE	83	VAL	1.5663	2.7355	0.0074
	EEEE	84	PHE	2.8317	0.6685	4.0678
	EEEE	85	SER	11.1097	5.8236	21.6819
	EEEE	86	ASP	6.3216	2.7103	9.9328
	EEEE	87	TRP	9.2509	0.2339	12.8578
25	EEEE	88	LEU	0.0596	0.1001	0.0191
	EEEE	89	LEU	0.1011	0.0000	0.2022
	EEEE	90	LEU	0.0000	0.0000	0.0000
	EEEE	91	GLN	0.2558	0.0000	0.4604
	EEEE	92	ALA	0.0564	0.0519	0.0745
30	EEEE	93	SER	4.5837	2.9367	7.8777
	EEEE	94	ALA	8.3906	1.2888	36.7978
	EEEE	95	GLU	4.4296	1.5357	6.7447
	EEEE	96	VAL	4.3010	4.6742	3.8035
	EEEE	97	VAL	1.4250	1.0740	1.8929
35	EEEE	98	MET	13.5431	0.2108	26.8754
	EEEE	99	GLU	7.1778	4.7822	9.0943
	EEEE	100	GLY	5.0685	5.0685	0.0000
	EEEE	101	GLN	9.8626	0.0125	17.7427
	EEEE	102	PRO	9.4878	1.6105	19.9908
40	EEEE	103	LEU	0.0128	0.0246	0.0009
	EEEE	104	PHE	6.2895	0.0000	9.8835
	EEEE	105	LEU	0.0574	0.0715	0.0432
	EEEE	106	ARG	2.3284	0.0000	3.6589
	EEEE	107	CYS	0.7794	1.1691	0.0000
45	EEEE	108	HIS	1.2031	0.2846	1.8155
	EEEE	109	GLY	1.3076	1.3076	0.0000
	EEEE	110	TRP	4.3507	0.3127	5.9659
	EEEE	111	ARG	14.5626	6.7438	19.0305
	EEEE	112	ASN	12.6107	3.8715	21.3499
50	EEEE	113	TRP	7.0410	3.3592	8.5138
	EEEE	114	ASP	11.4765	1.9258	21.0271
	EEEE	115	VAL	0.8593	0.6604	1.1244
	EEEE	116	TYR	5.8929	0.0005	8.8392
	EEEE	117	LYS	11.3051	0.9380	19.5988
55	EEEE	118	VAL	0.0000	0.0000	0.0000
	EEEE	119	ILE	4.8820	0.0000	9.7641

EEEE	120	TYR	0.0103	0.0000	0.0154
EEEE	121	TYR	3.6542	0.0005	5.4811
EEEE	122	LYS	3.7815	0.6097	6.3190
EEEE	123	ASP	10.9462	6.9829	14.9095
EEEE	124	GLY	13.7762	13.7762	0.0000
EEEE	125	GLU	13.1766	0.5548	23.2741
EEEE	126	ALA	14.6424	5.3245	51.9143
EEEE	127	LEU	9.2224	5.9305	12.5143
EEEE	128	LYS	11.5329	1.8633	19.2686
EEEE	129	TYR	10.3194	5.0683	12.9449
EEEE	130	TRP	8.0715	0.9722	10.9112
EEEE	131	TYR	11.8508	1.0518	17.2503
EEEE	132	GLU	12.7984	2.2087	21.2701
EEEE	133	ASN	5.2222	5.2458	5.1985
EEEE	134	HIS	8.275	1.2222	12.9775
EEEE	135	ASN	1.3104	0.3410	2.2798
EEEE	136	ILE	2.0064	1.3737	2.6391
EEEE	137	SER	10.1799	7.2553	16.0292
EEEE	138	ILE	3.5424	0.9990	6.0858
EEEE	139	THR	16.1230	2.4880	34.3029
EEEE	140	ASN	6.0914	3.7069	8.4760
EEEE	141	ALA	0.0000	0.0000	0.0000
EEEE	142	THR	7.1532	0.3267	16.2552
EEEE	143	VAL	4.0502	1.4721	7.4876
EEEE	144	GLU	14.1982	4.3093	22.1094
EEEE	145	ASP	4.2616	0.0294	8.4938
EEEE	146	SER	5.0852	3.1109	9.0339
EEEE	147	GLY	3.2633	3.2633	0.0000
EEEE	148	THR	5.3711	0.0808	12.4248
EEEE	149	TYR	0.2123	0.0000	0.3185
EEEE	150	TYR	3.8241	0.0000	5.7362
EEEE	151	CYS	0.0000	0.0000	0.0000
EEEE	152	THR	3.8973	0.0053	9.0866
EEEE	153	GLY	1.0506	1.0506	0.0000
EEEE	154	LYS	6.3259	0.0465	11.3493
EEEE	155	VAL	0.4347	0.0000	1.0143
EEEE	156	TRP	10.7736	3.6761	13.6126
EEEE	157	GLN	13.4826	3.3463	21.5916
EEEE	158	LEU	13.9288	0.1999	27.6578
EEEE	159	ASP	14.3643	5.1303	23.5982
EEEE	160	TYR	3.4607	2.4956	3.9432
EEEE	161	GLU	12.5195	4.7567	18.7297
EEEE	162	SER	1.0778	1.6166	0.0000
EEEE	163	GLU	9.3641	0.1874	16.7054
EEEE	164	PRO	9.7812	1.5531	20.7519
EEEE	165	LEU	1.6355	0.0916	3.1794
EEEE	166	ASN	3.8982	1.0603	6.7362
EEEE	167	ILE	0.5697	1.1379	0.0016
EEEE	168	THR	2.3606	0.0217	5.4780
EEEE	169	VAL	0.0074	0.0129	0.0000
EEEE	170	ILE	2.2300	0.0089	4.4512
EEEE	171	LYS	14.7618	13.0272	16.1495
EEEE	221	NAG	12.9978	0.0000	12.9978
EEEE	222	NAG	20.1629	0.0000	20.1629
EEEE	242	NAG	8.4007	0.0000	8.4007
EEEE	243	NAG	8.4488	0.0000	8.4488

	EEEE	244	MAN	16.3142	0.0000	16.3142
	EEEE	250	NAG	15.9751	0.0000	15.9754
	EEEE	274	NAG	18.4789	0.0000	18.4789
	EEEE	335	NAG	14.8589	0.0000	14.8589
5	EEEE	340	NAG	17.7265	0.0000	17.7265
	EEEE	366	NAG	11.7893	0.0000	11.7893
	EEEE	367	NAG	18.5598	0.0000	18.5598

Table 10. PhFcεRIα$_{1-172}$, Form T2, residue exposure

>>>>   coordinate set= pent74_11c1.pdb

seqid	resid	resname	access	access-main	access-side
CCCC	4	LYS	22.5230	10.8738	31.8424
CCCC	5	PRO	1.1416	1.5686	0.5722
CCCC	6	LYS	17.1986	1.4144	29.8259
CCCC	7	VAL	1.6270	2.8202	0.0362
CCCC	8	SER	8.6366	1.9053	22.0990
CCCC	9	LEU	4.4395	5.4841	3.3949
CCCC	10	ASN	12.0444	0.9261	23.1626
CCCC	11	PRO	7.7510	0.4778	17.4486
CCCC	12	PRO	10.0046	2.2549	20.3375
CCCC	13	TRP	1.5672	0.1129	2.1488
CCCC	14	ASN	3.3834	0.3515	6.4153
CCCC	15	ARG	1.7214	0.0000	2.7051
CCCC	16	ILE	0.9799	0.0000	1.9599
CCCC	17	PHE	0.2972	0.0000	0.4670
CCCC	18	LYS	11.0480	3.8504	16.8061
CCCC	19	GLY	5.6439	5.6439	0.0000
CCCC	20	GLU	3.6350	0.0352	6.5149
CCCC	21	ASN	5.3939	4.1927	6.5951
CCCC	22	VAL	0.2954	0.4493	0.0902
CCCC	23	THR	5.4708	0.0934	12.6405
CCCC	24	LEU	0.4978	0.0000	0.9957
CCCC	25	THR	5.1976	0.0006	12.1271
CCCC	26	CYS	0.3073	0.3299	0.2621
CCCC	27	ASN	8.5100	1.3260	15.6940
CCCC	28	GLY	6.8597	6.8597	0.0000
CCCC	29	ASN	17.2073	7.8659	26.5486
CCCC	30	ASN	14.4090	9.6919	19.1261
CCCC	31	PHE	18.6560	9.4593	23.9112
CCCC	32	PHE	7.3970	6.8547	7.7068
CCCC	33	GLU	17.4505	4.8495	27.5314
CCCC	34	VAL	10.1697	3.7420	18.7399
CCCC	35	SER	14.6634	2.2968	39.3965
CCCC	36	SER	7.1609	1.9487	17.5852
CCCC	37	THR	0.7165	1.2539	0.0000
CCCC	38	LYS	8.8073	0.3430	15.5788
CCCC	39	TRP	0.0048	0.0169	0.0000
CCCC	40	PHE	3.0029	0.0000	4.8131
CCCC	41	HIS	3.2953	0.2185	5.3465
CCCC	42	ASN	6.4333	7.3988	5.4678
CCCC	43	GLY	8.7787	8.7787	0.0000
CCCC	44	SER	12.5780	3.2206	31.2928
CCCC	45	LEU	14.3835	6.5311	22.2359
CCCC	46	SER	6.0642	4.1760	9.8407
CCCC	47	GLU	19.8848	8.0573	29.3468
CCCC	48	GLU	5.7325	2.1429	8.6042
CCCC	49	THR	11.1779	0.0000	26.0818
CCCC	50	ASN	3.7291	1.0808	6.3774
CCCC	51	SER	1.1927	0.0000	3.5780

	CCCC	52	SER	2.7289	0.0000	8.1866
	CCCC	53	LEU	2.8602	0.0189	5.7014
	CCCC	54	ASN	7.0896	4.0346	10.1446
	CCCC	55	ILE	1.9722	1.4947	2.4497
5	CCCC	56	VAL	11.4466	1.8119	24.2929
	CCCC	57	ASN	9.2079	1.1203	17.2954
	CCCC	58	ALA	0.2682	0.3352	0.0000
	CCCC	59	LYS	13.5663	0.0799	24.3554
	CCCC	60	PHE	4.2653	0.0614	6.6675
10	CCCC	61	GLU	9.3104	0.1429	16.6444
	CCCC	62	ASP	4.1004	0.0929	8.1079
	CCCC	63	SER	0.1952	0.0000	0.5857
	CCCC	64	GLY	0.0000	0.0000	0.0000
	CCCC	65	GLU	3.3950	0.0904	6.0387
15	CCCC	66	TYR	1.0210	0.0004	1.5313
	CCCC	67	LYS	3.2922	0.0006	5.9255
	CCCC	68	CYS	0.0000	0.0000	0.0000
	CCCC	69	GLN	4.0273	0.0000	7.2491
	CCCC	70	HIS	2.4293	0.2618	3.8743
20	CCCC	71	GLN	10.1947	6.5416	23.8992
	CCCC	72	GLN	18.7079	6.7237	28.2952
	CCCC	73	VAL	5.9018	2.0768	11.0019
	CCCC	74	ASN	7.6674	1.2523	14.0824
	CCCC	75	GLU	9.5618	4.3436	13.7363
25	CCCC	76	SER	0.7453	1.1107	0.0146
	CCCC	77	GLU	13.4902	1.2113	23.3134
	CCCC	78	PRO	3.7570	2.4424	5.5097
	CCCC	79	VAL	6.2786	1.0035	13.3121
	CCCC	80	TYR	4.8276	1.6806	6.4011
30	CCCC	81	LEU	0.4499	0.0000	0.8998
	CCCC	82	GLU	6.0083	0.0302	10.7907
	CCCC	83	VAL	1.5038	2.6317	0.0000
	CCCC	84	PHE	2.9396	0.6034	4.2746
	CCCC	85	SER	11.0379	5.9825	21.1488
35	CCCC	86	ASP	6.6954	2.8722	10.5186
	CCCC	87	TRP	5.7551	0.2523	7.9563
	CCCC	88	LEU	0.0496	0.0992	0.0000
	CCCC	89	LEU	0.0722	0.0000	0.1444
	CCCC	90	LEU	0.0039	0.0006	0.0071
40	CCCC	91	GLN	0.2715	0.0000	0.4886
	CCCC	92	ALA	0.1064	0.1238	0.0367
	CCCC	93	SER	4.5560	3.0073	7.6533
	CCCC	94	ALA	8.2925	1.3979	35.8708
	CCCC	95	GLU	5.1869	1.5220	8.1188
45	CCCC	96	VAL	5.3247	4.5540	6.3524
	CCCC	97	VAL	1.5905	0.9728	2.4141
	CCCC	98	MET	14.3166	0.0743	28.5590
	CCCC	99	GLU	7.0891	5.0739	8.7013
	CCCC	100	GLY	5.1879	5.1879	0.0000
50	CCCC	101	GLN	9.5976	0.0133	17.2651
	CCCC	102	PRO	9.4229	1.5439	19.9284
	CCCC	103	LEU	0.0333	0.0371	0.0295
	CCCC	104	PHE	6.3516	0.0000	9.9811
	CCCC	105	LEU	0.1059	0.0591	0.1526
55	CCCC	106	ARG	2.2520	0.0000	3.5388
	CCCC	107	CYS	0.6406	0.9609	0.0000

	CCCC	108	HIS	1.1793	0.2252	1.8153
	CCCC	109	GLY	1.3114	1.3114	0.0000
	CCCC	110	TRP	4.6295	0.3368	6.3465
	CCCC	111	ARG	13.1248	6.9961	16.6270
5	CCCC	112	ASN	12.8011	4.3120	21.2901
	CCCC	113	TRP	6.0437	3.3401	7.1251
	CCCC	114	ASP	11.9344	1.8804	21.9884
	CCCC	115	VAL	0.9151	0.7229	1.1714
	CCCC	116	TYR	5.9569	0.0000	8.9354
10	CCCC	117	LYS	11.0444	0.6651	19.3478
	CCCC	118	VAL	0.0000	0.0000	0.0000
	CCCC	119	ILE	4.4790	0.0001	8.9579
	CCCC	120	TYR	0.0043	0.0000	0.0064
	CCCC	121	TYR	3.7210	0.0085	5.5773
15	CCCC	122	LYS	4.0141	0.9317	6.4800
	CCCC	123	ASP	10.8032	6.5278	15.0786
	CCCC	124	GLY	14.5419	14.5419	0.0000
	CCCC	125	GLU	12.8310	0.4067	22.7705
	CCCC	126	ALA	14.9558	5.5670	52.5110
20	CCCC	127	LEU	9.4777	6.3362	12.6193
	CCCC	128	LYS	11.7644	1.7577	19.7697
	CCCC	129	TYR	10.4250	4.9480	13.1636
	CCCC	130	TRP	8.2395	1.0761	11.1049
	CCCC	131	TYR	12.1293	0.8795	17.7543
25	CCCC	132	GLU	12.7495	1.9453	21.3930
	CCCC	133	ASN	5.6282	5.4710	5.7854
	CCCC	134	HIS	8.2353	1.4518	12.7576
	CCCC	135	ASN	1.3610	0.3583	2.3637
	CCCC	136	ILE	2.1395	1.3206	2.9584
30	CCCC	137	SER	10.0045	7.3132	15.3872
	CCCC	138	ILE	3.5461	0.8905	6.2017
	CCCC	139	THR	15.6326	2.4796	33.1700
	CCCC	140	ASN	6.4183	3.6583	9.1784
	CCCC	141	ALA	0.0002	0.0000	0.0009
35	CCCC	142	THR	7.3418	0.3932	16.6068
	CCCC	143	VAL	5.5574	1.0899	11.5140
	CCCC	144	GLU	14.2578	4.3490	22.1849
	CCCC	145	ASP	4.1649	0.0654	8.2644
	CCCC	146	SER	5.4994	3.9946	8.5092
40	CCCC	147	GLY	2.9610	2.9610	0.0000
	CCCC	148	THR	5.8295	0.0862	13.4873
	CCCC	149	TYR	0.2839	0.0098	0.4210
	CCCC	150	TYR	3.8352	0.0141	5.7458
	CCCC	151	CYS	0.0000	0.0000	0.0000
45	CCCC	152	THR	3.7535	0.0000	8.7581
	CCCC	153	GLY	1.0847	1.0847	0.0000
	CCCC	154	LYS	6.0253	0.0000	10.8456
	CCCC	155	VAL	0.4796	0.0000	1.1192
	CCCC	156	TRP	5.6483	5.3816	5.7550
50	CCCC	157	GLN	13.9764	3.1848	22.6098
	CCCC	158	LEU	9.4587	0.2983	18.6191
	CCCC	159	ASP	14.1094	4.9876	23.2312
	CCCC	160	TYR	2.5046	2.3069	2.6034
	CCCC	161	GLU	13.4023	4.9331	20.1776
55	CCCC	162	SER	1.0596	1.5893	0.0000
	CCCC	163	GLU	9.9946	0.7061	17.4254

	CCCC	164	PRO	10.2249	1.5777	21.7546
	CCCC	165	LEU	1.6401	0.1628	3.1175
	CCCC	166	ASN	3.3684	1.0069	5.7299
	CCCC	167	ILE	0.5437	1.0633	0.0240
5	CCCC	168	THR	4.2337	0.0946	9.7525
	CCCC	169	VAL	0.1117	0.1954	0.0000
	CCCC	170	ILE	2.4168	0.0906	4.7430
	CCCC	171	LYS	14.4505	13.2729	15.3926
	CCCC	221	NAG	13.3692	0.0000	13.3692
10	CCCC	222	NAG	19.4652	0.0000	19.4652
	CCCC	242	NAG	9.4466	0.0000	9.4466
	CCCC	243	NAG	8.1868	0.0000	8.1868
	CCCC	244	MAN	18.7031	0.0000	18.7031
	CCCC	250	NAG	16.1904	0.0000	16.1904
15	CCCC	274	NAG	21.9195	0.0000	21.9195
	CCCC	335	NAG	15.0294	0.0000	15.0294
	CCCC	340	NAG	17.5228	0.0000	17.5228
	CCCC	366	NAG	12.1164	0.0000	12.1164
	CCCC	367	NAG	19.5921	0.0000	19.5921
20	AAAA	4	LYS	20.9627	10.5913	29.2599
	AAAA	5	PRO	1.1603	1.5921	0.5846
	AAAA	6	LYS	16.7967	1.3698	29.1382
	AAAA	7	VAL	1.6748	2.8323	0.1316
	AAAA	8	SER	8.1802	1.8708	20.7991
25	AAAA	9	LEU	4.4389	5.4321	3.4456
	AAAA	10	ASN	12.2932	0.9523	23.6341
	AAAA	11	PRO	7.8292	0.4916	17.6128
	AAAA	12	PRO	9.7721	2.2628	19.7845
	AAAA	13	TRP	1.5676	0.0823	2.1617
30	AAAA	14	ASN	3.0526	0.3315	5.7738
	AAAA	15	ARG	1.7626	0.0011	2.7691
	AAAA	16	ILE	0.9627	0.0000	1.9254
	AAAA	17	PHE	0.3249	0.0000	0.5105
	AAAA	18	LYS	10.8420	3.4841	16.7283
35	AAAA	19	GLY	5.4381	5.4381	0.0000
	AAAA	20	GLU	3.6790	0.0263	6.6011
	AAAA	21	ASN	5.3743	4.2040	6.5445
	AAAA	22	VAL	0.2940	0.4433	0.0951
	AAAA	23	THR	5.8035	0.1030	13.4041
40	AAAA	24	LEU	0.4614	0.0000	0.9228
	AAAA	25	THR	5.1305	0.0007	11.9704
	AAAA	26	CYS	0.2915	0.3512	0.1723
	AAAA	27	ASN	6.2421	1.5400	10.9443
	AAAA	28	GLY	6.9474	6.9474	0.0000
45	AAAA	29	ASN	17.1386	8.6715	25.6057
	AAAA	30	ASN	14.4072	9.6995	19.1150
	AAAA	31	PHE	15.4860	6.5595	20.5869
	AAAA	32	PHE	3.7024	5.7813	2.5144
	AAAA	33	GLU	6.0657	4.8688	7.0232
50	AAAA	34	VAL	5.5276	3.8118	7.8153
	AAAA	35	SER	14.1613	2.3658	37.7522
	AAAA	36	SER	7.1159	1.7815	17.7848
	AAAA	37	THR	0.7225	1.2641	0.0004
	AAAA	38	LYS	8.7294	0.3364	15.4439
55	AAAA	39	TRP	0.0092	0.0322	0.0000
	AAAA	40	PHE	3.1015	0.0000	4.8738

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	AAAA	41	HIS	3.4263	0.4703	5.3969
	AAAA	42	ASN	6.4271	7.3557	5.4985
	AAAA	43	GLY	8.7869	8.7869	0.0000
	AAAA	44	SER	12.6493	3.0960	31.7559
5	AAAA	45	LEU	14.5777	6.7914	22.3640
	AAAA	46	SER	5.5814	3.9481	8.8482
	AAAA	47	GLU	19.7555	7.9429	29.2055
	AAAA	48	GLU	5.9957	2.0924	9.1182
	AAAA	49	THR	11.1755	0.0000	26.0762
10	AAAA	50	ASN	3.7477	1.0911	6.4042
	AAAA	51	SER	1.1636	0.0000	3.4907
	AAAA	52	SER	2.7526	0.0004	8.2570
	AAAA	53	LEU	2.9437	0.0016	5.8859
	AAAA	54	ASN	7.0747	3.8236	10.3258
15	AAAA	55	ILE	1.9632	1.5156	2.4109
	AAAA	56	VAL	11.4314	1.7967	24.2777
	AAAA	57	ASN	8.8194	1.1924	16.4463
	AAAA	58	ALA	0.3818	0.4773	0.0000
	AAAA	59	LYS	14.0268	0.1179	25.1539
20	AAAA	60	PHE	4.2543	0.0600	6.6511
	AAAA	61	GLU	9.3832	0.1346	16.7820
	AAAA	62	ASP	4.0523	0.0770	8.0275
	AAAA	63	SER	0.1601	0.0000	0.4802
	AAAA	64	GLY	0.0003	0.0003	0.0000
25	AAAA	65	GLU	7.8567	0.0750	14.0821
	AAAA	66	TYR	1.0215	0.0000	1.5322
	AAAA	67	LYS	3.3027	0.0000	5.9449
	AAAA	68	CYS	0.0000	0.0000	0.0000
	AAAA	69	GLN	3.9650	0.0000	7.1371
30	AAAA	70	HIS	1.3538	0.2724	2.0747
	AAAA	71	GLN	16.3949	6.5138	24.2997
	AAAA	72	GLN	18.9827	6.9646	28.5973
	AAAA	73	VAL	4.9867	2.0211	8.9408
	AAAA	74	ASN	7.4791	1.0651	13.8931
35	AAAA	75	GLU	9.6144	4.2579	13.8996
	AAAA	76	SER	0.6674	0.9903	0.0214
	AAAA	77	GLU	15.9242	1.2854	27.6353
	AAAA	78	PRO	8.1677	4.8944	12.5320
	AAAA	79	VAL	6.4525	1.5909	12.9345
40	AAAA	80	TYR	7.2923	1.8827	9.9971
	AAAA	81	LEU	0.4642	0.0000	0.9283
	AAAA	82	GLU	6.0060	0.0321	10.7852
	AAAA	83	VAL	1.5422	2.6988	0.0000
	AAAA	84	PHE	2.9572	0.6545	4.2730
45	AAAA	85	SER	10.8486	6.1560	20.2338
	AAAA	86	ASP	6.1844	2.2433	10.1256
	AAAA	87	TRP	9.3655	0.2163	13.0252
	AAAA	88	LEU	0.0504	0.1008	0.0000
	AAAA	89	LEU	0.1469	0.0000	0.2937
50	AAAA	90	LEU	0.0016	0.0007	0.0025
	AAAA	91	GLN	0.2732	0.0066	0.4865
	AAAA	92	ALA	0.0432	0.0426	0.0458
	AAAA	93	SER	4.4502	2.9733	7.4040
	AAAA	94	ALA	8.7362	1.3963	38.0959
55	AAAA	95	GLU	7.1768	1.5655	11.6658
	AAAA	96	VAL	13.5692	4.6624	25.4450

	AAAA	97	VAL	1.5462	0.9380	2.3571
	AAAA	98	MET	14.3960	0.0702	28.7219
	AAAA	99	GLU	7.3826	4.6030	9.6063
	AAAA	100	GLY	4.9867	4.9867	0.0000
5	AAAA	101	GLN	9.6618	0.0164	17.3782
	AAAA	102	PRO	9.4982	1.5257	20.1283
	AAAA	103	LEU	0.0170	0.0095	0.0245
	AAAA	104	PHE	6.3600	0.0000	9.9943
	AAAA	105	LEU	0.0964	0.0678	0.1250
10	AAAA	106	ARG	2.2271	0.0002	3.4997
	AAAA	107	CYS	0.6410	0.9615	0.0000
	AAAA	108	HIS	1.1779	0.2061	1.8257
	AAAA	109	GLY	1.2835	1.2835	0.0000
	AAAA	110	TRP	4.3852	0.3446	6.0014
15	AAAA	111	ARG	14.5965	6.9788	18.9495
	AAAA	112	ASN	13.1375	4.4344	21.8406
	AAAA	113	TRP	7.1680	3.4865	8.6407
	AAAA	114	ASP	11.7831	1.8946	21.6716
	AAAA	115	VAL	0.9352	0.7629	1.1650
20	AAAA	116	TYR	5.3542	0.0000	8.0313
	AAAA	117	LYS	7.2506	0.7461	12.4542
	AAAA	118	VAL	0.0000	0.0000	0.0000
	AAAA	119	ILE	1.6994	0.0000	3.3988
	AAAA	120	TYR	0.0315	0.0007	0.0469
25	AAAA	121	TYR	2.9781	0.0007	4.4667
	AAAA	122	LYS	3.9855	0.7635	6.5630
	AAAA	123	ASP	10.6844	6.3101	15.0587
	AAAA	124	GLY	14.6459	14.6459	0.0000
	AAAA	125	GLU	7.8188	0.3898	13.7619
30	AAAA	126	ALA	2.0714	1.0926	5.9866
	AAAA	127	LEU	5.8795	1.4447	10.3142
	AAAA	128	LYS	11.0255	0.1820	19.7002
	AAAA	129	TYR	5.6220	4.2110	6.3275
	AAAA	130	TRP	6.9643	1.0858	9.3157
35	AAAA	131	TYR	2.7608	0.9482	3.6671
	AAAA	132	GLU	9.8508	1.9760	16.1507
	AAAA	133	ASN	5.7009	5.5383	5.8635
	AAAA	134	HIS	8.0039	1.5080	12.3344
	AAAA	135	ASN	1.3397	0.3105	2.3689
40	AAAA	136	ILE	2.1821	1.3384	3.0258
	AAAA	137	SER	9.9955	7.3477	15.2912
	AAAA	138	ILE	3.4842	0.8752	6.0933
	AAAA	139	THR	15.7464	2.4744	33.4424
	AAAA	140	ASN	6.4552	3.7317	9.1786
45	AAAA	141	ALA	0.0000	0.0000	0.0000
	AAAA	142	THR	7.4724	0.4042	16.8967
	AAAA	143	VAL	7.7469	1.0561	16.6680
	AAAA	144	GLU	14.1113	4.3219	21.9429
	AAAA	145	ASP	4.3240	0.0500	8.5980
50	AAAA	146	SER	5.4853	4.0599	8.3361
	AAAA	147	GLY	2.8492	2.8492	0.0000
	AAAA	148	THR	5.7830	0.0884	13.3757
	AAAA	149	TYR	0.2720	0.0018	0.4071
	AAAA	150	TYR	3.9253	0.0098	5.8831
55	AAAA	151	CYS	0.0000	0.0000	0.0000
	AAAA	152	THR	3.7350	0.0000	8.7151

AAAA	153	GLY	1.0268	1.0268	0.0000
AAAA	154	LYS	4.9160	0.0084	8.8421
AAAA	155	VAL	0.4691	0.0000	1.0946
AAAA	156	TRP	11.7056	5.3116	14.2632
AAAA	157	GLN	9.2515	3.3242	13.9933
AAAA	158	LEU	13.8847	0.2727	27.4967
AAAA	159	ASP	9.2336	3.2139	15.2533
AAAA	160	TYR	3.5492	2.3626	4.1425
AAAA	161	GLU	11.2704	5.0419	16.2531
AAAA	162	SER	1.1125	1.6687	0.0000
AAAA	163	GLU	9.7709	0.4328	17.2413
AAAA	164	PRO	10.3588	1.5740	22.0717
AAAA	165	LEU	1.6439	0.1655	3.1223
AAAA	166	ASN	4.0686	1.1039	7.0332
AAAA	167	ILE	0.5158	1.0240	0.0075
AAAA	168	THR	10.0323	0.1297	23.2358
AAAA	169	VAL	0.5330	0.8959	0.0491
AAAA	170	ILE	10.6523	1.5082	19.7963
AAAA	171	LYS	20.1585	15.5532	23.8428
AAAA	221	NAG	13.2449	0.0000	13.2449
AAAA	222	NAG	19.9892	0.0000	19.9892
AAAA	242	NAG	9.9407	0.0000	9.9407
AAAA	243	NAG	9.4600	0.0000	9.4600
AAAA	244	MAN	18.6631	0.0000	18.6631
AAAA	250	NAG	16.3080	0.0000	16.3080
AAAA	274	NAG	21.8749	0.0000	21.8749
AAAA	335	NAG	15.0157	0.0000	15.0157
AAAA	340	NAG	17.2280	0.0000	17.2280
AAAA	366	NAG	14.4545	0.0000	14.4545
AAAA	367	NAG	20.9042	0.0000	20.9042
BBBB	4	LYS	22.4434	10.6722	31.8604
BBBB	5	PRO	1.1609	1.5819	0.5996
BBBB	6	LYS	16.5842	1.4102	28.7235
BBBB	7	VAL	1.6862	2.8240	0.1692
BBBB	8	SER	8.2982	1.8668	21.1609
BBBB	9	LEU	4.4129	5.4051	3.4206
BBBB	10	ASN	11.9525	0.9175	22.9875
BBBB	11	PRO	7.8250	0.4752	17.6248
BBBB	12	PRO	10.1980	2.1957	20.8677
BBBB	13	TRP	1.5849	0.0977	2.1798
BBBB	14	ASN	3.3380	0.3318	6.3443
BBBB	15	ARG	1.7418	0.0000	2.7372
BBBB	16	ILE	0.9354	0.0001	1.8707
BBBB	17	PHE	0.3221	0.0000	0.5062
BBBB	18	LYS	11.1312	3.8205	16.9798
BBBB	19	GLY	5.3141	5.3141	0.0000
BBBB	20	GLU	3.5506	0.0401	6.3590
BBBB	21	ASN	5.3304	4.1079	6.5530
BBBB	22	VAL	0.2845	0.4466	0.0683
BBBB	23	THR	5.5150	0.0841	12.7561
BBBB	24	LEU	0.4740	0.0000	0.9480
BBBB	25	THR	5.1331	0.0000	11.9772
BBBB	26	CYS	0.2892	0.3174	0.2327
BBBB	27	ASN	6.4305	1.5210	11.3399
BBBB	28	GLY	7.2421	7.2421	0.0000
BBBB	29	ASN	17.3886	8.6086	26.1686

BBBB	30	ASN	14.2633	10.0072	18.5194
BBBB	31	PHE	18.8528	9.5505	24.1684
BBBB	32	PHE	6.5037	6.5617	6.4706
BBBB	33	GLU	12.9342	4.8992	19.3623
BBBB	34	VAL	8.3666	3.8085	14.4440
BBBB	35	SER	14.2536	2.2580	38.2448
BBBB	36	SER	7.1333	1.8956	17.6087
BBBB	37	THR	0.7187	1.2577	0.0000
BBBB	38	LYS	8.8478	0.3137	15.6751
BBBB	39	TRP	0.0155	0.0288	0.0102
BBBB	40	PHE	3.1021	0.0000	4.8747
BBBB	41	HIS	3.3964	0.4181	5.3819
BBBB	42	ASN	4.3570	5.3484	3.3656
BBBB	43	GLY	8.6389	8.6389	0.0000
BBBB	44	SER	12.5229	3.2589	31.0508
BBBB	45	LEU	14.4289	6.6263	22.2316
BBBB	46	SER	6.1946	4.5349	9.5141
BBBB	47	GLU	19.7813	8.0788	29.1432
BBBB	48	GLU	5.7938	2.2706	8.6124
BBBB	49	THR	11.0771	0.0000	25.8466
BBBB	50	ASN	3.6499	1.0731	6.2267
BBBB	51	SER	1.1954	0.0005	3.5851
BBBB	52	SER	2.7282	0.0002	8.1843
BBBB	53	LEU	2.6801	0.0033	5.3570
BBBB	54	ASN	7.0535	4.0402	10.0668
BBBB	55	ILE	1.9823	1.5180	2.4466
BBBB	56	VAL	11.5628	1.8317	24.5377
BBBB	57	ASN	8.8810	1.1220	16.6400
BBBB	58	ALA	0.3193	0.3991	0.0000
BBBB	59	LYS	13.7310	0.1005	24.6353
BBBB	60	PHE	4.2410	0.1526	6.5772
BBBB	61	GLU	9.1821	0.1249	16.4278
BBBB	62	ASP	4.1444	0.0742	8.2145
BBBB	63	SER	0.1404	0.0003	0.4207
BBBB	64	GLY	0.0115	0.0115	0.0000
BBBB	65	GLU	7.8724	0.0613	14.1212
BBBB	66	TYR	1.0150	0.0106	1.5171
BBBB	67	LYS	3.3196	0.0000	5.9752
BBBB	68	CYS	0.0000	0.0000	0.0000
BBBB	69	GLN	4.0029	0.0000	7.2052
BBBB	70	HIS	1.6317	0.2424	2.5580
BBBB	71	GLN	13.5234	6.2391	19.3508
BBBB	72	GLN	13.7415	5.5049	20.3307
BBBB	73	VAL	3.0796	1.9941	4.5269
BBBB	74	ASN	7.4362	0.9858	13.8867
BBBB	75	GLU	9.6630	4.3598	13.9056
BBBB	76	SER	0.6085	0.9051	0.0153
BBBB	77	GLU	15.8267	1.2423	27.4942
BBBB	78	PRO	8.2618	4.8501	12.8107
BBBB	79	VAL	6.6038	1.6215	13.2470
BBBB	80	TYR	7.2918	1.9227	9.9763
BBBB	81	LEU	0.4359	0.0011	0.8708
BBBB	82	GLU	5.5353	0.0340	9.9364
BBBB	83	VAL	1.5227	2.6648	0.0000
BBBB	84	PHE	2.9287	0.6127	4.2522
BBBB	85	SER	11.1963	6.1246	21.3396

BBBB	86	ASP	6.4970	2.8341	10.1599
BBBB	87	TRP	9.3025	0.2173	12.9366
BBBB	88	LEU	0.0466	0.0933	0.0000
BBBB	89	LEU	0.1325	0.0000	0.2650
BBBB	90	LEU	0.0000	0.0000	0.0000
BBBB	91	GLN	0.2715	0.0001	0.4887
BBBB	92	ALA	0.1140	0.1208	0.0870
BBBB	93	SER	4.3701	3.0355	7.0392
BBBB	94	ALA	8.8274	1.4714	38.2514
BBBB	95	GLU	7.1968	1.4526	11.7922
BBBB	96	VAL	13.4385	4.5929	25.2325
BBBB	97	VAL	1.5907	0.9613	2.4301
BBBB	98	MET	14.3698	0.0738	28.6658
BBBB	99	GLU	7.3281	4.9392	9.2392
BBBB	100	GLY	5.2577	5.2577	0.0000
BBBB	101	GLN	9.4091	0.0245	16.9168
BBBB	102	PRO	9.6291	1.5760	20.3666
BBBB	103	LEU	0.0129	0.0053	0.0206
BBBB	104	PHE	6.1594	0.0000	9.6790
BBBB	105	LEU	0.0613	0.0533	0.0693
BBBB	106	ARG	2.2836	0.0000	3.5885
BBBB	107	CYS	0.6725	1.0088	0.0000
BBBB	108	HIS	1.1253	0.2267	1.7244
BBBB	109	GLY	1.2775	1.2775	0.0000
BBBB	110	TRP	4.4509	0.3060	6.1089
BBBB	111	ARG	14.4604	6.9977	18.7248
BBBB	112	ASN	13.1855	4.3879	21.9831
BBBB	113	TRP	7.1019	3.5603	8.5186
BBBB	114	ASP	11.9934	2.2124	21.7745
BBBB	115	VAL	0.9738	0.8493	1.1398
BBBB	116	TYR	5.9699	0.0003	8.9548
BBBB	117	LYS	11.3675	0.6641	19.9301
BBBB	118	VAL	0.0000	0.0000	0.0000
BBBB	119	ILE	4.4231	0.0000	8.8463
BBBB	120	TYR	0.0060	0.0000	0.0090
BBBB	121	TYR	3.5477	0.0003	5.3215
BBBB	122	LYS	3.9640	0.7211	6.5584
BBBB	123	ASP	10.6309	6.1402	15.1215
BBBB	124	GLY	14.3673	14.3673	0.0000
BBBB	125	GLU	13.1648	0.4047	23.3729
BBBB	126	ALA	14.7406	5.6401	51.1429
BBBB	127	LEU	9.0669	6.2840	11.8498
BBBB	128	LYS	11.7318	1.7962	19.6802
BBBB	129	TYR	10.3977	5.0068	13.0932
BBBB	130	TRP	8.0404	1.1151	10.8105
BBBB	131	TYR	12.1527	0.8656	17.7962
BBBB	132	GLU	12.6929	2.0269	21.2256
BBBB	133	ASN	5.5740	5.4313	5.7167
BBBB	134	HIS	8.2722	1.4837	12.7979
BBBB	135	ASN	1.3495	0.3379	2.3611
BBBB	136	ILE	2.1772	1.2842	3.0701
BBBB	137	SER	10.0581	7.4531	15.2681
BBBB	138	ILE	3.4589	0.9040	6.0137
BBBB	139	THR	15.5520	2.5023	32.9516
BBBB	140	ASN	6.4140	3.6881	9.1399
BBBB	141	ALA	0.0003	0.0003	0.0000

BBBB	142	THR	6.5774	0.3047	14.9409
BBBB	143	VAL	7.8299	1.0449	16.8764
BBBB	144	GLU	14.1982	4.2567	22.1514
BBBB	145	ASP	4.3806	0.0466	8.7146
BBBB	146	SER	5.5841	4.1811	8.3902
BBBB	147	GLY	2.9485	2.9485	0.0000
BBBB	148	THR	5.5009	0.1035	12.6974
BBBB	149	TYR	0.2416	0.0180	0.3534
BBBB	150	TYR	3.8781	0.0000	5.8171
BBBB	151	CYS	0.0000	0.0000	0.0000
BBBB	152	THR	3.8579	0.0000	9.0018
BBBB	153	GLY	1.0286	1.0286	0.0000
BBBB	154	LYS	6.0883	0.0037	10.9561
BBBB	155	VAL	0.4604	0.0000	1.0742
BBBB	156	TRP	11.6843	⌐.2412	14.2615
BBBB	157	GLN	14.2169	3.2783	22.9678
BBBB	158	LEU	13.8111	0.3293	27.2930
BBBB	159	ASP	14.3170	4.9359	23.6980
BBBB	160	TYR	3.5010	2.3021	4.1004
BBBB	161	GLU	13.3785	5.0194	20.0658
BBBB	162	SER	1.1216	1.6824	0.0000
BBBB	163	GLU	9.8626	0.5373	17.3229
BBBB	164	PRO	10.0802	1.5190	21.4953
BBBB	165	LEU	1.6748	0.1571	3.1924
BBBB	166	ASN	4.0864	1.0418	7.1311
BBBB	167	ILE	0.5430	1.0598	0.0262
BBBB	168	THR	9.9575	0.1056	23.0934
BBBB	169	VAL	0.5482	0.9594	0.0000
BBBB	170	ILE	10.7170	1.5437	19.8904
BBBB	171	LYS	20.1725	15.3137	24.0596
BBBB	221	NAG	13.1802	0.0000	13.1802
BBBB	222	NAG	20.4108	0.0000	20.4108
BBBB	242	NAG	7.5051	0.0000	7.5051
BBBB	243	NAG	7.8194	0.0000	7.8194
BBBB	244	MAN	18.6420	0.0000	18.6420
BBBB	250	NAG	16.2628	0.0000	16.2628
BBBB	274	NAG	21.8856	0.0000	21.8856
BBBB	335	NAG	14.8369	0.0000	14.8369
BBBB	340	NAG	17.4016	0.0000	17.4016
BBBB	366	NAG	14.6038	0.0000	14.6038
BBBB	367	NAG	21.0874	0.0000	21.0874
DDDD	4	LYS	22.1244	10.4757	31.4434
DDDD	5	PRO	1.1536	1.5927	0.5680
DDDD	6	LYS	17.0471	1.3682	29.5902
DDDD	7	VAL	1.6664	2.8596	0.0755
DDDD	8	SER	8.3148	1.8918	21.1607
DDDD	9	LEU	4.3290	5.2653	3.3927
DDDD	10	ASN	12.0081	0.9613	23.0549
DDDD	11	PRO	8.1330	0.4813	18.3353
DDDD	12	PRO	10.2920	2.3028	20.9442
DDDD	13	TRP	1.5549	0.0701	2.1488
DDDD	14	ASN	3.1974	0.3117	6.0832
DDDD	15	ARG	1.7368	0.0000	2.7293
DDDD	16	ILE	0.9559	0.0003	1.9114
DDDD	17	PHE	0.3209	0.0000	0.5043
DDDD	18	LYS	10.9142	3.4868	16.8562

	DDDD	19	GLY	5.8859	5.8859	0.0000
	DDDD	20	GLU	3.5184	0.0001	6.3330
	DDDD	21	ASN	5.3913	4.1153	6.6672
	DDDD	22	VAL	0.2777	0.4369	0.0655
5	DDDD	23	THR	5.8162	0.1076	13.4277
	DDDD	24	LEU	0.4623	0.0006	0.9240
	DDDD	25	THR	5.1763	0.0000	12.0779
	DDDD	26	CYS	0.2817	0.3216	0.2020
	DDDD	27	ASN	8.2286	1.5680	14.8891
10	DDDD	28	GLY	7.4834	7.4834	0.0000
	DDDD	29	ASN	17.4431	8.5265	26.3597
	DDDD	30	ASN	14.3278	10.0224	18.6333
	DDDD	31	PHE	18.8219	8.9687	24.4524
	DDDD	32	PHE	7.0915	6.7608	7.2806
15	DDDD	33	GLU	17.4529	5.1261	27.3143
	DDDD	34	VAL	10.0069	3.7179	18.3922
	DDDD	35	SER	14.6436	2.2454	39.4399
	DDDD	36	SER	7.1471	1.9242	17.5931
	DDDD	37	THR	0.7333	1.2833	0.0000
20	DDDD	38	LYS	8.8058	0.3191	15.5951
	DDDD	39	TRP	0.0167	0.0569	0.0007
	DDDD	40	PHE	3.0699	0.0000	4.8241
	DDDD	41	HIS	3.3244	0.1639	5.4315
	DDDD	42	ASN	6.2564	7.1984	5.3143
25	DDDD	43	GLY	8.8245	8.8245	0.0000
	DDDD	44	SER	12.8423	3.1760	32.1749
	DDDD	45	LEU	14.8050	7.3234	22.2866
	DDDD	46	SER	6.2461	4.5119	9.7144
	DDDD	47	GLU	19.8403	7.8973	29.3948
30	DDDD	48	GLU	5.7613	2.1656	8.6379
	DDDD	49	THR	10.9341	0.0000	25.5128
	DDDD	50	ASN	3.7321	1.0782	6.3860
	DDDD	51	SER	1.1905	0.0000	3.5714
	DDDD	52	SER	2.7666	0.0003	8.2993
35	DDDD	53	LEU	2.7642	0.0050	5.5234
	DDDD	54	ASN	7.1762	4.1170	10.2353
	DDDD	55	ILE	1.9872	1.4615	2.5130
	DDDD	56	VAL	11.4848	1.8199	24.3713
	DDDD	57	ASN	9.2650	1.2272	17.3029
40	DDDD	58	ALA	0.3308	0.4134	0.0000
	DDDD	59	LYS	13.7555	0.1261	24.6591
	DDDD	60	PHE	4.2948	0.3462	6.5511
	DDDD	61	GLU	9.1485	0.1440	16.3520
	DDDD	62	ASP	4.0350	0.0620	8.0080
45	DDDD	63	SER	0.1959	0.0000	0.5877
	DDDD	64	GLY	0.0065	0.0065	0.0000
	DDDD	65	GLU	7.8394	0.0396	14.0791
	DDDD	66	TYR	1.0148	0.0000	1.5222
	DDDD	67	LYS	3.3208	0.0000	5.9774
50	DDDD	68	CYS	0.0002	0.0000	0.0005
	DDDD	69	GLN	3.9726	0.0000	7.1507
	DDDD	70	HIS	2.6810	0.2742	4.2855
	DDDD	71	GLN	16.6353	6.3493	24.8641
	DDDD	72	GLN	18.9785	6.9612	28.5924
55	DDDD	73	VAL	5.8822	1.9838	11.0801
	DDDD	74	ASN	7.4325	0.9456	13.9195

	DDDD	75	GLU	9.6342	4.3175	13.8875
	DDDD	76	SER	0.6597	0.9801	0.0188
	DDDD	77	GLU	15.8994	1.2593	27.6115
	DDDD	78	PRO	8.2500	4.9080	12.7060
5	DDDD	79	VAL	6.5718	1.5859	13.2197
	DDDD	80	TYR	7.3618	1.8414	10.1220
	DDDD	81	LEU	0.3727	0.0000	0.7455
	DDDD	82	GLU	5.7273	0.0000	10.3091
	DDDD	83	VAL	1.6083	2.8146	0.0000
10	DDDD	84	PHE	2.9246	0.6110	4.2466
	DDDD	85	SER	11.0966	6.0084	21.2730
	DDDD	86	ASP	6.2089	2.2133	10.2046
	DDDD	87	TRP	6.4962	0.2557	8.9923
	DDDD	88	LEU	0.0479	0.0958	0.0000
15	DDDD	89	LEU	0.1157	0.0000	0.2313
	DDDD	90	LEU	0.0002	0.0000	0.0004
	DDDD	91	GLN	0.2632	0.0000	0.4737
	DDDD	92	ALA	0.0436	0.0427	0.0472
	DDDD	93	SER	4.5089	2.9688	7.5891
20	DDDD	94	ALA	8.3925	1.3517	36.5557
	DDDD	95	GLU	7.1932	1.4693	11.7724
	DDDD	96	VAL	13.5421	4.7333	25.2870
	DDDD	97	VAL	1.5725	0.9243	2.4367
	DDDD	98	MET	14.2776	0.0883	28.4668
25	DDDD	99	GLU	7.6854	4.8779	9.9313
	DDDD	100	GLY	4.9621	4.9621	0.0000
	DDDD	101	GLN	9.7282	0.0319	17.4852
	DDDD	102	PRO	9.4269	1.5462	19.9345
	DDDD	103	LEU	0.0306	0.0330	0.0282
30	DDDD	104	PHE	6.2490	0.0000	9.8199
	DDDD	105	LEU	0.0962	0.0653	0.1272
	DDDD	106	ARG	2.2407	0.0007	3.5207
	DDDD	107	CYS	0.6463	0.9694	0.0000
	DDDD	108	HIS	1.1583	0.2394	1.7709
35	DDDD	109	GLY	1.3558	1.3558	0.0000
	DDDD	110	TRP	4.6167	0.3206	6.3351
	DDDD	111	ARG	13.1658	6.9018	16.7453
	DDDD	112	ASN	12.9428	4.3861	21.4995
	DDDD	113	TRP	6.0476	2.8196	7.3388
40	DDDD	114	ASP	11.3414	1.8363	20.8466
	DDDD	115	VAL	0.8809	0.7036	1.1174
	DDDD	116	TYR	5.3412	0.0000	8.0118
	DDDD	117	LYS	8.0269	0.7095	13.8809
	DDDD	118	VAL	0.0001	0.0000	0.0002
45	DDDD	119	ILE	1.6342	0.0000	3.2684
	DDDD	120	TYR	0.0131	0.0000	0.0197
	DDDD	121	TYR	2.9992	0.0083	4.4947
	DDDD	122	LYS	4.0023	0.8041	6.5609
	DDDD	123	ASP	10.7259	6.1708	15.2810
50	DDDD	124	GLY	14.3365	14.3365	0.0000
	DDDD	125	GLU	7.3185	0.3720	12.8756
	DDDD	126	ALA	2.1423	1.1064	6.2860
	DDDD	127	LEU	5.9569	1.4445	10.4694
	DDDD	128	LYS	11.1254	0.2785	19.8028
55	DDDD	129	TYR	5.7025	4.2384	6.4346
	DDDD	130	TRP	6.8913	1.0864	9.2132

DDDD	131	TYR	4.0982	0.8881	5.7033
DDDD	132	GLU	11.0810	2.0497	18.3061
DDDD	133	ASN	5.7438	5.5427	5.9449
DDDD	134	HIS	8.0681	1.4827	12.4583
DDDD	135	ASN	1.3522	0.3616	2.3429
DDDD	136	ILE	2.1277	1.2709	2.9846
DDDD	137	SER	10.0928	7.5360	15.2065
DDDD	138	ILE	3.4325	0.8858	5.9792
DDDD	139	THR	15.7856	2.5286	33.4616
DDDD	140	ASN	6.3849	3.6475	9.1223
DDDD	141	ALA	0.0000	0.0000	0.0000
DDDD	142	THR	7.3411	0.2496	16.7963
DDDD	143	VAL	7.7635	1.1808	16.5403
DDDD	144	GLU	13.9706	4.2430	21.7527
DDDD	145	ASP	4.2654	0.0465	8.4843
DDDD	146	SER	5.4380	3.9844	8.3451
DDDD	147	GLY	2.9908	2.9908	0.0000
DDDD	148	THR	5.6821	0.0926	13.1348
DDDD	149	TYR	0.2615	0.0000	0.3922
DDDD	150	TYR	3.8602	0.0001	5.7903
DDDD	151	CYS	0.0000	0.0000	0.0000
DDDD	152	THR	3.8063	0.0000	8.8814
DDDD	153	GLY	1.1071	1.1071	0.0000
DDDD	154	LYS	5.9720	0.0003	10.7494
DDDD	155	VAL	0.4744	0.0002	1.1066
DDDD	156	TRP	3.1754	2.8159	3.3193
DDDD	157	GLN	10.0034	3.2877	15.3759
DDDD	158	LEU	14.1226	0.2738	27.9715
DDDD	159	ASP	7.9805	2.3321	13.6289
DDDD	160	TYR	3.5343	2.4074	4.0978
DDDD	161	GLU	12.6759	4.6202	19.1204
DDDD	162	SER	1.1111	1.6667	0.0000
DDDD	163	GLU	9.9628	0.6047	17.4493
DDDD	164	PRO	10.2553	1.5732	21.8314
DDDD	165	LEU	1.6609	0.1704	3.1515
DDDD	166	ASN	4.3037	1.0892	7.5182
DDDD	167	ILE	0.5355	1.0632	0.0079
DDDD	168	THR	9.9863	0.0926	23.1779
DDDD	169	VAl	0.5843	0.9875	0.0466
DDDD	170	ILE	10.6158	1.4450	19.7865
DDDD	171	LYS	20.3127	15.3369	24.2933
DDDD	221	NAG	13.3953	0.0000	13.3953
DDDD	222	NAG	19.9723	0.0000	19.9723
DDDD	242	NAG	9.9493	0.0000	9.9493
DDDD	243	NAG	9.3637	0.0000	9.3637
DDDD	244	MAN	18.7429	0.0000	18.7429
DDDD	250	NAG	16.0945	0.0000	16.0945
DDDD	274	NAG	21.9996	0.0000	21.9996
DDDD	335	NAG	15.1906	0.0000	15.1906
DDDD	340	NAG	17.8940	0.0000	17.8940
DDDD	366	NAG	14.6791	0.0000	14.6791
DDDD	367	NAG	20.8557	0.0000	20.8557
EEEE	4	LYS	22.5960	10.2165	32.4995
EEEE	5	PRO	1.1597	1.6130	0.5553
EEEE	6	LYS	16.8781	1.3580	29.2941
EEEE	7	VAL	1.6131	2.7766	0.0619

	EEEE	8	SER	8.2297	1.9067	20.8757
	EEEE	9	LEU	4.4542	5.4841	3.4242
	EEEE	10	ASN	11.9578	0.9345	22.9812
	EEEE	11	PRO	8.0892	0.4787	18.2367
5	EEEE	12	PRO	10.2667	2.2261	20.9875
	EEEE	13	TRP	1.5846	0.0803	2.1863
	EEEE	14	ASN	3.3863	0.3258	6.4468
	EEEE	15	ARG	1.7357	0.0000	2.7275
	EEEE	16	ILE	0.9829	0.0000	1.9657
10	EEEE	17	PHE	0.3246	0.0002	0.5100
	EEEE	18	LYS	10.8388	3.5327	16.6837
	EEEE	19	GLY	5.3803	5.3803	0.0000
	EEEE	20	GLU	3.5458	0.0335	6.3557
	EEEE	21	ASN	5.3181	4.0487	6.5875
15	EEEE	22	VAL	0.2825	0.4415	0.0706
	EEEE	23	THR	5.3581	0.0670	12.4128
	EEEE	24	LEU	0.4756	0.0000	0.9513
	EEEE	25	THR	5.2190	0.0000	12.1778
	EEEE	26	CYS	0.3475	0.4090	0.2246
20	EEEE	27	ASN	8.6206	1.5643	15.6770
	EEEE	28	GLY	7.3744	7.3744	0.0000
	EEEE	29	ASN	16.8741	8.5078	25.2404
	EEEE	30	ASN	14.4860	9.6381	19.3339
	EEEE	31	PHE	18.9288	9.2491	24.4601
25	EEEE	32	PHE	7.2780	6.7628	7.5723
	EEEE	33	GLU	17.3776	4.9213	27.3427
	EEEE	34	VAL	9.8146	3.7193	17.9417
	EEEE	35	SER	14.4525	2.2438	38.8698
	EEEE	36	SER	7.1292	1.8233	17.7410
30	EEEE	37	THR	0.7268	1.2719	0.0000
	EEEE	38	LYS	8.8146	0.3416	15.5930
	EEEE	39	TRP	0.0112	0.0389	0.0002
	EEEE	40	PHE	3.0771	0.0000	4.8354
	EEEE	41	HIS	3.3339	0.3893	5.2969
35	EEEE	42	ASN	6.3403	7.2548	5.4259
	EEEE	43	GLY	8.8849	8.8849	0.0000
	EEEE	44	SER	12.3851	3.1501	30.8551
	EEEE	45	LEU	14.5997	6.7706	22.4287
	EEEE	46	SER	6.2344	4.5208	9.6615
40	EEEE	47	GLU	19.8124	8.1501	29.1422
	EEEE	48	GLU	5.5829	2.2603	8.2411
	EEEE	49	THR	11.1823	0.0000	26.0920
	EEEE	50	ASN	3.7514	1.0379	6.4648
	EEEE	51	SER	1.1828	0.0001	3.5482
45	EEEE	52	SER	2.6847	0.0000	8.0542
	EEEE	53	LEU	2.8988	0.0160	5.7815
	EEEE	54	ASN	7.0295	3.8406	10.2183
	EEEE	55	ILE	1.9774	1.5267	2.4282
	EEEE	56	VAL	11.4385	1.7455	24.3625
50	EEEE	57	ASN	8.9737	1.1309	16.8164
	EEEE	58	ALA	0.3534	0.4418	0.0000
	EEEE	59	LYS	14.0513	0.0995	25.2128
	EEEE	60	PHE	3.9435	0.0489	6.1690
	EEEE	61	GLU	9.2441	0.1331	16.5329
55	EEEE	62	ASP	4.0153	0.0793	7.9514
	EEEE	63	SER	0.1893	0.0000	0.5678

	EEEE	64	GLY	0.0000	0.0000	0.0000
	EEEE	65	GLU	2.9838	0.0460	5.3340
	EEEE	66	TYR	1.0048	0.0006	1.5069
	EEEE	67	LYS	3.2772	0.0001	5.8989
5	EEEE	68	CYS	0.0000	0.0000	0.0000
	EEEE	69	GLN	3.9654	0.0000	7.1378
	EEEE	70	HIS	2.6414	0.2451	4.2389
	EEEE	71	GLN	9.7531	6.2755	12.5353
	EEEE	72	GLN	15.3796	6.7847	22.2555
10	EEEE	73	VAL	6.0006	2.3479	10.8709
	EEEE	74	ASN	7.6007	0.9858	14.2156
	EEEE	75	GLU	9.6042	4.4474	13.7297
	EEEE	76	SER	0.6746	1.0066	0.0106
	EEEE	77	GLU	12.7067	1.2232	21.8935
15	EEEE	78	PRO	2.3956	1.5978	3.4593
	EEEE	79	VAL	6.0444	0.7862	13.0553
	EEEE	80	TYR	4.1212	1.3782	5.4928
	EEEE	81	LEU	0.4531	0.0000	0.9061
	EEEE	82	GLU	5.5155	0.0000	9.9279
20	EEEE	83	VAL	1.5309	2.6784	0.0008
	EEEE	84	PHE	2.8834	0.6355	4.1679
	EEEE	85	SER	11.0911	6.1575	20.9584
	EEEE	86	ASP	6.4143	2.5687	10.2598
	EEEE	87	TRP	9.2857	0.2426	12.9030
25	EEEE	88	LEU	0.0519	0.1037	0.0000
	EEEE	89	LEU	0.1205	0.0000	0.2410
	EEEE	90	LEU	0.0000	0.0000	0.0000
	EEEE	91	GLN	0.2686	0.0000	0.4835
	EEEE	92	ALA	0.0943	0.0991	0.0752
30	EEEE	93	SER	4.2341	2.9403	6.8217
	EEEE	94	ALA	8.4724	1.4590	36.5259
	EEEE	95	GLU	4.3753	1.4778	6.6933
	EEEE	96	VAL	4.5984	4.5523	4.6599
	EEEE	97	VAL	1.5521	0.9731	2.3241
35	EEEE	98	MET	14.3494	0.0687	28.6301
	EEEE	99	GLU	7.4147	5.0436	9.3116
	EEEE	100	GLY	5.3477	5.3477	0.0000
	EEEE	101	GLN	9.6429	0.0120	17.3476
	EEEE	102	PRO	9.4892	1.6653	19.9211
40	EEEE	103	LEU	0.0234	0.0192	0.0275
	EEEE	104	PHE	6.1968	0.0000	9.7379
	EEEE	105	LEU	0.0865	0.0657	0.1072
	EEEE	106	ARG	2.2169	0.0000	3.4838
	EEEE	107	CYS	0.6436	0.9654	0.0000
45	EEEE	108	HIS	1.1724	0.2409	1.7935
	EEEE	109	GLY	1.2996	1.2996	0.0000
	EEEE	110	TRP	4.6388	0.3429	6.3572
	EEEE	111	ARG	14.4865	6.9035	18.8197
	EEEE	112	ASN	13.2482	4.3960	22.1003
50	EEEE	113	TRP	7.0238	3.3035	8.5119
	EEEE	114	ASP	11.8883	1.9586	21.8181
	EEEE	115	VAL	0.8842	0.7257	1.0956
	EEEE	116	TYR	6.0204	0.0000	9.0306
	EEEE	117	LYS	11.3486	0.7247	19.8476
55	EEEE	118	VAL	0.0000	0.0000	0.0000
	EEEE	119	ILE	4.3850	0.0000	8.7700

	EEEE	120	TYR	0.0002	0.0005	0.0000
	EEEE	121	TYR	3.8442	0.0044	5.7642
	EEEE	122	LYS	4.0492	0.9747	6.5088
	EEEE	123	ASP	10.6363	6.3573	14.9153
5	EEEE	124	GLY	14.2853	14.2853	0.0000
	EEEE	125	GLU	13.3618	0.4051	23.7272
	EEEE	126	ALA	14.6809	5.6541	50.7878
	EEEE	127	LEU	9.2613	6.4361	12.0866
	EEEE	128	LYS	11.7127	1.6189	19.7878
10	EEEE	129	TYR	10.5042	5.1382	13.1872
	EEEE	130	TRP	8.3076	1.0723	11.2017
	EEEE	131	TYR	12.1072	0.8991	17.7113
	EEEE	132	GLU	12.7199	2.0028	21.2936
	EEEE	133	ASN	5.6925	5.5621	5.8228
15	FFEE	134	HIS	8.1921	1.5201	12.6401
	EEEE	135	ASN	1.3201	0.2942	2.3461
	EEEE	136	ILE	2.2145	1.3058	3.1231
	EEEE	137	SER	10.0571	7.3406	15.4902
	EEEE	138	ILE	3.4381	0.9086	5.9677
20	EEEE	139	THR	15.7625	2.5279	33.4087
	EEEE	140	ASN	6.4209	3.6811	9.1607
	EEEE	141	ALA	0.0000	0.0000	0.0000
	EEEE	142	THR	7.2538	0.3369	16.4763
	EEEE	143	VAL	5.2826	1.1302	10.8192
25	EEEE	144	GLU	14.2599	4.2746	22.2482
	EEEE	145	ASP	4.3200	0.0534	8.5866
	EEEE	146	SER	5.5098	4.0762	8.3771
	EEEE	147	GLY	2.9433	2.9433	0.0000
	EEEE	148	THR	5.7039	0.0995	13.1764
30	EEEE	149	TYR	0.2552	0.0130	0.3763
	EEEE	150	TYR	3.8275	0.0000	5.7413
	EEEE	151	CYS	0.0000	0.0000	0.0000
	EEEE	152	THR	3.7660	0.0000	8.7874
	EEEE	153	GLY	1.1095	1.1095	0.0000
35	EEEE	154	LYS	6.0705	0.0037	10.9239
	EEEE	155	VAL	0.4853	0.0000	1.1323
	EEEE	156	TRP	11.8745	5.3337	14.4908
	EEEE	157	GLN	14.3320	3.3004	23.1573
	EEEE	158	LEU	13.6525	0.2539	27.0512
40	EEEE	159	ASP	14.3336	5.0741	23.5931
	EEEE	160	TYR	3.5095	2.3905	4.0689
	EEEE	161	GLU	13.4677	5.2742	20.0225
	EEEE	162	SER	1.1284	1.6927	0.0000
	EEEE	163	GLU	9.6823	0.5318	17.0027
45	EEEE	164	PRO	10.3139	1.5274	22.0292
	EEEE	165	LEU	1.6379	0.1485	3.1273
	EEEE	166	ASN	3.3639	0.7774	5.9503
	EEEE	167	ILE	0.5534	1.0911	0.0157
	EEEE	168	THR	3.6331	0.0674	8.3873
50	EEEE	169	VAL	0.0817	0.1078	0.0468
	EEEE	170	ILE	2.1648	0.0777	4.2519
	EEEE	171	LYS	14.9019	13.4622	16.0537
	EEEE	221	NAG	13.0723	0.0000	13.0723
	EEEE	222	NAG	20.3453	0.0000	20.3453
55	EEEE	242	NAG	8.8452	0.0000	8.8452
	EEEE	243	NAG	7.6625	0.0000	7.6625

EEEE	244	MAN	18.6073	0.0000	18.6073
EEEE	250	NAG	16.1217	0.0000	16.1217
EEEE	274	NAG	22.0349	0.0000	22.0349
EEEE	335	NAG	15.0552	0.0000	15.0552
EEEE	340	NAG	17.7238	0.0000	17.7238
EEEE	366	NAG	12.1825	0.0000	12.1825
EEEE	367	NAG	19.5820	0.0000	19.5820

Table 11. PhFcεRIα₁₋₁₇₆, Form M2, residue exposure

>>>> coordinate set= md6c1.pdb

	segid	resid	resname	access	access-main	access-side
5	AAAA	1	VAL	23.3378	10.2131	40.8375
	AAAA	2	PRO	11.8969	4.7510	21.4247
	AAAA	3	GLN	4.0040	0.6188	6.7120
	AAAA	4	LYS	10.6487	3.0641	16.7164
	AAAA	5	PRO	0.2700	0.1467	0.4343
10	AAAA	6	LYS	14.5164	0.1128	26.0393
	AAAA	7	VAL	2.0175	3.5306	0.0002
	AAAA	8	SER	8.4156	1.5950	22.0570
	AAAA	9	LEU	3.4044	3.6981	3.1106
	AAAA	10	ASN	11.5698	0.5893	22.5503
15	AAAA	11	PRO	8.5175	0.1465	19.6787
	AAAA	12	PRO	9.1363	1.5259	19.2835
	AAAA	13	TRP	2.0981	0.0033	2.9360
	AAAA	14	ASN	2.7536	0.0000	5.5073
	AAAA	15	ARG	0.7887	0.0000	1.2394
20	AAAA	16	ILE	0.5825	0.0000	1.1649
	AAAA	17	PHE	0.1853	0.0000	0.2912
	AAAA	18	LYS	9.6106	1.2098	16.3312
	AAAA	19	GLY	4.3200	4.3200	0.0000
	AAAA	20	GLU	2.6272	0.0000	4.7290
25	AAAA	21	ASN	4.7245	2.9284	6.5206
	AAAA	22	VAL	0.4741	0.6955	0.1788
	AAAA	23	THR	4.7669	0.0001	11.1226
	AAAA	24	LEU	0.0001	0.0000	0.0002
	AAAA	25	THR	5.8774	0.0006	13.7131
30	AAAA	26	CYS	1.2474	1.8711	0.0000
	AAAA	27	ASN	9.8972	1.4492	18.3453
	AAAA	28	GLY	11.8125	11.8125	0.0000
	AAAA	29	ASN	10.4976	5.7985	15.1967
	AAAA	30	ASN	17.1596	4.7289	29.5903
35	AAAA	31	PHE	14.9024	9.0487	18.2474
	AAAA	32	PHE	6.9262	1.1011	10.2548
	AAAA	33	GLU	19.3638	7.9005	28.5344
	AAAA	34	VAL	10.5040	9.2873	12.1262
	AAAA	35	SER	20.0797	11.1239	37.9912
40	AAAA	36	SER	10.3115	2.5541	25.8262
	AAAA	37	THR	0.3123	0.1509	0.5275
	AAAA	38	LYS	9.1055	0.0303	16.3656
	AAAA	39	TRP	0.0125	0.0004	0.0173
	AAAA	40	PHE	3.3329	0.0507	5.2085
45	AAAA	41	HIS	3.3604	0.4369	5.3093
	AAAA	42	ASN	5.7196	5.9748	5.4644
	AAAA	43	GLY	11.0441	11.0441	0.0000
	AAAA	44	SER	12.3468	1.6054	33.8295
	AAAA	45	LEU	12.4194	6.6727	18.1661
50	AAAA	46	SER	6.2970	3.5164	11.8583
	AAAA	47	GLU	19.2754	6.3506	29.6153
	AAAA	48	GLU	5.5497	2.2183	8.2149
	AAAA	49	THR	10.8597	1.3240	23.5740

	AAAA	50	ASN	12.0836	1.0849	23.0822
	AAAA	51	SER	8.5667	0.8380	24.0243
	AAAA	52	SER	6.5795	0.5607	18.6170
	AAAA	53	LEU	2.0088	0.0000	4.0175
5	AAAA	54	ASN	10.4631	4.8106	16.1155
	AAAA	55	ILE	1.5373	1.3922	1.6825
	AAAA	56	VAL	9.8664	4.5674	16.9318
	AAAA	57	ASN	8.3728	1.0485	15.6970
	AAAA	58	ALA	0.1673	0.2091	0.0000
10	AAAA	59	LYS	12.7698	0.0135	22.9748
	AAAA	60	PHE	2.9685	0.0000	4.6647
	AAAA	61	GLU	10.1438	0.3798	17.9550
	AAAA	62	ASP	3.8187	0.0000	7.6375
	AAAA	63	SER	0.0423	0.0002	0.1265
15	AAAA	64	GLY	0.7550	0.7550	0.0000
	AAAA	65	GLU	4.0298	0.0243	7.2343
	AAAA	66	TYR	0.5144	0.0000	0.7716
	AAAA	67	LYS	4.6070	0.0021	8.2910
	AAAA	68	CYS	0.0643	0.0965	0.0000
20	AAAA	69	GLN	4.3129	0.5930	7.2889
	AAAA	70	HIS	2.2107	1.4131	2.7425
	AAAA	71	GLN	15.8607	4.7123	24.7794
	AAAA	72	GLN	10.1949	4.9757	14.3702
	AAAA	73	VAL	4.5886	3.4088	6.1618
25	AAAA	74	ASN	7.2228	1.6554	12.7903
	AAAA	75	GLU	11.1970	3.1686	17.6196
	AAAA	76	SER	0.7529	1.1293	0.0000
	AAAA	77	GLU	5.6624	0.5155	9.7799
	AAAA	78	PRO	9.4668	4.0586	16.6776
30	AAAA	79	VAL	4.2206	0.7903	8.7943
	AAAA	80	TYR	10.8696	1.6448	15.4820
	AAAA	81	LEU	0.3295	0.6590	0.0000
	AAAA	82	GLU	6.5599	0.0000	11.8078
	AAAA	83	VAL	1.2313	2.1548	0.0000
35	AAAA	84	PHE	2.6783	1.0628	3.6015
	AAAA	85	SER	10.4042	7.2453	16.7222
	AAAA	86	ASP	6.7155	3.1365	10.2944
	AAAA	87	TRP	7.9670	0.0000	11.1538
	AAAA	88	LEU	0.2303	0.4605	0.0000
40	AAAA	89	LEU	0.1824	0.0005	0.3643
	AAAA	90	LEU	0.0000	0.0000	0.0000
	AAAA	91	GLN	0.1542	0.0000	0.2776
	AAAA	92	ALA	0.0000	0.0000	0.0000
	AAAA	93	SER	6.4731	4.6474	10.1245
45	AAAA	94	ALA	6.9800	1.7371	27.9520
	AAAA	95	GLU	6.3625	0.8834	10.7457
	AAAA	96	VAL	12.7032	5.5496	22.2413
	AAAA	97	VAL	1.4127	0.9895	1.9769
	AAAA	98	MET	8.3663	0.9908	15.7417
50	AAAA	99	GLU	6.0466	3.8025	7.8419
	AAAA	100	GLY	1.3823	1.3823	0.0000
	AAAA	101	GLN	9.3401	0.0000	16.8122
	AAAA	102	PRO	11.5211	1.3350	25.1025
	AAAA	103	LEU	0.2239	0.2968	0.1510
55	AAAA	104	PHE	5.5960	0.0000	8.7937
	AAAA	105	LEU	0.2800	0.0000	0.5599

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	AAAA	106	ARG	5.6019	0.0000	8.8030
	AAAA	107	CYS	1.9041	2.6369	0.4387
	AAAA	108	HIS	1.2459	0.8447	1.5133
	AAAA	109	GLY	0.2958	0.2958	0.0000
5	AAAA	110	TRP	3.6776	0.2682	5.0414
	AAAA	111	ARG	13.9748	6.0118	18.5251
	AAAA	112	ASN	13.0426	5.9312	20.1540
	AAAA	113	TRP	8.4374	2.2626	10.9073
	AAAA	114	ASP	10.8862	0.8382	20.9341
10	AAAA	115	VAL	3.6736	4.0353	3.1913
	AAAA	116	TYR	10.8526	0.9359	15.8110
	AAAA	117	LYS	12.5729	4.0303	19.4070
	AAAA	118	VAL	1.5367	1.4181	1.6949
	AAAA	119	ILE	3.8886	0.4794	7.2979
15	AAAA	120	TYR	0.1235	0.0400	0.1653
	AAAA	121	TYR	3.2159	0.0000	4.8238
	AAAA	122	LYS	4.1348	0.5235	7.0239
	AAAA	123	ASP	9.0341	4.7242	13.3440
	AAAA	124	GLY	12.8886	12.8886	0.0000
20	AAAA	125	GLU	13.5568	0.5821	23.9366
	AAAA	126	ALA	5.4448	3.6508	12.6207
	AAAA	127	LEU	4.4392	1.2148	7.6637
	AAAA	128	LYS	6.6847	0.4089	11.7054
	AAAA	129	TYR	17.7661	6.5522	23.3730
25	AAAA	130	TRP	4.6781	0.2956	6.4311
	AAAA	131	TYR	5.9070	2.3743	7.6733
	AAAA	132	GLU	14.4146	6.3584	20.8595
	AAAA	133	ASN	9.2636	0.7631	17.7642
	AAAA	134	HIS	14.3143	1.4912	22.8630
30	AAAA	135	ASN	6.6861	0.2683	13.1040
	AAAA	136	ILE	0.1409	0.0100	0.2719
	AAAA	137	SER	9.4451	3.2255	21.8842
	AAAA	138	ILE	2.6491	0.8829	4.4154
	AAAA	139	THR	12.8859	1.4417	28.1448
35	AAAA	140	ASN	6.4432	3.5706	9.3157
	AAAA	141	ALA	1.3406	1.6757	0.0000
	AAAA	142	THR	7.2752	0.0020	16.9727
	AAAA	143	VAL	11.7608	1.2461	25.7803
	AAAA	144	GLU	14.7507	2.5626	24.5012
40	AAAA	145	ASP	3.5866	0.0546	7.1186
	AAAA	146	SER	4.2659	2.0709	8.6561
	AAAA	147	GLY	2.4870	2.4870	0.0000
	AAAA	148	THR	3.9797	0.0000	9.2860
	AAAA	149	TYR	0.3266	0.0000	0.4899
45	AAAA	150	TYR	3.1527	0.0005	4.7289
	AAAA	151	CYS	0.0003	0.0005	0.0000
	AAAA	152	THR	4.1824	0.6979	8.8283
	AAAA	153	GLY	0.7331	0.7331	0.0000
	AAAA	154	LYS	7.5163	0.0133	13.5188
50	AAAA	155	VAL	0.2906	0.0000	0.6781
	AAAA	156	TRP	11.8912	1.7474	15.9487
	AAAA	157	GLN	14.6241	5.4565	21.9582
	AAAA	158	LEU	13.5291	0.9340	26.1242
	AAAA	159	ASP	14.3755	5.4004	23.3507
55	AAAA	160	TYR	3.1668	2.6149	3.4428
	AAAA	161	GLU	10.8144	4.2630	16.0556

	AAAA	162	SER	0.5614	0.8334	0.0172
	AAAA	163	GLU	10.6063	0.2900	18.8593
	AAAA	164	PRO	10.9414	3.3661	21.0417
	AAAA	165	LEU	1.9287	0.7267	3.1308
5	AAAA	166	ASN	5.8142	3.0970	8.5314
	AAAA	167	ILE	0.2918	0.5835	0.0000
	AAAA	168	THR	9.3327	0.0000	21.7764
	AAAA	169	VAL	0.2835	0.4961	0.0000
	AAAA	170	ILE	10.1702	0.5659	19.7745
10	AAAA	171	LYS	14.8660	3.9580	23.5925
	AAAA	172	ALA	10.1636	3.7167	35.9516
	AAAA	173	PRO	16.8141	8.4692	27.9405
	AAAA	174	ARG	24.7335	21.3158	26.6865
	AAAA	221	NAG	10.3017	0.0000	10.3017
15	AAAA	222	NAG	20.4990	0.0000	20.4990
	AAAA	242	NAG	10.4998	0.0000	10.4998
	AAAA	243	NAG	9.1915	0.0000	9.1915
	AAAA	244	MAN	17.0951	0.0000	17.0951
	AAAA	274	NAG	8.2536	0.0000	8.2536
20	AAAA	275	FCA	13.5116	0.0000	13.5116
	AAAA	276	NAG	18.0492	0.0000	18.0492
	AAAA	340	NAG	18.2117	0.0000	18.2117
	AAAA	366	NAG	20.2201	0.0000	20.2201
	BBBB	1	VAL	23.2202	13.0224	36.8172
25	BBBB	2	PRO	12.9287	6.5376	21.4502
	BBBB	3	GLN	7.8969	1.1767	13.2731
	BBBB	4	LYS	10.9639	2.4069	17.8095
	BBBB	5	PRO	0.1485	0.1774	0.1101
	BBBB	6	LYS	13.6900	0.3136	24.3911
30	BBBB	7	VAL	2.0335	3.5586	0.0000
	BBBB	8	SER	8.6515	1.6168	22.7209
	BBBB	9	LEU	3.3843	3.6519	3.1168
	BBBB	10	ASN	11.2166	0.5892	21.8441
	BBBB	11	PRO	6.4967	0.0774	15.0558
35	BBBB	12	PRO	5.5258	1.4792	10.9213
	BBBB	13	TRP	0.5399	0.0000	0.7559
	BBBB	14	ASN	2.8551	0.0000	5.7102
	BBBB	15	ARG	0.8228	0.0000	1.2930
	BBBB	16	ILE	0.7004	0.0000	1.4007
40	BBBB	17	PHE	0.2062	0.0000	0.3240
	BBBB	18	LYS	10.1266	2.4178	16.2937
	BBBB	19	GLY	5.1193	5.1193	0.0000
	BBBB	20	GLU	3.6592	0.0000	6.5866
	BBBB	21	ASN	4.9980	2.8696	7.1265
45	BBBB	22	VAL	0.3086	0.5358	0.0056
	BBBB	23	THR	4.8914	0.0060	11.4053
	BBBB	24	LEU	0.0000	0.0000	0.0000
	BBBB	25	THR	5.3161	0.0000	12.4043
	BBBB	26	CYS	1.7698	1.9470	1.4152
50	BBBB	27	ASN	9.5595	2.4594	16.6596
	BBBB	28	GLY	5.1022	5.1022	0.0000
	BBBB	29	ASN	11.6239	9.1902	14.0577
	BBBB	30	ASN	11.1354	7.5265	14.7442
	BBBB	31	PHE	12.4823	0.9411	19.0773
55	BBBB	32	PHE	14.9629	4.4534	20.9683
	BBBB	33	GLU	10.0579	1.1430	17.1898

	BBBB	34	VAL	8.1169	2.1335	16.0948
	BBBB	35	SER	17.2091	9.6972	32.2329
	BBBB	36	SER	5.6660	1.8677	13.2627
	BBBB	37	THR	0.9190	0.7693	1.1187
5	BBBB	38	LYS	10.5493	0.0585	18.9418
	BBBB	39	TRP	0.0160	0.0000	0.0224
	BBBB	40	PHE	3.2085	0.1128	4.9774
	BBBB	41	HIS	3.2674	0.7993	4.9129
	BBBB	42	ASN	6.9206	7.0588	6.7824
10	BBBB	43	GLY	10.5521	10.5521	0.0000
	BBBB	44	SER	12.5873	1.8007	34.1606
	BBBB	45	LEU	12.5684	7.0671	18.0697
	BBBB	46	SER	5.8736	2.9025	11.8159
	BBBB	47	GLU	18.2898	4.6076	29.2356
15	BBBB	48	GLU	6.4732	2.2413	9.8587
	BBBB	49	THR	12.4950	1.2186	27.5302
	BBBB	50	ASN	10.6353	1.9696	19.3010
	BBBB	51	SER	2.7922	0.0131	8.3506
	BBBB	52	SER	5.4540	0.4267	15.5085
20	BBBB	53	LEU	2.2138	0.0004	4.4271
	BBBB	54	ASN	10.5005	4.6511	16.3499
	BBBB	55	ILE	1.3385	1.1102	1.5667
	BBBB	56	VAL	11.5067	3.9707	21.5548
	BBBB	57	ASN	8.7141	1.1097	16.3185
25	BBBB	58	ALA	0.1840	0.2300	0.0000
	BBBB	59	LYS	13.0236	0.0000	23.4424
	BBBB	60	PHE	2.3308	0.0000	3.6627
	BBBB	61	GLU	9.4233	0.1906	16.8095
	BBBB	62	ASP	3.8339	0.0000	7.6678
30	BBBB	63	SER	0.1605	0.0000	0.4815
	BBBB	64	GLY	1.6421	1.6421	0.0000
	BBBB	65	GLU	3.9224	0.0377	7.0302
	BBBB	66	TYR	0.5105	0.0000	0.7658
	BBBB	67	LYS	3.9749	0.0002	7.1547
35	BBBB	68	CYS	0.0929	0.1393	0.0000
	BBBB	69	GLN	5.4367	0.1443	9.6707
	BBBB	70	HIS	4.9806	0.9868	7.6431
	BBBB	71	GLN	14.5333	5.4826	21.7740
	BBBB	72	GLN	18.4063	11.6333	23.8247
40	BBBB	73	VAL	2.6548	3.2121	1.9118
	BBBB	74	ASN	12.0029	2.0287	21.9770
	BBBB	75	GLU	8.4921	2.6890	13.1345
	BBBB	76	SER	0.7254	1.0881	0.0000
	BBBB	77	GLU	7.7802	0.6132	13.5138
45	BBBB	78	PRO	9.3860	3.7419	16.9114
	BBBB	79	VAL	4.0363	0.8626	8.2679
	BBBB	80	TYR	11.1782	1.6916	15.9215
	BBBB	81	LEU	0.2983	0.5965	0.0000
	BBBB	82	GLU	7.4968	0.0000	13.4942
50	BBBB	83	VAL	1.2876	2.2532	0.0000
	BBBB	84	PHE	2.7723	1.0285	3.7688
	BBBB	85	SER	10.1939	7.3007	15.9804
	BBBB	86	ASP	6.5079	3.0391	9.9768
	BBBB	87	TRP	6.1336	0.0000	8.5870
55	BBBB	88	LEU	0.2766	0.5478	0.0054
	BBBB	89	LEU	0.2222	0.0049	0.4394

	BBBB	90	LEU	0.0152	0.0302	0.0001
	BBBB	91	GLN	0.1468	0.0000	0.2642
	BBBB	92	ALA	0.0005	0.0006	0.0000
	BBBB	93	SER	5.6156	4.5602	7.7265
5	BBBB	94	ALA	6.8297	1.8546	26.7302
	BBBB	95	GLU	6.8738	0.8762	11.6719
	BBBB	96	VAL	12.2316	5.3212	21.4456
	BBBB	97	VAL	1.4488	1.1013	1.9123
	BBBB	98	MET	11.2447	0.4365	22.0530
10	BBBB	99	GLU	6.9392	5.4744	8.1110
	BBBB	100	GLY	2.1371	2.1371	0.0000
	BBBB	101	GLN	10.3142	0.0031	18.5631
	BBBB	102	PRO	10.9007	1.3692	23.6094
	BBBB	103	LEU	0.1806	0.2907	0.0705
15	BBBB	104	PHE	0.9676	0.0002	1.5204
	BBBB	105	LEU	0.2088	0.0016	0.4161
	BBBB	106	ARG	3.6986	0.0002	5.8119
	BBBB	107	CYS	0.0292	0.0438	0.0000
	BBBB	108	HIS	1.4195	0.6184	1.9535
20	BBBB	109	GLY	0.5887	0.5887	0.0000
	BBBB	110	TRP	3.6590	0.0000	5.4025
	BBBB	111	ARG	12.1336	6.9873	15.0744
	BBBB	112	ASN	13.9325	3.3709	24.4942
	BBBB	113	TRP	3.3478	2.2053	3.8048
25	BBBB	114	ASP	7.6950	3.0188	12.3711
	BBBB	115	VAL	0.1840	0.2489	0.0975
	BBBB	116	TYR	4.9222	0.0000	7.3832
	BBBB	117	LYS	10.4451	0.8887	18.0902
	BBBB	118	VAL	0.0000	0.0000	0.0000
30	BBBB	119	ILE	4.6639	0.0004	9.3274
	BBBB	120	TYR	0.0002	0.0000	0.0003
	BBBB	121	TYR	3.8872	0.0000	5.8308
	BBBB	122	LYS	4.3212	0.6213	7.2812
	BBBB	123	ASP	9.3317	5.1768	13.4866
35	BBBB	124	GLY	14.0149	14.0149	0.0000
	BBBB	125	GLU	14.1323	1.6253	24.1378
	BBBB	126	ALA	12.2018	6.3993	35.4121
	BBBB	127	LEU	9.7819	5.9893	13.5746
	BBBB	128	LYS	10.6006	2.2370	17.2915
40	BBBB	129	TYR	9.1175	4.6166	11.3680
	BBBB	130	TRP	11.8627	0.8908	16.2515
	BBBB	131	TYR	9.3270	0.4323	13.7744
	BBBB	132	GLU	10.1438	0.0000	18.2588
	BBBB	133	ASN	4.9699	1.6521	8.2877
45	BBBB	134	HIS	2.1605	0.1201	3.5207
	BBBB	135	ASN	3.4385	4.8744	2.0027
	BBBB	136	ILE	0.1878	0.2608	0.1149
	BBBB	137	SER	10.4452	5.0394	21.2570
	BBBB	138	ILE	4.4124	0.8988	7.9260
50	BBBB	139	THR	13.3105	0.5909	30.2701
	BBBB	140	ASN	6.8155	3.1228	10.5082
	BBBB	141	ALA	1.3398	1.6747	0.0000
	BBBB	142	THR	7.5421	0.0097	17.5852
	BBBB	143	VAL	11.6452	1.2806	25.4646
55	BBBB	144	GLU	14.1708	1.1173	24.6136
	BBBB	145	ASP	3.4895	0.0584	6.9206

	BBBB	146	SER	4.2945	1.9825	8.9184
	BBBB	147	GLY	4.3457	4.3457	0.0000
	BBBB	148	THR	4.4415	0.0000	10.3634
	BBBB	149	TYR	0.0214	0.0001	0.0321
5	BBBB	150	TYR	3.1691	0.0000	4.7537
	BBBB	151	CYS	0.0000	0.0000	0.0000
	BBBB	152	THR	3.5053	0.0000	8.1791
	BBBB	153	GLY	0.6931	0.6931	0.0000
	BBBB	154	LYS	6.3103	0.0180	11.3441
10	BBBB	155	VAL	0.0365	0.0044	0.0793
	BBBB	156	TRP	3.3899	5.9121	2.3810
	BBBB	157	GLN	16.5870	5.2100	25.6886
	BBBB	158	LEU	13.1911	0.1922	26.1899
	BBBB	159	ASP	13.0965	5.2133	20.9797
15	BBBB	160	TYR	3.2939	3.1627	3.3595
	BBBB	161	GLU	10.8490	4.6790	15.7851
	BBBB	162	SER	0.5960	0.7781	0.2318
	BBBB	163	GLU	10.5937	0.3366	18.7993
	BBBB	164	PRO	11.6713	3.2190	22.9411
20	BBBB	165	LEU	1.9716	0.7957	3.1476
	BBBB	166	ASN	5.2287	2.2398	8.2176
	BBBB	167	ILE	0.2784	0.5568	0.0000
	BBBB	168	THR	9.3922	0.0000	21.9152
	BBBB	169	VAL	0.2895	0.5066	0.0000
25	BBBB	170	ILE	9.7952	0.6056	18.9848
	BBBB	171	LYS	14.9992	3.9650	23.8265
	BBBB	172	ALA	8.6682	3.2571	30.3128
	BBBB	173	PRO	17.2332	8.4405	28.9567
	BBBB	174	ARG	24.5074	21.0894	26.4605
30	BBBB	221	NAG	17.4850	0.0000	17.4850
	BBBB	242	NAG	10.4355	0.0000	10.4355
	BBBB	243	NAG	10.3502	0.0000	10.3502
	BBBB	244	MAN	15.8885	0.0000	15.8885
	BBBB	335	NAG	8.8279	0.0000	8.8279
35	BBBB	336	NAG	16.5384	0.0000	16.5384
	BBBB	337	FCA	16.2107	0.0000	16.2107
	BBBB	340	NAG	13.5916	0.0000	13.5916
	BBBB	341	NAG	21.2819	0.0000	21.2819
	BBBB	366	NAG	21.9238	0.0000	21.9238

Table 12. PhFcεRIα₁₋₁₇₂, Form H1, residue exposure

>>>>   coordinate set= c703f.pdb

	segid			average accessible area	
	sidechain	resid	resname	residue	mainchain
5	1	VAL	22.5900	15.0637	32.6251
	2	PRO	11.2478	3.9295	21.0055
	3	GLN	15.8860	3.9559	25.4300
	4	LYS	7.8658	4.1508	10.8378
	5	PRO	0.7859	0.7412	0.8456
10	6	LYS	15.0743	0.2689	26.9185
	7	VAL	2.5158	4.4026	0.0000
	8	SER	8.7041	1.7476	22.6170
	9	LEU	3.4804	4.2930	2.6678
	10	ASN	13.3748	1.0394	25.7103
15	11	PRO	6.4372	0.6223	14.1904
	12	PRO	9.9906	1.9726	20.6812
	13	TRP	1.6444	0.0463	2.2837
	14	ASN	2.4971	0.0178	4.9764
	15	ARG	1.2172	0.0001	1.9127
20	16	ILE	0.3947	0.0000	0.7895
	17	PHE	0.1203	0.0000	0.1890
	18	LYS	9.6134	1.5661	16.0512
	19	GLY	6.4465	6.4465	0.0000
	20	GLU	2.9946	0.0000	5.3903
25	21	ASN	4.7501	2.8416	6.6586
	22	VAL	0.3670	0.6423	0.0000
	23	THR	5.0060	0.1082	11.5364
	24	LEU	0.2483	0.0000	0.4966
	25	THR	4.0121	0.0000	9.3616
30	26	CYS	0.1821	0.1881	0.1702
	27	ASN	6.6425	2.1781	11.1069
	28	GLY	5.3679	5.3679	0.0000
	29	ASN	17.4099	6.2098	28.6100
	30	ASN	10.2762	3.8525	16.6998
35	31	PHE	8.0955	2.8330	11.1027
	32	PHE	13.6377	6.1749	17.9021
	33	GLU	14.0698	3.4930	22.5313
	34	VAL	17.4046	4.8614	34.1288
	35	SER	19.6721	12.8131	33.3901
40	36	SER	11.0819	4.5899	24.0659
	37	THR	0.8916	0.1902	1.8268
	38	LYS	8.3803	0.0158	15.0719
	39	TRP	0.0119	0.0000	0.0167
	40	PHE	3.9461	0.0636	6.1646
45	41	HIS	3.7169	0.6731	5.7461
	42	ASN	6.6160	8.2911	4.9408
	43	GLY	11.9937	11.9937	0.0000
	44	SER	11.8169	1.4187	32.6133
	45	LEU	12.1877	6.2251	18.1503
50	46	SER	4.5272	3.1407	7.3002
	47	GLU	18.3989	5.5809	28.6533
	48	GLU	1.6700	0.3535	2.7232

	49	THR	6.8437	0.4232	15.4044
	50	ASN	6.1820	1.4496	10.9145
	51	SER	8.4271	1.0315	23.2182
	52	SER	6.0403	0.9347	16.2516
5	53	LEU	1.9666	0.0000	3.9331
	54	ASN	10.6560	4.7155	16.5965
	55	ILE	1.5407	1.0849	1.9965
	56	VAL	8.4966	4.2813	14.1170
	57	ASN	8.0710	0.2994	15.8427
10	58	ALA	0.4475	0.5594	0.0000
	59	LYS	12.6628	0.0000	22.7931
	60	PHE	2.0470	0.0207	3.2050
	61	GLU	9.1096	0.1120	16.3076
	62	ASP	3.9382	0.0000	7.8765
15	63	SER	0.1178	0.0000	0.3535
	64	GLY	0.5477	0.5477	0.0000
	65	GLU	3.5925	0.1947	6.3107
	66	TYR	0.3061	0.0000	0.4592
	67	LYS	4.9263	0.0000	8.8674
20	68	CYS	0.0002	0.0002	0.0000
	69	GLN	3.1065	0.1191	5.4965
	70	HIS	4.3287	0.5494	6.8482
	71	GLN	14.4511	4.6243	22.3126
	72	GLN	16.7254	5.5984	25.6271
25	73	VAL	4.6849	0.0239	10.8997
	74	ASN	3.7390	2.2152	5.2628
	75	GLU	9.8220	1.6123	16.3897
	76	SER	0.9279	1.3599	0.0638
	77	GLU	10.2035	0.8100	17.7182
30	78	PRO	6.8952	4.7323	9.7791
	79	VAL	4.4704	0.8249	9.3311
	80	TYR	10.8485	1.3619	15.5919
	81	LEU	0.8740	1.0895	0.6586
	82	GLU	6.2336	0.0000	11.2205
35	83	VAL	1.6724	2.9266	0.0000
	84	PHE	3.0301	0.8580	4.2712
	85	SER	10.9935	6.5698	19.8409
	86	ASP	6.6012	2.2575	10.9449
	87	TRP	9.0703	0.2059	12.6161
40	88	LEU	0.4451	0.8570	0.0331
	89	LEU	0.5432	0.0676	1.0187
	90	LEU	0.0913	0.1298	0.0527
	91	GLN	0.0763	0.0000	0.1373
	92	ALA	0.0388	0.0480	0.0022
45	93	SER	4.5675	4.1995	5.3034
	94	ALA	7.1276	1.0786	31.3237
	95	GLU	6.8795	1.2919	11.3495
	96	VAL	13.0247	4.2238	24.7593
	97	VAL	1.0770	0.5985	1.7150
50	98	MET	16.7988	0.4914	33.1061
	99	GLU	7.5393	3.3688	10.8758
	100	GLY	3.1157	3.1157	0.0000
	101	GLN	10.1587	0.2304	18.1014
	102	PRO	8.7856	1.4883	18.5154
55	103	LEU	0.0405	0.0000	0.0810
	104	PHE	5.7390	0.0000	9.0184

	105	LEU	0.0000	0.0000	0.0000
	106	ARG	4.9770	0.0000	7.8210
	107	CYS	2.8329	3.8594	0.7800
	108	HIS	1.0226	0.3429	1.4757
5	109	GLY	0.7524	0.7524	0.0000
	110	TRP	4.3881	0.0000	6.1433
	111	ARG	13.1221	5.0820	17.7164
	112	ASN	12.3893	5.7597	19.0188
	113	TRP	6.4754	2.8590	7.9219
10	114	ASP	11.2956	2.1441	20.4471
	115	VAL	2.0499	2.1826	1.8731
	116	TYR	11.1258	1.0112	16.1831
	117	LYS	16.7863	4.7622	26.4055
	118	VAL	8.1424	6.0958	10.8711
15	119	ILE	6.8012	0.9964	12.6060
	120	TYR	2.8442	0.9061	3.8133
	121	TYR	3.5867	0.0012	5.3794
	122	LYS	5.1214	0.6012	8.7376
	123	ASP	7.4941	4.6376	10.3507
20	124	GLY	12.2128	12.2128	0.0000
	125	GLU	15.1128	1.2362	26.2141
	126	ALA	11.6923	3.6139	44.0058
	127	LEU	4.6471	5.4019	3.8923
	128	LYS	18.8922	6.6649	28.6740
25	129	TYR	17.4834	7.0989	·22.6757
	130	TRP	2.4961	4.3542	1.7528
	131	TYR	12.7233	5.2485	16.4608
	132	GLU	13.6661	0.7556	23.9944
	133	ASN	9.3922	6.3761	12.4084
30	134	HIS	15.2795	8.2917	19.9381
	135	ASN	11.1940	2.7459	19.6420
	136	ILE	5.4540	0.6821	10.2259
	137	SER	0.6915	0.0000	2.0744
	138	ILE	6.3883	1.6352	11.1413
35	139	THR	4.7987	2.2363	8.2152
	140	ASN	5.2615	2.7779	7.7451
	141	ALA	0.9545	1.1931	0.0000
	142	THR	6.9219	0.6069	15.3420
	143	VAL	9.5663	1.8575	19.8448
40	144	GLU	14.4371	3.2860	23.3579
	145	ASP	2.2220	0.0056	4.4384
	146	SER	5.2393	2.1712	11.3756
	147	GLY	3.0536	3.0536	0.0000
	148	THR	2.8393	0.0000	6.6250
45	149	TYR	0.0489	0.0000	0.0734
	150	TYR	3.3061	0.0181	4.9500
	151	CYS	0.0000	0.0000	0.0000
	152	THR	3.7148	0.0000	8.6679
	153	GLY	0.9412	0.9412	0.0000
50	154	LYS	8.4275	0.1238	15.0704
	155	VAL	0.3174	0.0138	0.7223
	156	TRP	14.1884	7.2900	16.9477
	157	GLN	15.4584	4.5161	24.2122
	158	LEU	11.5234	0.7276	22.3193
55	159	ASP	15.3714	7.3517	23.3910
	160	TYR	·4.5849	·1.8192	5.9678

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	161	GLU	12.0528	4.8779	17.7927
	162	SER	0.9680	1.3220	0.2601
	163	GLU	10.9265	0.9944	18.8722
	164	PRO	11.4182	2.7638	22.9575
5	165	LEU	1.8797	0.4866	3.2727
	166	ASN	5.1428	2.5621	7.7235
	167	ILE	0.3717	0.7433	0.0000
	168	THR	9.9155	0.0000	23.1363
	169	VAL	0.2713	0.4747	0.0000
10	170	ILE	12.6290	1.6535	23.6046
	171	LYS	18.1223	11.6928	23.2660
	221	NAG	10.3807	0.0000	10.3807
	222	NAG	20.2927	0.0000	20.2927
	242	NAG	10.3379	0.0000	10.3379
15	243	NAG	10.0051	0.0000	10.0051
	244	MAN	17.1981	0.0000	17.1981
	250	NAG	15.4600	0.0000	15.4600
	274	NAG	20.0516	0.0000	20.0516
	340	NAG	16.0149	0.0000	16.0149
20	341	NAG	20.8951	0.0000	20.8951
	366	NAG	14.4348	0.0000	14.4348
	367	NAG	20.6913	0.0000	20.6913

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Table 13. Crystallographic data and model refinement

Data Set	Form H	Form M2	Form I	Form I2
res.	3.2	3.2	3.1	3.8
wavel(A)	1.0039	1.0047	0.914	0.92
comp/(last shell)	93.2(95.4)	99.3(100)	97.0(83.3)	85.7(80.2)
av. red. (last shell)	8.0(7.1)	4.1(4.2)	7.3(2.2)	2.0(1.6)
Rmerge (last shell)	10.3(51.6)	9.7(43.6)	11.2(76.6)	6.3(60.9)
I/sigI (last shell)	11.8(5.3)	9.2(3.0)	7.9(1.1)	7.5(1.1)
#refl(free)	4030(412)	11640(620)	23318(1180)	14239(740)
Rfactor/Rfree	28.8/31.3	25.4/28.3	29.1/32.9	27.8/30.4
# atoms	1537	3120	7660	7660
# waters	0	0	0	0
RMSD bonds	0.0084	0.0096	0.0100	0.0086
RMSD angles	1.53	1.60	1.50	1.40
Ave. B	97.1	69.4	137.6	191.1

Table 14. Root mean square deviations for alpha carbon positions

model	RMSD v' ong (Angs)	#CA	segments
H1	0.855	155	4-27/28-31/36-70/73-129/137-171
H1 30 loop	3.667	6	27-31, 36
H1 130 loop	4.176	9	129-137
M2 copy A	0.880	157	4-27/36-130/134-171
M2A 30 loop	5.212	6	27-31, 36
M2A 130 loop	3.818	5	130-134
M2 copy B	0.766	155	4-27/36-127/133-171
M2B 30 loop	4.258	6	27-31, 36
M2B 130 loop	6.938	7	127-133
T1 copy C	0.839	155	4-28/36-71/73-127/133-171
T1C 30 loop	6.372	5	28-31, 36
T1C 130 loop	7.449	7	127-133
T2 copy C	0.867	155	4-28/36-71/73-127/133-171
T1C 30 loop	6.319	5	28-31, 36
T1C 130 loop	7.476	7	127-133

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While various embodiments of the present invention have been described in
detail, it is apparent that modifications and adaptations of those embodiments will occur
to those skilled in the art. It is to be expressly understood, however, that such
modifications and adaptations are within the scope of the present invention, as set forth
5   in the following claims.

What is claimed is:

1.   A three-dimensional model selected from the group consisting of: (a) a three-dimensional model of an extracellular domain of a human high affinity Fc epsilon receptor alpha chain (FcεRIα) protein, wherein said model substantially represents the atomic coordinates specified in a table selected from the group consisting of Table 1, Table 5, Table 6, Table 7, and Table 8; and (b) a three-dimensional model comprising a modification of said model of (a), wherein said modification represents a protein that binds to a Fc domain of an antibody.

2.   A method to produce a three-dimensional model of an extracellular domain of a human FcεRIα protein, said method comprising representing amino acids of said protein at substantially the atomic coordinates specified in a table selected from the group consisting of Table 1, Table 5, Table 6, Table 7 and Table 8.

3.   .   A method to produce a three-dimensional model of an antibody receptor protein other than a human FcεRIα protein represented by the three-dimensional model substantially representing the atomic coordinates specified in a table selected from the group consisting of Table 1, Table 5, Table 6, Table 7 and Table 8, said method comprising homology modeling.

4.   An isolated crystal of an extracellular domain of a FcεRIα protein.

5.   A method to produce an isolated crystal of an extracellular domain of a FcεRIα protein, said method comprising vapor diffusion.

6.   An isolated FcεRIα protein selected from the group consisting of: (a) a protein consisting of SEQ ID NO:2; (b) a protein consisting of SEQ ID NO:4 except that the isoleucine at position 170 is replaced with a cysteine; and (c) a protein that is structurally homologous to a protein of (a) or (b), wherein said protein of (c) binds to a Fc domain of an antibody.

7.   A method to identify a compound that inhibits the binding between an IgE antibody and a FcεRIα protein, said method comprising using a three-dimensional model of an extracellular domain of a human high affinity FcεRIα protein to identify said compound, wherein said model substantially represents the atomic coordinates

specified in a table selected from the group consisting of Table 1, Table 5, Table 6, Table 7 and Table 8.

8.   A mutein that binds to a Fc domain of an antibody, wherein said mutein has an improved function compared to a protein comprising an amino acid sequence selected from the group consisting of SEQ ID NO:2 and SEQ ID NO:4, wherein said improved function is selected from the group consisting of increased stability, increased affinity for an Fc domain of an antibody, altered substrate specificity, and increased solubility, wherein said mutein is produced by a method comprising:

(a)   analyzing a three-dimensional model substantially representing the atomic coordinates specified in a table selected from the group consisting of Table 1, Table 5, Table 6, Table 7 and Table 8 to identify at least one amino acid of the protein represented by said model which if replaced by a specified amino acid would effect said improved function of said protein; and

(b)   replacing said identified amino acid(s) to produce said mutein having said improved function.

9.   A mutein having an improved function compared to an unmodified FcεRIα protein, wherein said improved function is selected from the group consisting of increased stability, increased affinity for an Fc domain of an antibody, altered substrate specificity, and increased solubility, wherein the amino acid sequence of said mutein differs in at least one position from the amino acid sequence of said unmodified protein, said position being in a region selected from the group consisting of a crystal contact cluster, a tryptophan-containing hydrophobic ridge, a FG loop in D2, a D1D2 interface, a cleft between D1 and D2, a domain 1, a domain 2, a hydrophobic core, a A'B loop of D1, a EF loop of D1, a BC loop of D2, a C strand of D2, a CC' loop of D2, a C'E loop of D2, a strand of D2, the amino terminal five residues of said protein, and the carboxyl terminal five residues of said protein.

10.   A method to improve a function of a FcεRIα protein, said improved function being selected from the group consisting of increased stability, increased affinity for an Fc domain of an antibody, altered substrate specificity, and increased solubility, said method comprising:

(a)   analyzing a three-dimensional model of an extracellular domain of a human high affinity FcεRIα protein substantially representing the atomic coordinates specified in a table selected from the group consisting of Table 1, Table 5, Table 6, Table 7 and Table 8 to identify at least one amino acid of said protein which if replaced by a specified amino acid improves at least one of said functions of said protein; and

(b)   replacing said identified amino acid(s) to produce a mutein having at least one of said improved functions.

11.   An isolated FcεRIα protein selected from the group consisting of: a crystal contact cluster involved in IgE binding; a tryptophan-containing hydrophobic ridge; a FG loop in D2; a D1D2 interface; a cleft between D1 and D2; a domain 1; a domain 2; a hydrophobic core; a A'B loop of D1; a EF loop of D1; a BC loop of D2; a C strand of D2; a CC' loop of D2; a C'E loop of D2; and a strand of D2.

12.   The invention of Claim 1, 2, 3, 7, 8 or 10, wherein said model is represented by a method selected from the group consisting of listing the coordinates of all atoms comprising said model, providing a physical three-dimensional model, imaging said model on a computer screen, providing a picture of said model, and deriving a set of coordinates based of a picture of said model.

13.   The invention of Claim 1, 2, 3, 7, 8 or 10, wherein said model identifies the solvent accessibility of amino acid residues of said protein listed in a table selected from the group consisting of Table 2, Table 9, Table 10, Table 11 and Table 12.

14.   The invention of Claim 1, 2, 3, 7, 8 or 10, wherein said model represents a protein that binds to a Fc domain of an IgE antibody with an affinity that is at least equivalent to the affinity of the extracellular domain of human FcεRIα for an IgE antibody selected from the group consisting of a human IgE antibody, a canine IgF antibody, a feline IgE antibody, an equine IgE antibody, a rat IgE antibody, and a murine IgE antibody.

15.   The invention of Claim 1, 2, 3, 7, 8 or 10, wherein said model represents a protein that selectively binds to a mammalian antibody selected from the group consisting of an IgE antibody and an IgG antibody.

16.   The invention of Claim 1, 2, 3, 7, 8 or 10, wherein said model represents an extracellular domain of a protein selected from the group consisting of a human FcεRIα protein, a canine FcεRIα protein, a feline FcεRIα protein, an equine FcεRIα protein, a murine FcεRIα protein, and a rat FcεRIα protein.

17.   The invention of Claim 1, 2, 3, 7, 8 or 10, wherein said model comprises a three-dimensional model of an extracellular antibody binding domain of an antibody receptor protein other than human FcεRIα.

18.   The invention of Claim 17, wherein said model is produced by incorporating all or any part of the amino acid sequence of said other antibody receptor protein into a three-dimensional model of said extracellular domain of said human FcεRIα protein to produce said model of said other antibody receptor protein.

19.   The invention of Claim 1, 2, 3, 7, 8 or 10, wherein said model represents an IgE binding domain.

20.   The invention of Claim 1, 2, 3, 7, 8 or 10, wherein said model is produced by a method comprising:

        (a)   crystallizing an extracellular domain of a human FcεRIα protein;

        (b)   collecting X-ray diffraction data from said crystallized protein; and

        (c)   determining said model from said data and amino acid sequence of said protein.

21.   The invention of Claim 20, wherein said protein has an amino acid sequence selected from the group consisting of SEQ ID NO:2, SEQ ID NO:4 and SEQ ID NO:4 except that the isoleucine at position 170 is replaced with a cysteine.

22.   The invention of Claim 1, 2, 3, 7, 8 or 10, wherein said model has a three-dimensional structure comprising atomic coordinates that have a root mean square deviation of protein backbone atoms of less than 10 angstroms when superimposed on said three-dimensional model substantially represented by the atomic coordinates specified in a table selected from the group consisting of Table 1, Table 5, Table 6, Table 7, and Table 8.

23.　.　The invention of Claim 1, wherein said modification has an amino acid sequence that shares at least about 30% amino acid sequence homology with a FcεRIα protein having an amino acid sequence selected from the group consisting of SEQ ID NO:2 and SEQ ID NO:4.

24.　The invention of Claim 1 or 3, wherein said model represents a FcεRIα protein having increased stability compared to the stability of a human FcεRIα protein having an amino acid sequence selected from the group consisting of SEQ ID NO:2 and SEQ ID NO:4.

25.　The invention of Claim 1 or 3, wherein said model represents a FcεRIα protein having increased affinity for IgE compared to the affinity of a human FcεRIα protein having an amino acid sequence selected from the group consisting of SEQ ID NO:2 and SEQ ID NO:4 for IgE.

26.　The invention of Claim 1 or 3, wherein said model represents a FcεRIα protein having altered substrate affinity compared to the affinity of a human FcεRIα protein having an amino acid sequence selected from the group consisting of SEQ ID NO:2 and SEQ ID NO:4 for IgE.

27.　The invention of Claim 1 or 3, wherein said model comprises a three-dimensional model of a FcεRIα protein having increased solubility compared to the solubility of a human FcεRIα protein having an amino acid sequence selected from the group consisting of SEQ ID NO:2 and SEQ ID NO:4.

28.　The invention of Claim 1, 2 or 3, wherein said model is used to identify an inhibitor of the selective binding between a FcεRIα protein and an IgE antibody.

29.　The invention of Claim 1, 2, 3, 7, 8 or 10, wherein said model identifies crystal contacts between a FcεRIα protein and a Fc domain of an IgE antibody.

30.　The invention of Claim 1, 2, 3, 4, 5, 6, 7, 8, 9, 10 or 11, wherein domain 1 and domain 2 are oriented in a manner as specified by the structural coordinates specified in a table selected from the group consisting of Table 1, Table 5, Table 6, Table 7 and Table 8.

31.　The invention of Claim 1, 2, 3, 7, 8, or 10, wherein said model identifies amino acids in the D1D2 interface.

32.   The invention of Claim 3, wherein said method of homology modeling comprises incorporating at least a portion of the amino acid sequence of said other antibody receptor protein into said three-dimensional model substantially representing the atomic coordinates specified in a table selected from the group consisting of Table 1, Table 5, Table 6, Table 7 and Table 8 to produce said model of said other antibody receptor protein.

33.   The invention of Claim 1, 2, 3, 4, 5, or 6, wherein said protein has an amino acid sequence selected from the group consisting of SEQ ID NO:2, SEQ ID NO:4, and SEQ ID NO:4 except that the isoleucine at position 170 is replaced with a cysteine.

34.   The invention of Claim 4 or 5, wherein said crystal belongs to a space group selected from the group consisting of monoclinic space group C2, hexagonal space group $P6_122$, and tetragonal space group $P4_3$.

35.   The invention of Claim 4 or 5, wherein said crystal is selected from the group consisting of: a monoclinic space group C2 having cell dimensions of 88.6 angstroms x 69.6 angstroms x 49.3 angstroms, alpha=gamma=90.0 degrees, beta=116.69 degrees; a monoclinic space group C2 having cell dimensions of 136.02 angstroms x 75.01 angstroms x 79.28 angstroms, alpha=gamma=90 degrees, beta=117.8 degrees; a monoclinic space group C2 having cell dimensions of 136.90 angstroms x 73.79 angstroms x 79.40 angstroms, alpha=gamma=90 degrees, beta=117.74 degrees; a tetragonal space group $P4_3$ having cell dimensions of 145.08 angstroms x 145.08 angstroms x 62.74 angstroms, alpha=beta=gamma=90 degrees; a tetragonal space group $P4_3$ having cell dimensions of 150.50 angstroms x 150.50 angstroms x 74.18 angstroms, alpha=beta=gamma=90 degrees; a hexagonal space group $P6_122$ having cell dimensions of 58 angstroms x 58 angstroms x 226 angstroms, alpha=beta=90 degrees, gamma=120 degrees; and a hexagonal space group $P6_122$ having cell dimensions of 58.62 angstroms x 58.62 angstroms x 229.19 angstroms, alpha=beta=90 degrees, gamma=120 degrees.

36.   The invention of Claim 4, 5, 6, or 11, wherein said protein is produced in insect cells or Chinese hamster ovary cells.

37.   The invention of Claim 4 or 5, wherein said crystal diffracts X-rays to a resolution selected from the group consisting of about 2.4 angstroms, about 3.1 angstroms, about 3.2 angstroms, and about 3.8 angstroms.

38.   The invention of Claim 1, 3, 4, 5, 6, 7, 9 or 11, wherein said protein represented by said modification of Claim 1, said antibody receptor protein of Claim 3, or said FcεRIα protein of Claim 4, 5, 6, 7, 9 or 11 is selected from the group consisting of a human FcεRIα protein, a feline FcεRIα protein, a canine FcεRIα protein, an equine FcεRIα protein, a murine FcεRIα protein, and a rat FcεRIα protein..

39.   A nucleic acid molecule comprising a nucleic acid sequence that encodes a protein selected from the group consisting of said protein of Claim 6 or 11 and said mutein of Claim 8, 9, or 10.

40.   A recombinant molecule comprising a nucleic acid sequence of Claim 39.

41.   A recombinant virus comprising a nucleic acid sequence of Claim 39.

42.   A recombinant cell comprising a nucleic acid sequence of Claim 39.

43.   A method to produce a protein comprising culturing a recombinant cell of Claim 42.

44.   An inhibitory compound identified in accordance with the method of Claim 7.

45.   A therapeutic composition comprising an inhibitory compound of Claim 44.

46.   A method to protect an animal from allergy, said method comprising administering to said animal an inhibitory compound of Claim 44.

47.   The invention of Claim 7, 44, 45, or 46, wherein said compound interacts with a region of said model selected from the group consisting of the IgE binding domain, the D1D2 interface, and the cleft between domain 1 and domain 2.

48.   The invention of Claim 7, 44, 45, or 46, wherein said compound interacts with a region of said model selected from the group consisting of a A'B loop of domain 1, a EF loop of domain 1, a BC loop of domain 2, a C strand of domain 2, a CC' loop of domain 2, a C'E loop of domain 2, a F strand of domain 2, a FG loop of domain 2, and a tryptophan-containing hydrophobic ridge.

49.   The invention of Claim 7, 44, 45, or 46, wherein said compound interacts with a region of said model in which N-linked glycosylation sites are absent.

50.   The invention of Claim 7, 44, 45, or 46, wherein said compound interacts with an amino acid selected from the group consisting of: (a) a residue having a position in SEQ ID NO:2 or SEQ ID NO:4 selected from the group consisting of position 87, 115, 117, 118, 120-123, 128, 129, 131, 149, 153, 155 and 159; and (b) a surface residue within about 10 angstroms of any of said residues of (a).

51.   The invention of Claim 7, 44, 45, or 46, wherein said compound interacts with an amino acid selected from the group consisting of: (a) a residue having a position in SEQ ID NO:2 or SEQ ID NO:4 selected from the group consisting of position 87, 117, 121, 123, 128, and 159; and (b) a surface residue within about 10 angstroms of any of said residues of (a).

52.   The invention of Claim 7, wherein said method comprises:

        (a)   generating said model, or a model of an IgE binding domain thereof, on a computer screen;

        (b)   generating the spacial structure of a compound to be tested; and

        (c)   testing to determine if said compound interacts with said IgE binding domain, wherein such an interaction indicates that said compound is capable of inhibiting said binding of an IgE antibody to a FcεRIα protein.

53.   The invention of Claim 52, wherein said step (a) includes the step of identifying one or more amino acid(s) in the IgE binding domain of said model that interact directly with the Fc domain of an IgE antibody when said Fc domain binds to said IgE binding domain.

54.   The invention of Claim 53, wherein said compound interacts directly with one or more of said amino acid(s).

55.   A diagnostic reagent comprising a mutein of Claim 8, 9 or 10.

56.   A therapeutic composition comprising a mutein of Claim 8, 9 or 10.

57.   A method to use a mutein of Claim 8, 9 or 10, wherein said method is selected from the group consisting of: (a) a method to protect an animal from allergy, said method comprising administering a therapeutic composition comprising said mutein

to said animal; (b) a method to detect allergy, or susceptibility thereto, in an animal, said method comprising using said mutein to detect said allergy; and (c) a method to enhance the performance of an IgE binding assay, said method comprising incorporating into said assay said mutein.

58.   The invention of Claim 8 or 10, wherein said step of replacing does not substantially disrupt the three-dimensional structure of said protein.

59.   The invention of Claim 8, 9, 10, 55, 56 or 57, wherein said mutein has an increased stability compared to an unmodified antibody receptor protein.

60.   The invention of Claim 8, 9, 10, 55, 56 or 57, wherein said mutein has an increased shelf-life compared to an unmodified antibody receptor protein.

61.   The invention of Claim 8, 9, 10, 55, 56 or 57, wherein said mutein has a K_A for said Fc domain of at least about 3×10^9 liters/mole.

62.   The invention of Claim 8, 9, 10, 55, 56 or 57, wherein said mutein has a k_a for said Fc domain of at least about 1×10^5 liters/mole-second.

63.   The invention of Claim 8, 9, 10, 55, 56 or 57, wherein said mutein has a k_d for said Fc domain of less than or equal to 3×10^{-5}/second.

64.   The invention of Claim 8, 9 or 10, wherein said antibody is an IgE antibody.

65.   The invention of Claim 8, 55, 56 or 57, wherein said mutein is produced by a method comprising:

(a) comparing the IgE binding domain on said model with amino acid sequence of an antibody receptor protein with an improved function to identify at least one amino acid segment of said antibody receptor protein with said improved function that if incorporated into said FcεRIα protein represented by said model would give said FcεRIα protein said improved function; and

(b) incorporating said segment into said FcεRIα protein, thereby producing a mutein with said improved function.

66.   The invention of Claim 8, 10, 55, 56 or 57, wherein said mutein is produced by a method comprising:

(a)   using said model to identify a three-dimensional arrangement of residues that can be randomized by mutagenesis to allow the construction of a library of molecules from which an improved function can be selected; and

(b)   identifying at least one member of said mutagenized library having said improved function.

67.   The invention of Claim 8, 9, 10, 55, 56 or 57, wherein said mutein is produced by a method comprising:

(a)   effecting random mutagenesis of nucleic acid molecules encoding a target of a FcεRIα protein as identified by analyzing a model of that protein;

(b)   cloning said mutagenized nucleic acid molecules into a phage display library, wherein said phage display library expresses said target; and

(c)   identifying at least one member of the library that expresses said target, said target having an improved function.

68.   The invention of Claim 67, wherein said target comprises an IgE binding domain and wherein said improved function comprises increased affinity of said domain for an antibody.

69.   The invention of Claim 8 or 10, wherein said step of replacing is selected from the group consisting of:

(a)   replacing at least one amino acid in at least one non-constrained loop of domain 1 in an area proximal to the FceRI gamma chain putative binding site;

(b)   joining an amino-terminal amino acid residue to a carboxyl-terminal amino acid residue of an extracellular domain of a FcεRIα protein;

(c)   replacing at least one amino acid site with an amino acid suitable for derivatization;

(d)   replacing at least one pair of amino acids of said protein with a cysteine pair to enable the formation of a disulfide bond that stabilizes said mutein;

(e)   removing at least a portion of the region between the B strand and C strand of domain 1;

(f)   removing at least a portion of the region between the C strand and E strand of domain 1;

(g)   replacing at least one amino acid in the IgE binding domain in order to increase the affinity between an IgE antibody and said protein;

(h)   replacing at least one amino acid of said protein with an amino acid such that said replacement decreases the entropy of unfolding of said protein;

(i)   replacing at least one amino acid of said protein selected from the group consisting of asparagines and glutami :s with an amino acid that is less susceptible to deamidation than is said amino acid to be replaced;

(j)   replacing at least one aminc acid of said protein selected from the group consisting of methionines, histidines and tryptophans with an amino acid that is less susceptible to an oxidation or reduction reaction than is said amino acid to be replaced;

(k)   replacing at least one arginine of said protein with an amino acid that is less susceptible to dicarbonyl compound modification than is said amino acid to be replaced;

(l)   replacing at least one amino acid of said protein susceptible to reaction with a reducing sugar sufficient to reduce said protein function with an amino acid less susceptible to said reaction;

(m)   replacing at least one amino acid of said protein with an amino acid capable of increasing the stability of the inner core of said protein;

(n)   replacing at least one amino acid of said protein with at least one N-linked glycosylation site;

(o)   replacing at least one N-linked glycosylation site of said protein with at least one amino acid that does not comprise an N-linked glycosylation site; and

(p)   replacing at least one amino acid of said protein with an amino acid that reduces aggregation of said protein.

70.   The invention of Claim 8, 9, 10, 55, 56 or 57, further comprising a
substance attached to an amino acid of said mutein such that said substance does not
substantially interfere with the antibody binding activity of said protein.

1/8

A
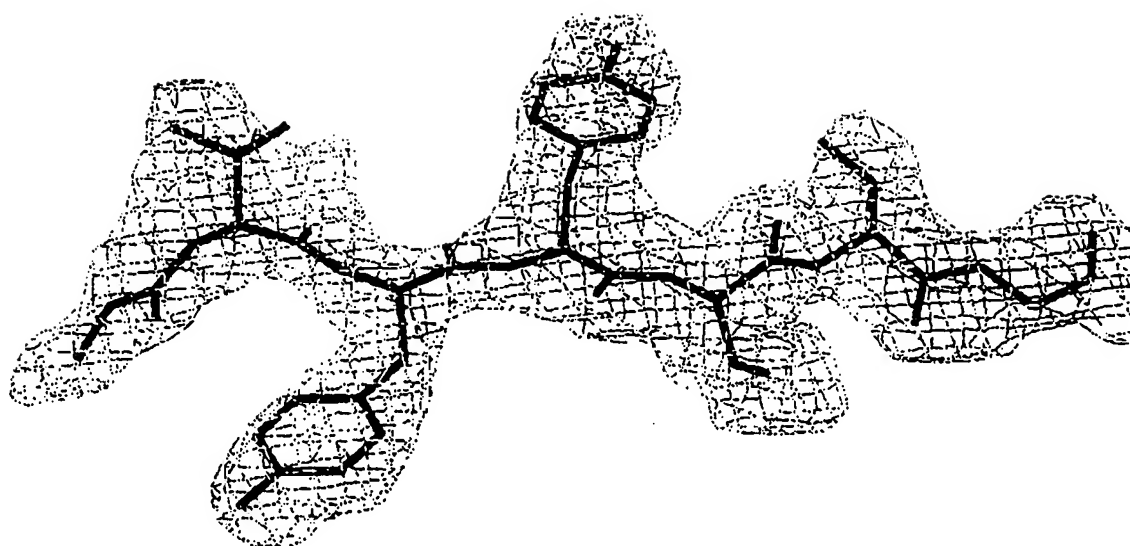
B

Asn42

Fig. 1A, 1B
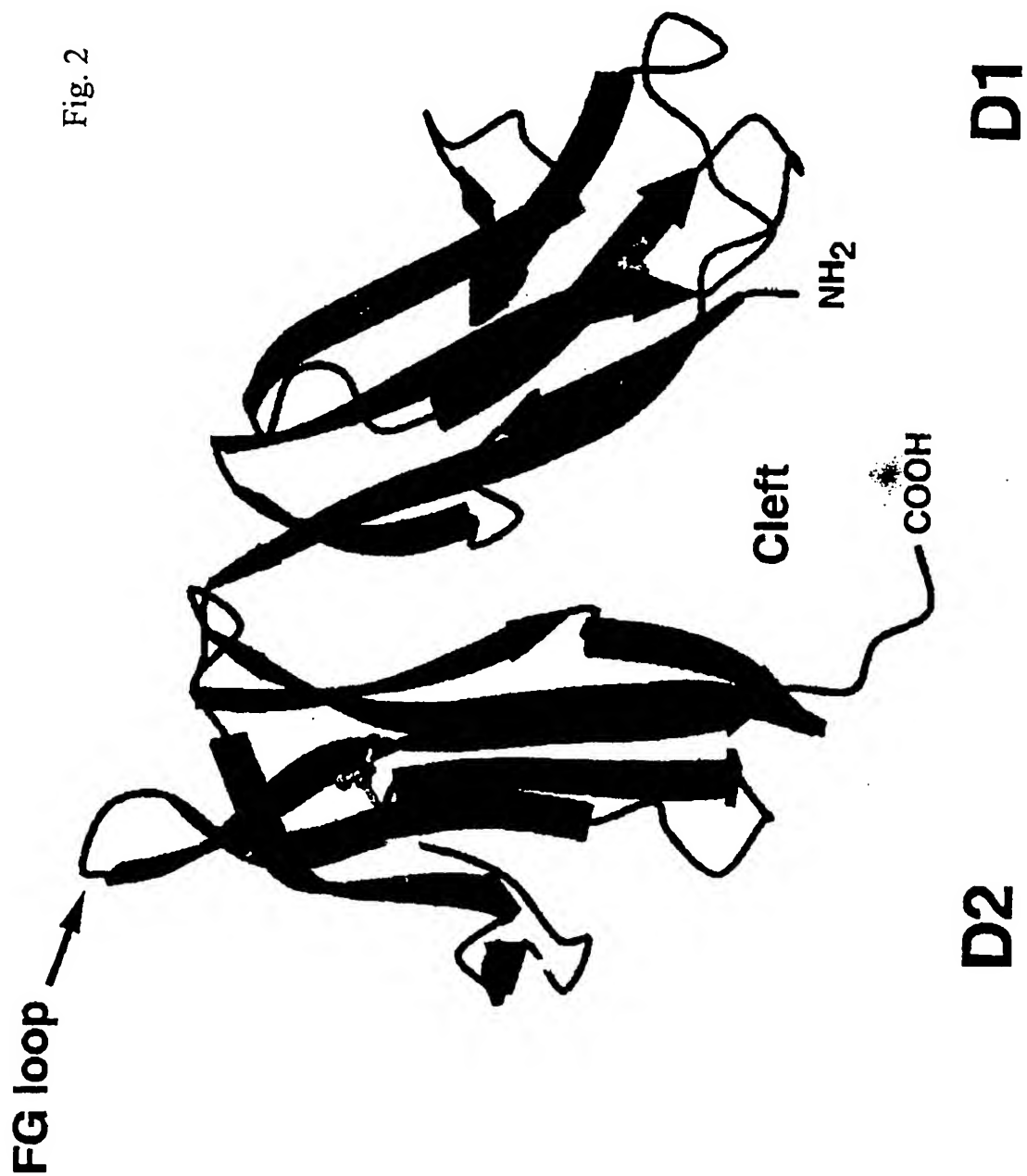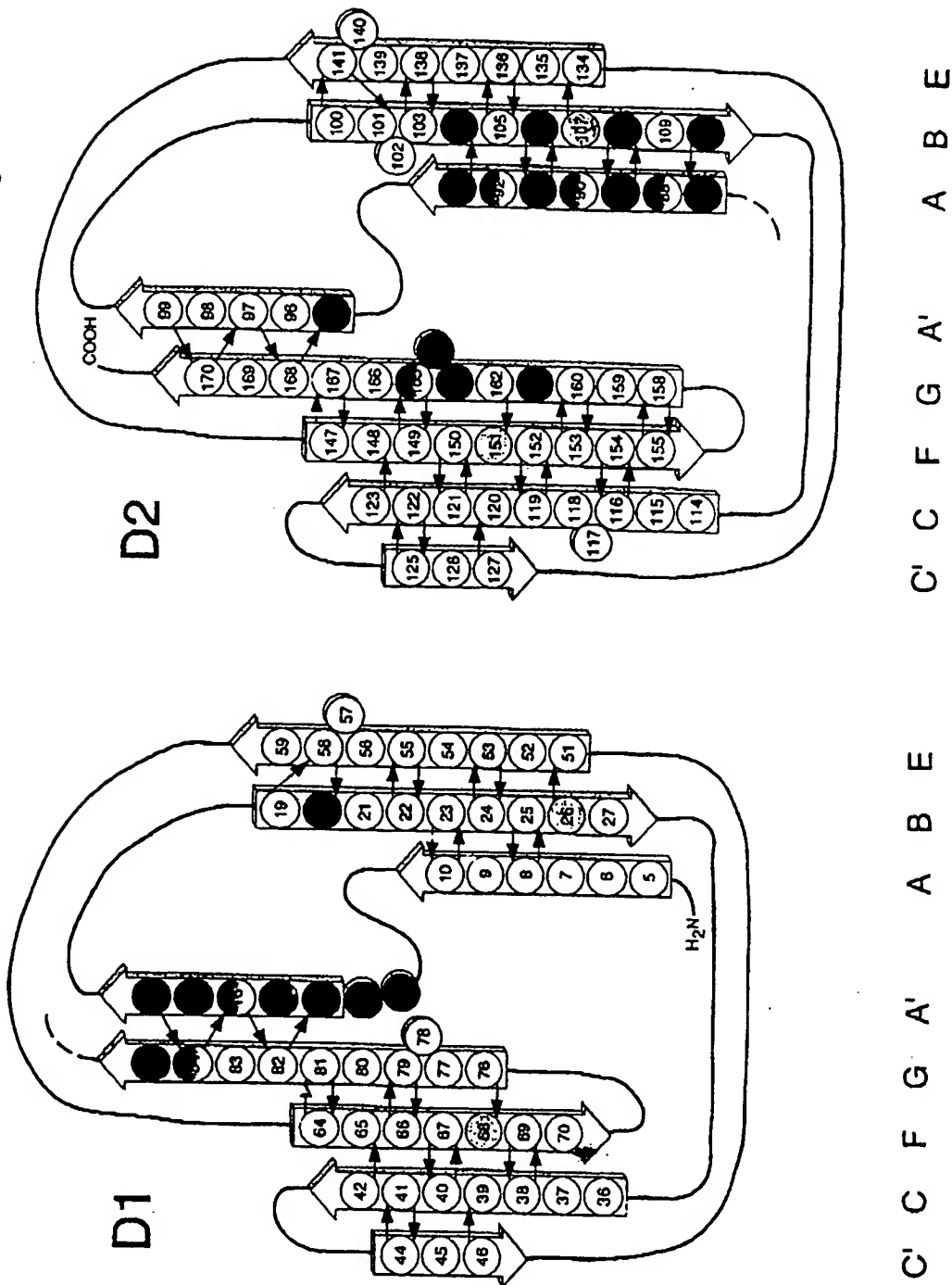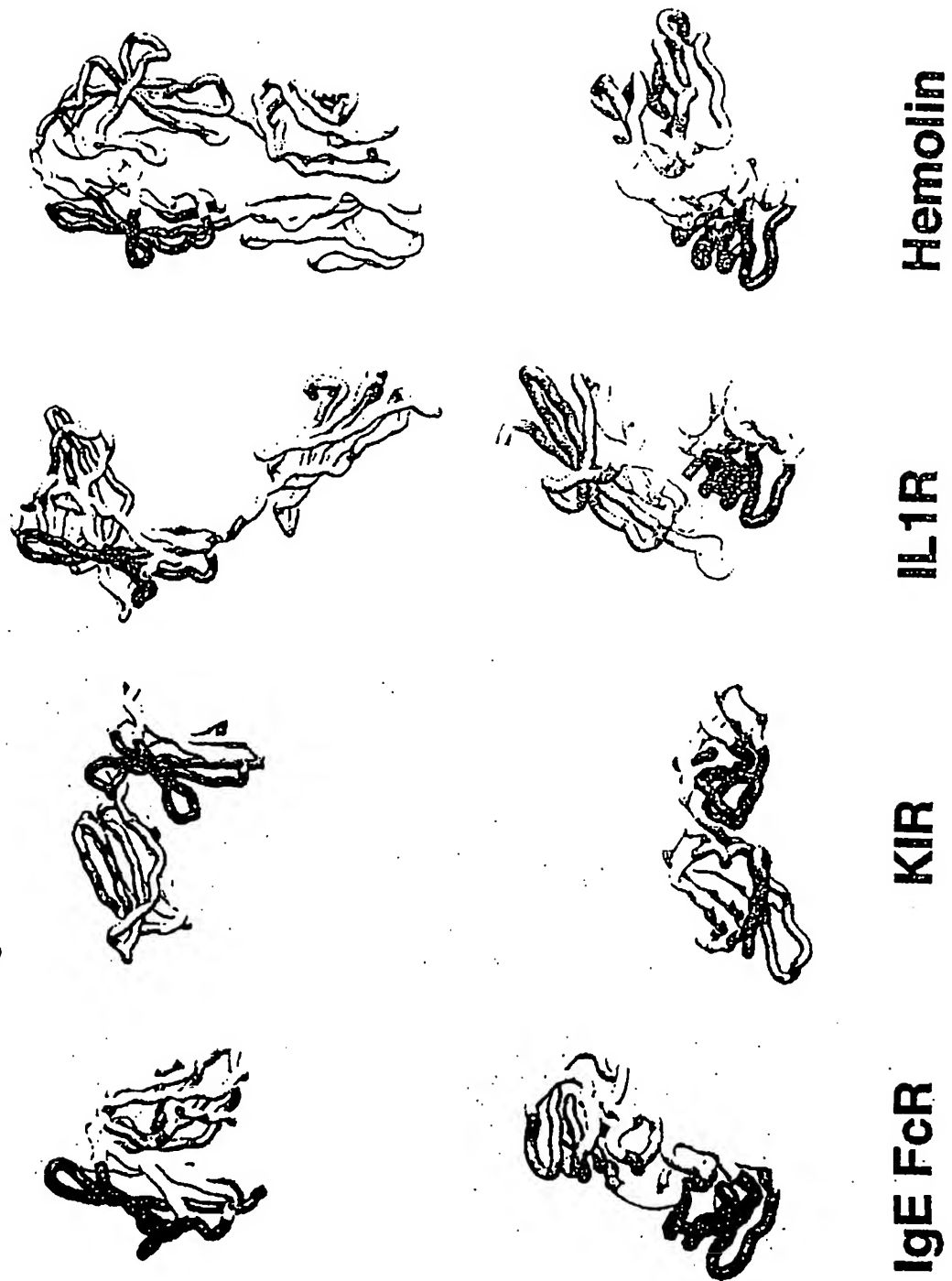
Fig. 2

Fig. 3

Fig. 4

Fig. 5

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           A          A'         B          C          C'
           ▬▬         ▬▬         ▬▬         ▬▬         ▬▬
1                                                              50
FcγRIA     ATTKAVTSLQ PPWVSVFQEE TVTLRCEVLH LPGSSTQWF  LNGTATQTST
FcγRIB     ATTKAVITLQ PPWVSVFQEE TVTLHCEVLH LPGSSTQWF  LNGTATQTST
FcγRIIA    APPKAVLKLE PPWINVLQED SVTLTCQGAR SPESDSIQWF HNGNLIPTHT
FcγRIIC    APPKAVLKLE PQWINVLQED SVTLTCRGTH SPESDSIQWF HNGNLIPTHT
FcγRIIB    APPKAVLKLE PQWINVLQED SVTLTCRGTH SPEDNSTQWF HNGNLIPTHT
FcγRIII-1  DLPKAVVFLE PQWYRVLEKD SVTLKCQGAY SPEDNSTQWF HNESLISSQA
FcɛRI      VPQKPKVSLN PPWNRIFKGE NVTLTCNGNN FFEVSSTKWF HNGSLSEETN
           2331223412 124■322332 31113■2■2  3223312211 2123233■3
           +              ++       ++       ●+        ++

           E          F          G          A          A'
           ▬▬         ▬▬         ▬▬         ▬▬         ▬▬
51                                                            100
FcγRIA     PSYRITSASV NDSGEYRCQR GLSGRSDPIQ LEIHRGWLLL QVSSRVFTEG
FcγRIB     PSYRITSASV NDSGEYRCQR GLSGRSDPIQ LEIHRGWLLL QVSSRVFTEG
FcγRIIA    QPSYRFKANN NDSGEYTCQT GQTSLSDPVH LTVLSEWLVL QTPHLEFQEG
Fcγ.IIC    QPSYRFKANN NDSGEYTCQT GQTSLSDPVH LTVLSEWLVL QTPHLEFQEG
FcγIIB     QPSYRFKANN NDSGEYTCQT GQTSLSDPVH LTVLSEWLVL QTPHLEFQEG
FcγRIII-1  SSYFIDAATV DDSGEYRCQT NLSTLSDPVQ LEVHIGWLLL QAPRWVFKEE
FcɛRI      SSLNIVNAKF EDSGEYKCQH QQVNESEPVY LEVFSDWLLL QASAEVVMEG
           323■3■1■3  3111113113 323■312123 1224331121 13■■722■12
           +                    ●          +          +

           B          C          C'         E          F
           ▬▬         ▬▬         ▬▬         ▬▬         ▬▬
101                                                           150
FcγRIA     EPLALRCHAW KDKLVYNVLY YRNGKAPKFF HWNSNLTILK TNISHNGTYH
FcγRIB     EPLALRCHAW KDKLVYNVLY YRNGKAPKFF HWNSNLTILK TNISHNGTYH
FcγRIIA    ETIMLRCHSW KDKPLVKVTF FQNGKSQKFS RLDPTFSIPQ ANHSHSGDYH
FcγRIIC    ETIVLRCHSW KDKPLVKVTF FQNGKSKKFS RSDPNFSIPQ ANHSHSGDYH
FcγRIIB    ETIVLRCHSW KDKPLVKVTF FQNGKSKKFS RSDPNFSIPQ ANHSHSGDYH
FcγRIII-1  DPIHLRCHSW KNTALHKVTY LQNGKGRKYF HHNSDFYIPK ATLKDSGSYF
FcɛRI      QPLFLRCHGW RNWDVYKVIY YKDGEALKYW YENHNISITN ATVEDSGTYY
           322■111131 223■232132 3321235123 3■233333133 22■3221313
           +                    +          ●          +  +

           G
           ▬▬
151                  176
FcγRIA     CSG.MGKHRY TSAGISVTVK ELFPAP
FcγRIB     CSG.MGKHRY TSAGISVTVK ELFPAP
FcγRIIA    CTGNIGYTLF SSKPVTITV. QVPSMG
FcγRIIC    CTGNIGYTLY SSKPVTITV. QAPSSS
FcγRIIB    CTGNIGYTLF SSKPVTITV. QAPSSS
FcγRIII-1  CRGLFGSKNV SSETVNITIT QGLAVS
FcɛRI      CTGKVWQLDY ESEPLNITVI KAPREK
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           +
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+ - CHO site in human/nonhuman FcR

● - Highly conserved CHO site in all FcRs (> 9/17)
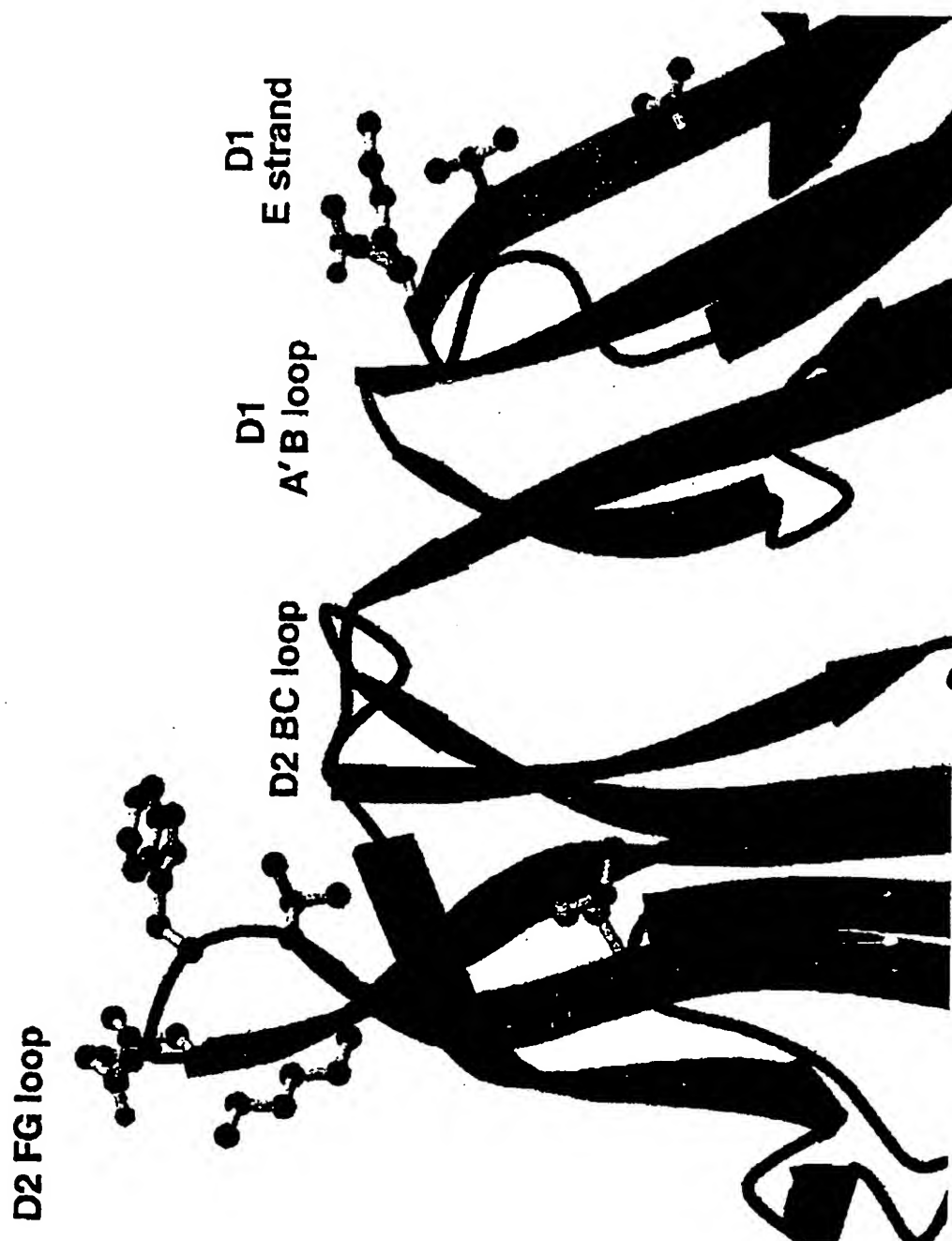
Fig. 6

Fig. 7

Fig. 8

IgE

FcεRIα

Mast Cell Membrane

-1-
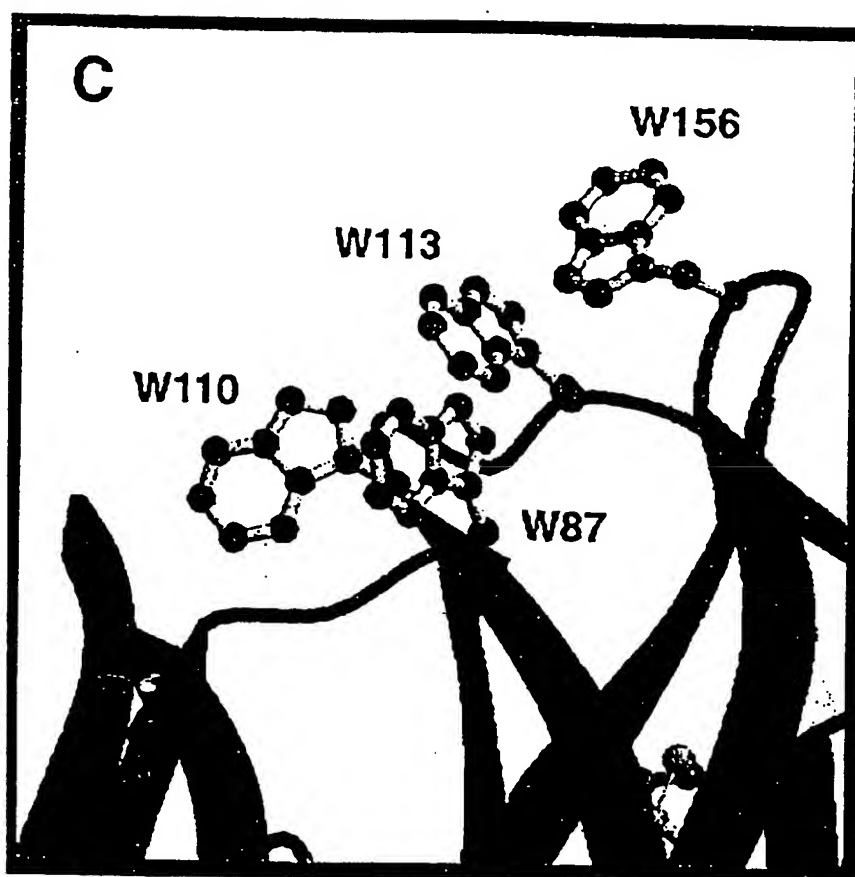
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     Northwestern University
     Jardetzky, Theodore S.
     Garman, Scott Clayton
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     CHAIN AND USES THEREOF

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ttt aaa gga gag aat gtg act ctt aca tgt aat ggg aac aat ttc ttt   96
Phe Lys Gly Glu Asn Val Thr Leu Thr Cys Asn Gly Asn Asn Phe Phe
                20   25   30

gaa gtc agt tcc acc aaa tgg ttc cac aat ggc agc ctt tca gaa gag   144
Glu Val Ser Ser Thr Lys Trp Phe His Asn Gly Ser Leu Ser Glu Glu
            35   40   45

aca aat tca agt ttg aat att gtg aat gcc aaa ttt gaa gac agt gga   192
Thr Asn Ser Ser Leu Asn Ile Val Asn Ala Lys Phe Glu Asp Ser Gly
        50   55   60

gaa tac aaa tgt cag cac caa caa gtt aat gag agt gaa cct gtg tac   240
Glu Tyr Lys Cys Gln His Gln Gln Val Asn Glu Ser Glu Pro Val Tyr
 65   70   75   80

ctg gaa gtc ttc agt gac tgg ctg ctc ctt cag gcc tct gct gag gtg   288
Leu Glu Val Phe Ser Asp Trp Leu Leu Leu Gln Ala Ser Ala Glu Val
                85   90   95

gtg atg gag ggc cag ccc ctc ttc ctc agg tgc cat ggt tgg agg aac   336
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	100					105				110					

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            100                    105                    110

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tac tgg tat gag aac cac aac atc tcc att aca aat gcc aca gtt gaa    432
Tyr Trp Tyr Glu Asn His Asn Ile Ser Ile Thr Asn Ala Thr Val Glu
    130                135                140

gac agt gga acc tac tac tgt acg ggc aaa gtg tgg cag ctg gac tat    480
Asp Ser Gly Thr Tyr Tyr Cys Thr Gly Lys Val Trp Gln Leu Asp Tyr
145                150                155                160

gag tct gag ccc ctc aac att act gta ata aaa gct ccg cgt gag aag    528
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Glu Val Ser Ser Thr Lys Trp Phe His Asn Gly Ser Leu Ser Glu Glu
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Thr Asn Ser Ser Leu Asn Ile Val Asn Ala Lys Phe Glu Asp Ser Gly
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Glu Tyr Lys Cys Gln His Gln Gln Val Asn Glu Ser Glu Pro Val Tyr
 65               70                 75                 80

Leu Glu Val Phe Ser Asp Trp Leu Leu Leu Gln Ala Ser Ala Glu Val
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Val Met Glu Gly Gln Pro Leu Phe Leu Arg Cys His Gly Trp Arg Asn
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Trp Asp Val Tyr Lys Val Ile Tyr Tyr Lys Asp Gly Glu Ala Leu Lys
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Tyr Trp Tyr Glu Asn His Asn Ile Ser Ile Thr Asn Ala Thr Val Glu
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Asp Ser Gly Thr Tyr Tyr Cys Thr Gly Lys Val Trp Gln Leu Asp Tyr
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Phe Lys Gly Glu Asn Val Thr Leu Thr Cys Asn Gly Asn Asn Phe Phe
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gaa gtc agt tcc acc aaa tgg ttc cac aat ggc agc ctt tca gaa gag     144
Glu Val Ser Ser Thr Lys Trp Phe His Asn Gly Ser Leu Ser Glu Glu
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Thr Asn Ser Ser Leu Asn Ile Val Asn Ala Lys Phe Glu Asp Ser Gly
     50                  55                  60

gaa tac aaa tgt cag cac caa caa gtt aat gag agt gaa cct gtg tac     240
Glu Tyr Lys Cys Gln His Gln Gln Val Asn Glu Ser Glu Pro Val Tyr
 65                  70                  75                  80

ctg gaa gtc ttc agt gac tgg ctg ctc ctt cag gcc tct gct gag gtg     288
Leu Glu Val Phe Ser Asp Trp Leu Leu Leu Gln Ala Ser Ala Glu Val
                 85                  90                  95

gtg atg gag ggc cag ccc ctc ttc ctc agg tgc cat ggt tgg agg aac     336
Val Met Glu Gly Gln Pro Leu Phe Leu Arg Cys His Gly Trp Arg Asn
            100                 105                 110

tgg gat gtg tac aag gtg atc tat tat aag gat ggt gaa gct ctc aag     384
Trp Asp Val Tyr Lys Val Ile Tyr Tyr Lys Asp Gly Glu Ala Leu Lys
        115                 120                 125

tac tgg tat gag aac cac aac atc tcc att aca aat gcc aca gtt gaa     432
Tyr Trp Tyr Glu Asn His Asn Ile Ser Ile Thr Asn Ala Thr Val Glu
    130                 135                 140

gac agt gga acc tac tac tgt acg ggc aaa gtg tgg cag ctg gac tat     480
Asp Ser Gly Thr Tyr Tyr Cys Thr Gly Lys Val Trp Gln Leu Asp Tyr
145                 150                 155                 160

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			20				25						30		

Glu	Val	Ser	Ser	Thr	Lys	Trp	Phe	His	Asn	Gly	Ser	Leu	Ser	Glu	Glu
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Thr	Asn	Ser	Ser	Leu	Asn	Ile	Val	Asn	Ala	Lys	Phe	Glu	Asp	Ser	Gly
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Glu	Tyr	Lys	Cys	Gln	His	Gln	Gln	Val	Asn	Glu	Ser	Glu	Pro	Val	Tyr
65					70					75					80

Leu	Glu	Val	Phe	Ser	Asp	Trp	Leu	Leu	Leu	Gln	Ala	Ser	Ala	Glu	Val
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Val	Met	Glu	Gly	Gln	Pro	Leu	Phe	Leu	Arg	Cys	His	Gly	Trp	Arg	Asn
			100					105					110		

Trp	Asp	Val	Tyr	Lys	Val	Ile	Tyr	Tyr	Lys	Asp	Gly	Glu	Ala	Leu	Lys
		115					120					125			

Tyr	Trp	Tyr	Glu	Asn	His	Asn	Ile	Ser	Ile	Thr	Asn	Ala	Thr	Val	Glu
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Asp	Ser	Gly	Thr	Tyr	Tyr	Cys	Thr	Gly	Lys	Val	Trp	Gln	Leu	Asp	Tyr
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